

## STIC Search Report Biotech-Chem Library

## STIC Database Tracking Number 122814

TO: David Lukton

Location: REM-3B75/3C70

Art Unit: 1653

Tuesday, May 25, 2004

Case Serial Number: 09/594978

From: Toby Port

**Location: Biotech-Chem Library** 

Remsen 1A59

Phone: 571-272-2523

toby.port@uspto.gov

## Search Notes

Dear Examiner Lukton,

Here are the results of your search.

Please feel free to contact me if you have any questions.

**Toby Port** 



Peptide #
Human liv
Human pep
Streptcoc
Human imm
Human imm
Human imm
Human imm
Human imm
Human imm

Abg55464 Abg55464 Abg43601 Aaw62760 Aam82654

Human aqu Tbp2 anti Human aqu H. influe UDP-N-ace

Human exc Human kid

Aao09024 E
Aav1793 Aav1793 Aav1793 Aav1703 Aav1703 Aav1703 Aav100 Aav100

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AAUS3554
AAU66465
ABP06455
ABM50073
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AART7953

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AAW51785

AAW51705

AAW54106

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AAM12648

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Aab56241 Vascular
Aau28720 DPI trypt
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ALIGNMENTS

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S chrysomallus actinomycin biosynthase protein acmC fragment #9.
AAM47151 standard; peptide; 6 AA.
     AAM47151;
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12-FEB-2002 (first entry)

Modular enzyme system; cyclic gene synthesis; repetitive coding sequence; antibiotic; non-ribosomal peptide synthetase; NRPS; PKS; polyketide synthase; actinomycin biosynthase.

Streptomyces chrysomallus Synthetic.

01-NOV-2001.

WO200181564-A2.

25-APR-2001; 2001WO-DE001578.

26-APR-2000; 2000DE-01021267,

(ACTI-) ACTINODRUG PHARM GMBH.

Schauwecker F;

2002-049276/06. WPI; 2002-049276/ N-PSDB; ABA03345.

Preparing DNA encoding modular protein for e.g. producing new enzymes for synthesis of polyketide antibiotics, comprises cyclic integration of fragments into a vector.

Example 3; Page 54; 83pp; German.

The present invention relates to the preparation of DNA, in a circular vector, that encodes one or more segments of a modular polypeptide. DNA or DNA libraries produced this way are used to produce modular polypeptides, particularly enzymes, which can be used to act on

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substrates to produce compounds for therapeutic testing. Bnzymes of particular interest are those involved in non-ribosomal peptide synthesis or polyketide synthesis, and compounds for testing are particularly macrolide antibiotics, including penicillins, vancomycins or erythromycins, but may also be modular receptors. The present sequence is a fragment of a protein encoded by a Streptomyces chrysomallus actinomycin blosynthesis gene which was used in a plasmid in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The specification describes a beta-secretase enzyme. The enzyme cleaves beta-amyloid precursor protein to produce beta-amyloid peptide. This enzyme is therefore implicated in the production of amyloid plaque components which accumulate in the brains of individuals afflicted with Alzheimer's disease. Inhibitors of beta-secretase are administered to a mammalian subject e.g. with Alzheimer's disease or Alzheimer's disease. It ike pathology to test if they maintain or improve cognitive ability or reduce the plaque burden. The compounds are used for the treatment of amyloidogenic diseases e.g. Alzheimer's disease. The present sequence represents an inhibitor of beta-secretase enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Purified beta-secretase protein used in assays to discover inhibitors which can be used for the treatment of amyloidogenic diseases e.g. Alzheimer's disease.
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Tung J, Wang S, Mcconlogue L;
                                                                                                                                                                                      100.0%; Score 19; DB 5; I
100.0%; Pred. No. 1.4e+06;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A beta-secretase inhibitor peptide.
                                                                                                                                                                                                                                                                                                                                                                              AAB07871 standard; peptide; 7 AA.
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Best Local Similarity 100.
Matches 4; Conservative
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Sinha S, Tatsuno G,
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                                                                                                                                                       Sequence 6 AA;
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Modified-site
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15-JUN-1999;
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Sequence 7 AA;

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AAB07872;

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The invention relates to screening, diagnosis or prognosis of Vascular Dementia (VD) in a subject comprising analysing body fluud from the subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of features containing at least one chosen feature whose relative abundance correlates with the presence, absence, stage or severity of VD or predicts the onest or course of VD, especially detecting in a sample of cerebrospinal fluid (CSP) from the subject one of 223 VD-associated protein isoforms (VPIS) (ABB55801-ABB56295) as fully defined in the specification. Detecting VD-associated features and VPI is useful for the screening, diagnosis or prognosis of VD, for determining the stage or severity of VD, for identifying a subject at risk of VD or for monitoring the effect of therapy administered to a subject having VD. Nucleic acids encoding a VPI or inhibiting the function of a VPI are useful for the treatment of VD and for gene therapy
                                                                                                                                                                                                             VD; VD-associated protein isoform; VPI; screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Screening, diagnosis or prognosis of vascular dementia (VD), useful determining stage of VD and monitoring the effect of VD therapy, comprises analyzing body fluid by 2-dimensional electrophoresis for features correlated with VD.
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                                                                                                                                                                   Vascular dementia-associated protein isoform (VPI) 441.
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                                                                                                                                                                                                                                 diagnosis; prognosis; gene therapy
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                                            ABB56241 standard; peptide; 8 AA.
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24-NOV-2000; 2000GB-00028734.
28-NOV-2000; 2000US-00724391.
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                                                                                                                           (first entry)
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                                                                                                                                                                                                           Vascular Dementia;
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                                                                                                                                                                                                                                                                                                                                                                                            Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide;
amyloid plaque component; Alzheimer's disease; amyloidogenic disease;
inhibitor.
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100.0%; Score 19; DB 3; Length 7; 100.0%; Pred. No. 1.4e+06; ive 0; Mismatches 0; Indels
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Wang S, Mcconlogue L;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                          A beta-secretase inhibitor peptide.
                                                                                                                                                                                                                               AAB07872 standard; peptide; 8 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Basi G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tatsuno G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-533011/48.
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Query Match
Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
                                                                                   1 VAEF 4
                                                                                                                         VAEF 7
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Modified-site
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15-JUN-1999;
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                                                                                                                                                                                                                                                                                                                14-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
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Sinha S,

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Gaps

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The present invention relates to the identification of depression associated protein isoforms (DPIs), particularly the tryptic digest peptides of these proteins. Some of the DPIs (AAU28404-AAU28655) described are decreased in the cerebrospinal fluid (CSF) of BAD (Bipolar affective disorder) subjects, whilst other DPIs (AAU28625-AAU28887) are increased in BAD subjects, whilst other DPIs (AAU28625-AAU28887) are increased in BAD subjects, whilst other DPIs (AAU28625-AAU28887) are increased in BAD subjects, Millst other DPIs (DPIS) are increased in BAD subjects, whilst other DPIs (AAU28625-AAU28887) are increased in BAD subjects, the invention are useful for clinical screening, diagnosis, prognosis, therapy and prophylaxis of neuropsychiatric disorders e.g. BAD (also known as bipolar mood disorder, schizoaffective disorders, and unipolar affective disorders. The present sequence represents one of the DPI tryptic digest peptides of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schizophrenia-associated protein isoform; SPI; SPI-206; SPI-238; SPI-240; neuroleptic; gene therapy; cerebrospinal fluid; serum; plasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel nucleic acid encoding a protein associated with bipolar affective disorder, which is used for diagnosis, prophylaxis and therapy of neuropsychiatric disorders, such as bipolar affective disorder.
                                                 Human; depression associated protein isoform; tryptic digest peptide; DPI; cerebrospinal fluid; CSF; BAD; bipolar affective disorder; neuropsychiatric disorder; bipolar mood disorder; neuroleptic; maniac-depressive illness; schizoaffective disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schizophrenia-Associated Protein Isoform (SPI) peptide #343.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 19; DB 4; I 100.0%; Pred. No. 1.4e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                        Parekh RB, Rohlff C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 37; 153pp; English.
                                                                                                                                                                                                                                                                                                                                                                    (OXFO-) OXFORD GLYCOSCIENCES UK LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU25114 standard; peptide; 8 AA
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                 DPI tryptic digest peptide #317
                                                                                                                                                                                                                                                                                          24-FEB-2000; 2000GB-0004412.
08-DEC-2000; 2000GB-00030050.
12-DEC-2000; 2000US-0254830P.
                                                                                                                                                                                                                                                       23-FEB-2001; 2001WO-GB000786.
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Best Local Similarity
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                                                                                                                                                                              WO200162787-A1.
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                                                                                                                                             Homo sapiens.
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Tyson KL

Terrett JA,

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                                                                                                                                                                                                                          New schizophrenia associated protein isoforms and encoding nucleic acid molecules, useful for treatment, diagnosis and prognosis of schizophrenia and screening for potential drugs for treatment and new drug targets.
                                                                                                                                                                                                                                                                                                                The sequence represents a schizophrenia-associated protein isoform (SPI). These protein isoforms, e.g. SFI-206, SPI-238 and SPI-240 are detectable in cerebrospinal fluid, serum or plasma and are useful markers of schizophrenia. The sequences can be used for treatment and diagnosis of schizophrenia, screening, prognosis, monitoring the results of therapy, identifying patients most likely to respond to a particular therapy and identification of new targets for drug treatment. SPI DNA is useful as a nucleic acid probe to detect the presence of nucleic acids or SPIs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, Bipolar Affective Disorder, BAD; Depression-Associated feature; DF; Depression-Associated protein isoform; DPI; Cerebro-epinal fluid; CSF; antidepressant, antimanic; nootropic, tranquiliser; neuroleptic; attention deficient disorder; schizoaffective disorder;
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                                                                                                                                                               Tyson KL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 8;
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                                                                                                                                                                 Terrett JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Depression-Associated Protein isoform DPI-124,
                                                                                                                                                              Herath HMAC, Parekh RB, Rohlff C,
                                                                                                                                                                                                                                                                                        Disclosure; Page 36; 148pp; English.
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                                                                                                                                  (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
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                                                                                      24-FEB-2000; 2000GB-00004415.
28-DEC-2000; 2000US-00750395.
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08-DEC-2000; 2000GB-00030050.
12-DEC-2000; 2000US-0254830P.
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                                                          23-FEB-2001; 2001WO-GB000792
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les 4; Conserv
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WO200162785-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8 AA;
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                             30-AUG-2001
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Matches
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Gaps ö

Length 8; 0; Indels

WPI; 2001-582081/65.

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The invention relates to a preparation comprising an isolated Bipolar Affected Disorder (BAD)-Associated Protein Isoform (DPIS). The DPI's are used to screen, diagnose or prognose of BAD or unipolar depression, identify a subject at risk of developing BAD or unipolar depression, identify a caffect of therapy in a subject. They are also used to screen for or identify agents that interact with a DPI. These agents, antibodies against the DPIs, and nucleic acids encoding the DPIs are used to treat or prevent BAD or unipolar depression. Diseases that can be treated are attention deficient disorder. As exhizosffective disorder, a bipolar or unipolar affective disorder. The DPIs are used in proteomics. The Unipolar depression overcomes the problems of using gene expression analysis, such as not being able to obtain central nervous green (CNS) tissue from a living patient under normal circumstances. The present sequence is a DIP increased in the CSF (cerebro-spinal fluid) of subjects having BAD
Preparation for diagnosing or treating bipolar affected disorder (BAD) unipolar depression, or for screening for modulators, comprises a BAD-associated protein isoform.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Diagnosing and monitoring Schizophrenia by detecting the presence of Schizophrenia Associated Features and Schizophrenia Associated Protein Isoforms in samples of cerebrospinal fluid.
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                                                                                                                                                              Claim 8; Page 37; 163pp; English.
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28-DEC-2000; 2000US-00750395.
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Best Local Similarity
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(first entry)

Rohlff C;

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The invention relates to methods and compositions for screening, diagnosis and prognosis of Schizophrenia. The method involves detecting the presence of Schizophrenia (SCH) Associated Features (SFS) and SCH. Associated Protein Isoforms (SPIS) in samples, e.g. by electrophoresis, immunoassay or hybridisation assay, for diagnosing and monitoring SCH, studying the effectiveness of treatments and for identifying potential therapeutic agents. The method is used for (1) screening or diagnosis of SCH and the relative abundance of at least 1 chosen feature correlates with the presence or absence of SCH; and (2) monitoring the effect of therapy administered to a subject with SCH and the relative abundance of at least 1 chosen feature which correlates with the severity of SCH. The expression and activity of the SFs, SPIs and related molecules (e.g. secondary messengers) are studied to diagnose SCH, monitor the progress of the disorder and the effectiveness of treatment and as targets to identify and produce potential therapeutic agents for the treatment of SCH. The paucity of detectable neuralgic defects distinguishes neuropsychiatric disorders such as SCH from neurological disorders, where manifestations of anatomical and biochemical changes have been identified in many cases. Consequently the identification and characterisation of cellular and/or molecular causative defects and neuropathies are necessary for improved treatment of sections of schizophrenia-associated contract the programment of sections of schizophrenia-associated sections of sequences of schizophrenia-associate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A compsn. which induces a cytotoxic T lymphocyte (CTL) response to a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 19; DB 4; I 100.0%; Pred. No. 1.4e+06; Live 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                isoforms used in the method of the invention
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(first entry)
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Best Local Similarity
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27-MAR-1996
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Gaps

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Length 8; 0; Indels

100.0%; Score 19; DB 4; L 100.0%; Pred. No. 1.4e+06; ive 0; Mismatches 0;

4; Conservative

1 VAEF 4

2 VAEF

us-09-594-978a-2.rag

Length 9;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Crystallized complex of beta-site amyloid precursor protein (APP) cleaving enzyme (BACE) and APP inhibitor peptide useful for identifying agents that interact with active site of BACE or active site of APP
human MAGE antigen (Ag) in a mammal comprises, a MAGE CTL Ag response inducing peptide (i.e. AAR78904 to AAR78917) and a lipid conjugated helper T cell inducing peptide. The compsn. is useful in the treatment and prevention of MAGE tumour Ag associated diseases, e.g. melanoma cancers. (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                   Beta-amyloid precursor protein; APP; APP inhibitor peptide; BACE; beta site APP cleaving enzyme; protein coordinate data; APP751; Swedish family mutation; Alzheimer's disease.
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                                                                                                    100.0%; Score 19; DB 2; Length 9; 100.0%; Pred. No. 1.4e+06; rative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                            A beta-amyloid precursor protein (APP) inhibitor peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Svenson K, Annis B, Akopian TN, Bard J,
                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                ABB77871 standard; peptide; 9 AA.
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/note= "statine"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-SEP-2001; 2001WO-US029387.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               binding protein or peptide.
                                                                                                                                                                                                                                                                                                 27-SEP-2002 (first entry)
                                                                                                                                4; Conservative
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Best Local Similarity
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Misc-difference
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                                                                              Sequence 9 AA;
                                                                                                                                                                                2 VAEF
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Somers WS;
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ABB77871
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The present sequence represents a beta-amyloid precursor protein (APP) inhibitor peptide. This peptide inhibits binding between APP and BACE lebta site APP cleaving enzyme). The specification describes a crystallized complex of BACE and the present APP inhibitor. Protein coordinate data for BACE is given in the specification. The APP inhibitor peptide is based on the P10 to P4' APP751 Swedish family mutation. The crystallized complex is used for identifying an agent that interacts with an active site of BACE or an active site of an APP binding protein or peptide. The agents are useful in the treatment and/or prevention of

Sequence 9 AA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes an isolated peptide (I) comprising a sequence of at least four amino acids, where the peptide is a substrate for conducting asparey1 protease assays. (I) has neuroprotective and nootropic activities, and can be used as an inhibitor of beta-secretase activity. A beta-secretase modulator from the present invention can be used for inhibiting beta-secretase activity in vio, and in the manufacture of a medicament for the treatment of Alzheimer's disease. Pharmaceutical compositions from the present invention can be used for treating a disease or condition characterised by an abnormal beta-secretase activity (I) is useful for identifying agents that modulate the activity of human Asp2 asparty1 protease (Hu-Asp2). (I) is useful as a core structure to construct derivatives. ABL49914 to ABL49925 and ABB06609 to ABB06593 represent sequences used in the exemplification of
                                                                                                                                                                                                                                                                         retase, enzyme, cleavage site, amyloid protein precursor, APP, protease, neuroprotective, nootropic, beta-secretase inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel substrates for human aspartyl protease useful for identifying modulators of beta secretase activity of aspartyl protease for treating
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Score 19; DB 5; I Pred. No. 1.4e+06;
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                          0; Mismatches
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                                                                                                                                                          ABB06593 standard; peptide; 10 AA.
100.0%;
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12-MAR-2001; 2001US-0275251P.
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Alzheimer's disease.
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                                                        1 VAEF
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Query Match
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Memapsin 2 substrate specificity determination peptide #10
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(first entry)
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15-NOV-2002
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                                                                                                                                                                                                                                                                                                                                                                 Beta-secretase; enzyme; cleavage site; amyloid protein precursor; APP; aspartyl protease; neuroprotective; nootropic; beta-secretase inhibitor; Alzheimer's disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel substrates for human aspartyl protease useful for identifying modulators of beta secretase activity of aspartyl protease for treating
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                                                                                                                                                                                                                                                                                                        Beta-secretase related peptide SEQ ID NO:196.
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12-MAR-2001; 2001US-0275251P.
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Matches

ESULT 13 BG78404 D ABG7

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The invention relates to an inhibitor of catalytically active memapsin 2 binds to the aspartic protease which can cleave at beta secretaes sites), which binds to the active site of memapsin 2 defined by the presence of two catalytic aspartic residues and substrate binding cleft. Also included is method of determination of the substrate side-chain preference in substrates with memapsin 2, and determining the sub-site preference in memapsin 2 by determining relative initial hydrolysis rates of the memapsin 2 inhibitors containing a base sequence taken from (My9-2 (Glu-val-Asn-Leu-Ala-Ala-Glu-phe), probing the library of inhibitors with memapsin 2 inhibitors containing a base sequence taken from (My9-2 (Glu-val-Asn-Leu-Ala-Ala-Glu-phe), probing the library of inhibitors with memapsin 2 which binds to several inhibitors to generate several bound memapsin 2, and detecting the bound memapsin 2 with an antibody raised to memapsin 2 and an alkaline phosphatase conjugated secondary antibody. The inhibitors may be used in the manufacture of a medicament for the treatment of Alzheimer's disease since memapsin 2 medicament for the treatment of Alzheimer's disease since memapsin 2 with be involved in the cleavage of amyloid precursor protein (App), and for determining the substrate side-chain preference in memapsin 2 sub-sites. The present sequence represents a subsite variant peptide used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New memapsin 2 activity inhibitor useful in treatment of e.g. Alzheimer's
Human; memapsin 2; aspartic protease; beta secretase; degenerative disease; Alzheimer's disease; amyloid precursor protein; APP; neuroprotective; nootropic; inhibitor; substrate side-chain preference.
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100.0%; Pred. No. 1.5e+02;
.ive 0; Mismatches 0; Indels
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inhibitor
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                           The invention comprises a crystallised recombinant protein that is involved in general metabolism, the recombinant protein may be from Staphylococcus aureus, Streptococcus pneumoniae, Helicobacter pylori, Escherichia coli or Pesudomonas aeruginosa. The crystallised recombinant protein of the invention is useful in the prevention (vaccine) or treatment of a disease or disorder caused by S. pneumoniae, H. pylori, E. coli or P. aeruginosa. The present amino acid sequence was used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                          Awrey D, Beattie B;
/ K, Necakov S, Nethery K;
                                                                                                                                                                                                                                                                                                                                                      New crystallized recombinant polypeptides from Staphylococcus aureus, Streptococcus pneumoniae, Helicobacter pylori or Pseudomonas aeruginosa involved in general metabolism, useful as drug targets for pathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide; amyloid plaque component; Alzheimer's disease; amyloidogenic disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                  crystallised recombinant protein; metabolism; Staphylococcus aureus; Streptococcus pneumoniae; Helicobacter pylori; Escherichia coli; Pseudomonas aeruginosa; vaccine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 19; DB 7; Length 12; 100.0%; Pred. No. 1.5e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                         edadi M, Alam MZ, Awrey l
Houston S, Mansoury K, N
k B, Vallee F, Wrezel O;
                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 66; 277pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A beta-secretase inhibitor peptide.
                                                                                                                                                                                                                                                                                          Vedadi M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB07889 standard; peptide; 13 AA
Escherichia coli DnaK peptide #3
                                                                                                                                                                                                                                                                                                     Canadien V, Domagala M, Housto
Ng I, Pinder B, Sheldrick B,
                                                                                                                                         2001US-0332160P.
2001US-0333661P.
2001US-0333665P.
2001US-034170P.
2001US-0341954P.
2001US-0342003P.
                                                                                                                                                                                                      20-DEC-2001; 2001US-03425422.
28-DEC-2001; 2001US-0344252P.
28-DEC-2001; 2001US-0343570P.
28-DEC-2001; 2001US-0343666P.
                                                                                                                       21-NOV-2002; 2002WO-CA001768
                                                                                                                                                                                                                                                                      (AFFI-) AFFINIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                   Dharamsi A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                          Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 VAEF 12
                                                                               WO2003044185-A2
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                                                                                                                                                                        18-DEC-2001, 2
19-DEC-2001, 2
19-DEC-2001, 2
20-DEC-2001, 2
21-DEC-2001, 2
28-DEC-2001, 2
                                                                                                                                                     27-NOV-2001;
27-NOV-2001;
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                                                                                                   30-MAY-2003
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Canadien V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB07889
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Matches
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Glutamic acid; glutamine; vaccine; major histocompatibility complex; MHC immunomodulator; antiallergic; endocrine; neuroprotectant; virucidal; bactericidal; antiparasitic; fungicidal; cytostatic; medicine; pharmaceutical; immune disorder; immune deficiency; autoimmune; hypersensitivity; allergy; graft rejection; infection; hormonal disorder central nervous system disease; cancer; melanoma; anti-melanoma vaccine; human immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The specification describes a beta-secretase enzyme. The enzyme cleaves beta-amyloid precursor protein to produce beta-amyloid peptide. This enzyme is therefore implicated in the production of amyloid plaque components which accumulate in the brains of individuals afflicted with Alzheimer's disease. Inhibitors of beta-secretase are administered to a mammalian subject e.g. with Alzheimer's disease or Alzheimer's disease. Is they maintain or improve cognitive ability or reduce the plaque burden. The compounds are used for the treatment of amyloidogenic diseases e.g. Alzheimer's disease. The present sequence represents an inhibitor of beta-secretase enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Purified beta-secretase protein used in assays to discover inhibitors which can be used for the treatment of amyloidogenic diseases e.g. Alzheimer's disease.
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                                                                                                                                                                                                                                                                                                                                                  Doane MT, Friger. T. Wang S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 33; Page 24; 121pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                          Tung J,
                                                                                                                                                                     10-FEB-2000; 2000WO-US003819.
                                                                                                                                                                                                                              99US-0119571P.
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                                                                                                                                                                                                                                                                                                                  (BLAN-) ELAN PHARM INC
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Sinha S, Tatsuno G,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-533011/48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13 AA;
                                                     WO200047618-A2
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                                                                                                                                                                                                                           10-FEB-1999;
15-JUN-1999;
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Synthetic
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amyloid pl
inhibitor.
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neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer; amyloid protein; angiopoietin; apoptosis related protein; cadherin; cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor; complement related protein; cytonome; kinase; colony stimulating factor; interleukin; G-protein coupled receptor; thiosesterase; inflammation; multifactorial disease; autoimmune disease; infection;
                                                                                                                                                                                                                                                                                                                                 beta-amyloid precursor protein to produce beta-amyloid peptide. This enzyme is therefore implicated in the production of amyloid peptide. This components which accumulate in the brains of individuals affiliated with Alzheimer's disease are administered to a mammalian subject e.g. with Alzheimer's disease or Alzheimer's disease. like pathology to test if they maintain or improve cognitive ability or reduce the plaque burden. The compounds are used for the treatment of amyloidogenic diseases e.g. Alzheimer's disease. The present sequence represents a peptide derived from beta-amyloid precursor protein
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                                                                                                                                                                                                                                                                                                                    specification describes a beta-secretase enzyme. The enzyme cleaves amyloid precursor protein to produce beta-amyloid peptide. This
                                                                                                                                                               Purified beta-secretase protein used in assays to discover inhibitors which can be used for the treatment of amyloidogenic diseases e.g. Alzheimer's disease.
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                                               Power
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                                         n N, John V,
Mcconlogue L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human peptide #735 encoded by a SNP oligonucleotide.
                                               Frigon N,
                       Doane MT, Frig.
                                                                                                                                                                                                                                                                     Disclosure, Page 12, 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM97460 standard; peptide; 14 AA.
                                                                   Tung J,
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27-DEC-2000; 2000US-00173419.
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(ELAN-) ELAN PHARM INC
                                            Anderson JP, Basi G,
Sinha S, Tatsuno G,
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                                                                                                                     WPI; 2000-533011/48.
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ID AAM9
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                                                                                                                                                                                                                                                                                                                                                              The present invention describes a pharmaceutical compound (I) that contains an N-terminal glutamic acid (Glu) or glutamine (Glu) residue in the form of an addition salt with a strong, physiologically acceptable acid (II). Also described are: (a) a pharmaceutical composition containing at least one (I); (b) a vaccine containing at least one (I) where this is a major histocompatibility complex (MHC) ligand (Ia); (c) a method for in vitro diagnosis of diseases associated with the presence of (Ia); (d) a kit for method (c) that includes a (Ia); and (e) a process for preparing (I). (I) has immunomodilator, endocribe, antiallergic, neuroprotectant, virucidal, bactericidal, antiparasitic, fungicidal and cytostatic activities. (I) are useful, in human or veterinary medicine, in pharmaceutical compositions (for treating immune disorders e.g. in pharmaceutical composition is a MHC lighand (Ia), in vaccines for treatment or prevention of: (i) viral, bacterial, parasitic or fungal infections, or (ii) of cancers. A particular application is in antimelator associated with interactions between MHC and (I), e.g. melanoma and human immunodeficiency virus infection: Anylessys to AAM99592 represent invention immunodeficiency virus infection compounds from the present invention immunedeficiency with pharmaceutical compounds from the present invention
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                                                                                                                                                                                                                   Stabilized pharmaceutical containing N-terminal glutamic acid or glutamine, useful e.g. in anti-melanoma vaccines, is an addition salt with strong acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide; amyloid plaque component; Alzheimer's disease; amyloidogenic disease;
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                                                                                                                          Goetsch L;
                                                                                                                          Corvaia N, Beck A,
                                                                         (FABR ) FABRE MEDICAMENT SA PIERRE.
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                                                                                                                                                                                                                                                                                                                         Claim 9; Page 96; 149pp; French
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99US-0139172P
                          23-MAR-2000; 2000FR-00003711.
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                                                                                                                                                                         WPI; 2001-611470/70
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Best Local Similarity
Matches 4; Conserv
                                                                                                                        Klinguer-Hamour C,
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15-JUN-1999;
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The present invention relates to oligonucleotides (see AAL26793-AAL34659)
encoding polymorphic variants of proteins related to amylases, amyloid
proteins, anglopolettin, apoptosis related proteins, cadherin, cyclin,
polymerase, oncogenes, histones, kinases, colony timulating factors,
complement related proteins, cytochromes, kinesins, cytokines,
interferons, interleukins, G-protein coupled receptors and thioesterases.
The present sequence is a peptide encoded by one such oligonucleotide.
The oligonucleotides and the peptides encoded by them may be used in the
prevention, diagnosis and treatment of diseases associated with
chaptopriate expression of the proteins listed above. Disorders that may
be prevented, diagnosed and/or treated include multifactorial diseases
with a genetic component, such as autoimmune diseases (e.g. rheumatoid
arthritis, multiple solerosis, diabetes, systemic lupus erythromatosus
arthritis, multiple solerosis, diabetes, systemic lupus erythromatosus
arthritis, multiple solerosis, diabetes, systemic lupus erythromatosus
brain, breast, colon and kidney, leukaemial, diseases of the nervous
system and an infection of pathogenic organisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genomic database, mass spectrometer; proteomic business; pharmaceutical; nuclear transport; signalling pathway; cellular organelle.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a method for identifying coding sequence in genomic databases, by using polypeptide sequence information obtained from peptide sequencing projects, especially those using mass spectrometers. It is useful for conducting a proteomics business. It is
                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 19; DB 4; Length 14; 100.0%; Pred. No. 1.8e+02; ive 0; Mismatches 0; Indels
                                     Disclosure; Page 3829; 4143pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana S11 peptide #6.
  autoimmune diseases and infections.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE32223 standard; peptide; 15 AA.
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20-APR-2001; 2001US-0285362P.
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Matches
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also used for establishing a distribution system for distributing the pharmaceutical preparation for sale, and may optionally include stabilishing a sales group for marketing the pharmaceutical preparation. It is also used for predicting the gene structure, such as intron/exon boundaries, for searching genomic databases for sequences derived from multi-protein complexes e.g. assemblies with a particular function such as splicing, transport or nuclear import or export, for elucidating transient rather than structural complexes (that are involved in signalling pathways) and for identifying proteins in cellular organelles. The present sequence is Arabidopsis thaliana peptide used to illustrate the method of the invention
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; Pred. No. 1.9e+02;
0; Mismatches 0;
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Similarity 100.0%;
4; Conservative 0;
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Best Local Similarity
Matches 4; Conserv
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Hepatitis A virus.
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Gaps ö Length 20;

DB 2;

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100.08;

Query Match

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Hepatitis A virus.
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                                                                                          Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptides AAW42943-46 are immunogenic peptides corresponding to immunogenic epitops of the Hepatitis A virus (HAN). The peptides are substantially similar to a portion of the amino acid sequence of the P3A protein of HAV corresponding to amino acids 1423-1496. The present peptide is derived from amino acids 1421-1440 and has a reactivity of 63.4% with acute sera. Compositions containing the peptides can be used to induce an immune response to HAV in a mammal. The peptides can also be used to detect the presence of antibodies against HAV in mammalian serum. The peptides can also be used to make an antibody against HAV by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunogenic Hepatitis A Virus (HAV) peptide(s) - used to induce an immune response to HAV in a mammal or to detect the presence of antibodies against HAV in a mammal.
                                                                                                                                                                                                                                 Immunogenic peptide; immunogenic epitope; P3A protein; immune response;
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 100.0%; Pred. No. 2.6e+02; tive 0; Mismatches 0;
                                                                                                                                                                                                        Immunogenic Hepatitis A virus peptide YK-1368.
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                                                                                                                              AAW42943 standard; peptide; 20 AA.
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              4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        Khudyakov YE
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                   Hepatitis A virus.
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The present sequence is one of a number of synthetic peptides which are immunoreactive with hepatitis A virus (HAV) antibodies. The peptides comprise antigenic epitopes of the major structural capsid polypeptides or or non-structural polypeptides of HAV with one or more glutamine or non-structural polypeptides of HAV with one or more glutamine correct the presence of antibodies against HAV in mammalian serum, to detect the presence of AHV in a human or animal through the binding of the peptide to an antibody, to detect acute phase infection by detecting is mammalian serum and detecting convalescence in a nammalian serum and detecting convalescence in a mammalian serum and detecting convalescence in a mammalian serum and assets serving immunoblotting, fluorescence in situ hybridisation analysis, gel-mobility shift assays, tracking of radioactive or bioluminescent markers, chromatography or electrophoresis. The peptides are used to induce an immune response to HAV when administered to a human or animal. Glutamine at the carboxy end of the peptides enhances the IgM antibody reactivity
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                                                                                 Hepatitis A virus; HAV; immunogen; immunostimulant; virucide; vaccine;
antigen; major structural capsid polypeptide; HAV antibody detection.
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Synthetic HAV P3A peptide, SEQ ID NO:
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Query Match
Best Local Similarity luv.v.
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99US-0144412P

Khudyakov YE;

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The present sequence is one of a number of synthetic peptides which are immunoreactive with hepatitis A virus (HAV) antibodies. The peptides comprise antigenic epitopes of the major structural applyeptides of the major structural applyeptides of molecules at the carboxy end of the peptide. The peptides are used to detect the presence of Antibodies against HAV in mammalian serum, to detect the presence of HAV in a human or animal through the binding of the peptide to an antibody, to detect acute phase infection by detecting ISM antibodies in mammalian serum and detecting convalescence in a mammalian serum and detecting convalescence in a mammalian serum the detecting of samples in clinical or research-based assays using immunoblotting, fluorescence in situ hybridiation analysis, gel-mobility shift assays, tracking of radioactive or bioluminescent markers, chromatography or electrophoresis. The peptides are used to induce an immune response to HAV when administered to a human or animal. Glutamine at the carboxy end of the peptides enhances the ISM antibody reactivity
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antibody.
                                                                                                                                                                                                            Synthetic peptides used as antigen sources for enzyme immunoassays detecting anti-hepatitis A virus and as vaccines.
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                                             14-JUL-2000; 2000WO-US019267.
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Best Local Similarity 100.
Matches 4; Conservative
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                                                                                                                                             Fields HA,
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                                                                                                                                          The present immunogenic peptide corresponds to an immunogenic epitope of the Hepatitis A virus (HAV). The peptide is substantially similar to a portion of the amino acid sequence of the Pla protein of HAV corresponding to amino acids 1423-1496. Compositions containing the peptide can be used to induce an immune response to HAV in a mammal. The peptide can also be used to detect the presence of antibodies against HAV in mammalian serum. The peptide can also be used to make an also be used to make an antibody against HAV by administering the peptide to a mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is one of a number of synthetic peptides which are immunoreactive with hepatitis A virus (HAV) antibodies. The peptides comprise antigenic epitopes of the major structural capsid polypeptides or non-structural polypeptides of HAV with one or more glutamine molecules at the carboxy end of the peptide. The peptides are used to detect the presence of antibodies against HAV in mammalian serum, to the peptide to an antibody, to detect acute phase infection by detecting ISM antibodies in mammalian serum and detecting convalescence in a
                                          an immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis A virus; HAV; immunogen; immunostimulant; virucide; vaccine; antigen; major structural capsid polypeptide; HAV antibody detection.
                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                   Immunogenic Hepatitis A Virus (HAV) peptide(s) - used to induce an :response to HAV in a mammal or to detect the presence of antibodies against HAV in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic peptides used as antigen sources for enzyme immunoassays detecting anti-hepatitis A virus and as vaccines.
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                                                                                                                                                                                                                                                                                                                                              Length 25;
                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                            100.0%; Score 19; DB 2; I
100.0%; Pred. No. 3.3e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic HAV P3A peptide, SEQ ID NO: 65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 22, Page 110; 130pp; English
                                                                                                                Claim 33; Page 115; 140pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB69465 standard; peptide; 25 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-JUL-2000; 2000WO-US019267.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0144412P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Khudyakov YE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-112681/12.
                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis A virus.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                       1 VAEF 4
                                                                                                                                                                                                                                                                                                              Sequence 25 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fields HA,
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4; Length 21; 0; Indels

100.0%; Score 19; DB 4; I 100.0%; Pred. No. 2.7e+02; ive 0; Mismatches 0;

97WO-US006891 96US-0015644P

Khudyakov YE;

(first entry)

Best Loca Matches

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AW17832

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Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and disaplaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                                                                        Peptide #7947 encoded by probe for measuring placental gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, liver, cirrhosis, hyperlipoproteinaemia, hyperlipidaemia,
hypercholesterolaemia, coronary heart disease.
                                                                                                                                                      Probe; microarray; human; placenta; antenatal diagnosis; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 19; DB 4; I
llarity 100.0%; Pred. No. 3.7e+02;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 27; SEQ ID NO 34179; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human liver peptide, SEQ ID No 34112.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ż
                 AAM33910 standard; protein; 28 AA.
                                                                                                                                                                                                                                                                                                                                                        04-FEB-2000; 2000US-0180312P.
26-MX-2200; 2000US-020745EP.
30-UJX-2200; 2000US-020745EP.
03-AUG-2000; 2000US-00632366.
21-SFP-2000; 2000US-023468PP.
04-OCT-2000; 2000GS-023459P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABG55464 standard; peptide; 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen W,
                                                                                                                                                                                                                                                                                                                        30-JAN-2001; 2001WO-US000663
                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from human placenta. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-488897/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                   WO200157272-A2.
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                                                                                                                                                                                                                   Homo sapiens.
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                                                                                       17-OCT-2001
                                                                                                                                                                                                                                                                                        09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide NT71 (AAW17812) was obtd. by trypsin digestion of human liver mevalonate pyrophosphate decarboxylase (MPD) (AAW17831), an enzyme of the cholesterol biosynthetic pathway. The sequence of the peptide was used to design PCR primers utilised in the amplification of cDMA from a rat liver cDNA library. A rat MPD partial clone was obtd. and used as a probe to screen a human liver cDNA library. A 1800 bp sequence (AAT66464) coding for human MPD was identified
                 samples in clinical or research-based assays using immunoblotting, fluorescence in situ hybridisation analysis, gel-mobility shift assays, tracking of radioactive or bioluminescent markers, chromatography or electrophoresis. The peptides are used to induce an immune response to HAV when administered to a human or animal. Glutamine at the carboxy end of the peptides enhances the IgM antibody reactivity
 The peptides are used to detect or quantify HAV antibodies in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human mevalonate pyrophosphate decarboxylase coding sequence - used screening for MPD inhibitors, which regulate and control cholesterol
                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
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                                                                                                                                                                             100.0%; Score 19; DB 4; Length 25; 100.0%; Pred. No. 3.3e+02; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human mevalonate pyrophosphate decarboxylase peptide NT71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mevalonate pyrophosphate decarboxylase; MPD; cholesterol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 19; DB 2; Lt
llarity 100.0%; Pred. No. 3.7e+02;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                 AAW17832 standard; peptide; 28 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; Page 10; 37pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95US-0005652P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96WO-EP004394
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Huwyler LR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (NOVS ) NOVARTIS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-245104/22.
                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                     1 VAEF 4
                                                                                                                                                                                                                                                                                        3 VAEF 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 28 AA;
                                                                                                                                             Sequence 25 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-APR-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               synthesis
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Gaps

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WO200157273-A2.

RESULT 27

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Homo sapiens.

Length 28; Indels

09-AUG-2001

Chen W, Rank DR;

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measuring human gene expression in a sample derived from human adult liver. Comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG47348-ABG59930 represent human liver single exon encoded peptides of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from MIPO at
                                                                                                                                                                                                                                                                                                                                Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.
                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a single exon nucleic acid probe (SENP) (I) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human peptide encoded by genome-derived single exon probe SEQ ID 33266.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomcosis; Karagener syndrome; pulmonary histocytosis; pulmonary alveolar proteinosis; fibrocystic pulmonary dyskinesis; pulmonary hypertension; hyaline membrane disease.
                                                                                                                                                                                                                                                                                                                                                                                       Claim 27; SEQ ID NO 34112; 658pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABG43601 standard; peptide; 28 AA.
                                                                                                  26-MAY-2000; 2000US-0207456P.
30-UTN-2000; 2000US-00608408.
03-AUG-2000; 2000US-0053366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                           (MOLE-) MOLECULAR DYNAMICS INC
                                               30-JAN-2001; 2001WO-US000664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hanzel DK,
                                                                                                                                                                                                                                                                                                 WPI; 2001-488898/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 28 AA;
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                                                                                   04-FEB-2000;
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                                                                                                                                                                                                                                                               Penn SG,
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The invention relates to a patially addressable set or shall be computed to the computed of th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention relates to a spatially-addressable set of single
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100.0%; Pred. No. 3.7e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                 measure gene expression in human lung samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 27; SEQ ID NO 33266; 634pp; English
                                                                                                                                                                                                                                                                                                            Chen W, Rank DR;
                                                                                                                                                                                                                                                                    (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                            03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
                                                           30-JAN-2001; 2001WO-US000665
                                                                                                                       2000US-0207456P.
2000US-00608408.
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Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                         Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-114183/15
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                                                                                                                                                                                                                                                                                                         Penn SG,
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100.0%; Score 19; DB 4; Length 28; 100.0%; Pred. No. 3.7e+02; Azive 0; Mismatches 0; Indels

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2000US-0190076P.
2000US-0198123P.
                     17-JAN-2001; 2001WO-US001354
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                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus pneumoniae polynucleotides - useful for developing products for diagnosis, prevention and treatment of infections e.g. pneumonia, bacteremia, meningitis or endocarditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence is that of a Streptococcal polypeptide. The polypeptide can potentially be used for the diagnosis and prevention of bacterial infections, especially SP infection. It may be used for the trearment of diseases such as otitis media, conjunctivitis, pneumonia, bacteremia, meningitis, sinusitis, pleural empyema, endocarditis or infection of the cerebrospinal fluid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                            Hodgson JE, Knowles DJC, Lonetto MA, Nicholas RO;
Zarfos PN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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                                                                                                                                Polypeptide; ORF; open reading frame; infection; bacterial; streptococcal; bacteremia; diagnosis; prophylaxis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immune/haematopoietic antigen SEQ ID NO:10247
                                                                                                         Streptococcus pneumoniae polypeptide.
                                 AAW62760 standard; protein; 30 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAM82654 standard; protein; 32 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5; Page 32; 181pp; English
                                                                                                                                                                                                                                                                                        (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                  96US-0031879P.
                                                                                                                                                                                                                                           97WO-US021976
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                                                                                 (first entry)
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Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                    Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-322654/28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 30 AA;
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                                                                                                                                                                                                                                                                  27-NOV-1996;
                                                                                                                                                                                          WO9823631-A1
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                                                                                  09-NOV-1998
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                                                                                                                                                                                                                                                                                                                             Black MT,
Reid RH, 2
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                                                         AAW62760;
           ESULT 30
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N-PSDB; AAK55435

7-NOV-2000;

(HUMA-) HUMAN GENOME SCI INC.

Barash SC, Ruben SM;

Claim 20; SEQ ID NO 22916; 1399pp + Sequence Listing; English

AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (1) and action sequences given in AAM91210 to AAM91921. (1) have cytostatic activity, and can be used in gene therapy and vaccine production. (1) proteins and polymucleotides may be used in the prevention, diagnosis and teatment of diseases associated with inappropriate (1) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (1) by expressing inactive proteins or to supplement the patients own production of (1). Additionally, (1) polymucleotides may be used to produce the secreted (1), by inserting the pulling into a host cell and culturing the cell to express the protein. (1) proteins and polymucleotides may be used to protein. (2) proteins and polymucleotides may be used to protein. (2) concers and creat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 concers from the present invention. AAK5492 to AAK54950 and AAM92169 crepresent sequences used in the exemplification of the present invention ö Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders. Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis. Human, cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation. Gaps . 0 Claim 11; SEQ ID NO 10247; 3071pp + Sequence Listing; English Query Match
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels Human polypeptide SEQ ID NO 22916. AA009024 standard; protein; 33 AA. 28-FEB-2000; 2000US-00515126. 18-MAY-2000; 2000US-00577409. 26-FEB-2001; 2001WO-US004927 Tang YT, Liu C, Drmanac RT 06-NOV-2001 (first entry) WPI; 2001-514838/56. (HYSE-) HYSEQ INC 13 VAEF 16 N-PSDB; AAI88955 1 VAEF 4 Sequence 32 AA; WO200164835-A2. Homo sapiens 07-SEP-2001 AA009024; RESULT 32 AA009024 ò 원 

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The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to prytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, nematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tbp1, Tbp2, transferrin receptor operon; vaccine, antigen;
non-typable strain, Haemophilus influenzae, meningitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR77953 standard; peptide; 35 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antigenic Tbp2 peptide TBP2-21
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93US-00175116
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Yang Y, Murdin A, Klein M,
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Best Local Similarity
Local 4; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 33 AA;
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29-DEC-1993;
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Gaps ö

Length 33;

100.0%; Score 19; DB 4; Length 33 100.0%; Pred. No. 4.4e+02; Viamatches 0; Indels

AAR77933-969 are predicted antigenic peptides derived from conserved regions of the Tbp2 protein from H. influenzae strains Eagan, MinnA, DL63 and non-typable strain PAK12085. The transferrin receptor (TER) operon consists of two genes (Tpb1 and Tbp2) arranged in tandem and which are transcribed from a single promoter. H. influenzae TfR is iron- and/or haemin-regulated and a putative fur-binding site has been identified upstream of tbp2. Antibodies blocking this binding site may prevent bacterial growth. Fragments of the TfR (or its genes) are useful in advantage to provide protection against, e.g. bacterial meningitis. An advantage of using the TfR is that it shares homology with TfR of other Nucleic acids encoding Haemophilus transferrin receptor - used to develop prods for detection and in diagnosis, prevention and treatment of Haemophilus infection. Example 16; Page 72; 231pp; English.

Gray-Owen S;

Chong P,

Schryvers A,

94WO-CA000616

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protein of Haemophilus influenzae type b. Thp2 is part of the transferrin receptor, of which Thp1 is also a subunit. The deduced amino acid sequences of Thp1 and Thp2 were compared, and regions of conservation identified. The above peptides are derived from these regions, the present peptide being derived from these regions, the present peptide being derived from these regions, the mutical from the growth of these bacteria, and they can utilise human transferrin as a source of iron. Antibodies which block the access of the transferrin receptor to its iron source prevent bacterial growth. The transferrin receptor, or fragments, therefore, are good vaccine candidates. An immunogenic composition comprising (or encoding) the immunogenic truncated analogue to induce protection against disease caused by a bacterial pathogen that produces the transferrin in immunosasays for the detection of Haemophilus transferrin receptor. The immunogenic truncated analogue is also useful as an antigen in immunosasays for the detection of Haemophilus transferrin receptor.
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H. influenzae strains including non-typable strains. According to the specification the present sequence shows residues 449-484 of Tbp2 from the H. influenzae strain Eagan
                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             Transferrin receptor, Haemophilus influenzae type 'b; iron; human transferrin; iron source; antibody; bacterial growth; vaccine; immunogenic truncated analogue; antigen; Tbp1; Tbp2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haemophilus truncated transferrin receptor protein analogue, Tbp2 - to induce protection against disease caused by transferrin producing pathogens, or as antigen to detect Haemophilus TfR antibodies.
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                                                                                                         100.0%; Score 19; DB 2; Length 35; 100.0%; Pred. No. 4.7e+02;
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                                                                                                                                               0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                             Predicted antigenic Tbp1 peptide TBP2-21.
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                                                                                                                                                                                                                                                                                                       AAW46146 standard; protein; 35 AA.
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96US-00649518.
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                                                                                                                                             4; Conservative
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Haemophilus influenzae.
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Yang Y, Murdin AD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-052329/05.
                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                 14 VAEF 17
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                                                                         Sequence 35 AA;
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17-MAY-1996;
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                                                                                                           Query Match
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                                                                                                                                                                                                                                                                     RESULT 34
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RESULT 35 **AAY**51751

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The present sequence represents the NH2-terminal amino acid sequence of aquaporin-1 (AQD-1), isolated from human erythrocytes. AQD-11s a water channel proteins regulate the passage of water and out of cells, in response to osmotic changes. The DNA encoding AQP-1 is useful for the recombinant production of AQP-1, found in mammalian erythrocytes, and is useful in the study to identify reagents which enhance or inhibit water channel function. This can lead to therapeutics which enhance secretion e.g. in the case of dryness of eyes which can be obtaindness or to hydrate large respiratory airways, as their dryness can precipitate asthma
                                                                                                                                                                                                                                                                                                             /label= Unknown
/note= "not specified but is given as Ser in the full
length protein given in AAW55786"
                                                                                                                                                           Human, aquaporin-1; AQP-1; water channel protein; regulation; osmotic change; erythrocyte; dryness; blindness; hydration; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polynucleotide(s) encoding water channel protein Aquaporin-1 for recombinant production of protein for activity studies.
                                                                                                                           Human aquaporin-1 NH2-terminal amino acid sequence CHIP28.
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100.0%; Pred. No. 4.7e+02;
ive 0; Mismatches 0;
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                   AAW55788 standard; peptide; 35 AA.
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                                                                                           14-JUL-1998 (first entry)
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Best Local Similarity luv...
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24-FEB-1995;
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                                                                                                                                                                                                       secretion.
                                                       AAW55788;
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AC AAW5
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DT 20-C
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to induce protection against disease caused by transferrin producing
pathogens, or as antigen to detect Haemophilus TfR antibodies.
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   Length 35;
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                                 0; Indels
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 100.0%; Score 19; DB 2; I
100.0%; Pred. No. 4.7e+02;
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                                   Mismatches
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lein M, Chong P;
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93US-00175116.
94US-00337483.
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                                   4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-052329/05
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Best Local Similarity
Matches 4; Conserv
                   Similarity
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29-DEC-1993;
08-NOV-1994;
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                                                                                                                                                                                                                                                                                                                                                                            diagnosis.
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Query Match
Best Local S:
Matches 4
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Gaps

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5 (AQPS). The polynucleotide encoding AQPS is useful for producing recombinant AQPS, which can be incorporated into proteoliposomes or cell membrane vosicles which are able to be used in screening assays for water channel agoniets or antagoniets. The present sequence represents the N-terminal peptide from AQP1 (also called CHIP28), from an example of the
                                                                                                                                                                                                                       The present invention describes a water channel protein called aquaporin
                                                                                                                                   DNA encoding aquaporin-5 water channel protein - useful for producing recombinant protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antibodies specific for transferrin receptor proteins of Haemophilus influenzae, useful for treating otitis media, epiglottitis, pneumonia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antibacterial; antiinflammatory; auditory; respiratory; antibody; antiserum; transferrin receptor; immunogen; epitope; otitis media; bacterial meningitis; epiglottitis; pneumonia; tracheobronchitis.
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    influenzae transferrin receptor Tbp1 epitope TBP2-21.

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100.0%; Pred. No. 4.7e+02;
ive 0; Mismatches 0;
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                                                                                                                                                                                      Example 2; Col 20; 47pp; English
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95US-00337483.
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                               (UYJO ) UNIV JOHNS HOPKINS
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Best Local Similarity luv...
A, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schryvers A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-096387/08.
                                                                                                  WPI; 1999-152100/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               influenzae, ūseful
:racheobronchitis.
                                                                                                                                                                                                                                                                                                                            present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 VAEF 17
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                                                                                                                                                                                                                                                                                                                                                              Sequence 35 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-JUN-1995;
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08-NOV-1995;
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Murdin A, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY80448;
                                                               Agre PC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptides AAW53086-W53100 and peptides AAW54100-W54122 are derived from the Tbp2 protein is one of two proteins with genes found on the transferrin operon. These peptides can be used along with the genes, DNA sequences and recombinant proteins for diagnosis, immunisation and the generation of diagnostic and immunological reagents. They can also be used to protect from bacteria that produce transferrin
                                                                                                                                                                                                                                                                                                                                                                                           Purification of recombinant Haemophilus transferrin-binding protein - by solubilising inclusion bodies separated from cell lysate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rat; aquaporin-5; AQP5; AQP1; transmembrane water channel protein; major intrinsic protein; MIP; CHIP28.
                                                                                                                                                                                                                                                                                                         Chong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 19; DB 2; Length 35; 100.0%; Pred. No. 4.7e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                           Yang Y,
            tbp1; tbp2; vaccine; H. influenzae; antibody; diagnosis; passive immunisation; transferrin receptor operon.
                                                                                                                                                                                                                                                                                                           Loosmore S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human aquaporin-1 (CHIP28) N-terminal peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 16/17; Column 37-38; 261pp; English.
                                                                                                                                                                                                                                                                                                           Harkness R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "unspecified"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW94320 standard; peptide; 35 AA
                                                                                                                                                                                                   93US-00148968.
93US-00175116.
94US-00337483.
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Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                       S, Klein M,
Schryvers A;
                                                              Haemophilus influenzae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptor protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 35 AA;
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08-NOV-1994;
                                                                                                                                                                  07-JUN-1995;
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                                                                                                                                                                                                                                                                                                           Gray-Owen S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-APR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-FEB-1995;
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                                                                                                US5708149-A
                                                                                                                                 13-JAN-1998
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Indels

Length 35;

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Klein M;

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               corresponds to an epitope from the H. influenzae transferrin receptor protein TDP2. The antibodies may be used for preventing and treating infections and disorders caused by H. influenzae, including bacterial meningitis, otitis media, epiglotitis, pneumonia and tracheobronchitis. The antibodies may also be used detect the presence of H. influenzae proteins in samples according to standard methodologies (e.g. enzyme linked immunosorbant assay (ELISA)) and hence diagnose infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus aureus protein; ribozyme; antisense sequence; control; Staphylococcal gene; regulatory element; bacterial gene expression; vaccine; Staphylococcal infection; food poisoning; scaled skin syndrome;
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                                                                                                                                                                                                                                       Gaps
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 This sequence
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Ward JM;
                                                                                                                                                                                           Similarity 100.0%; Pred. No. 4.7e+02; 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UDP-N-acetylglucosamine 1-carboxyvinyltransferase.
 fragment) from strains of Haemophilus influenzae.
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Rosenberg M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                             AAW27782 standard; protein; 36 AA.
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Pratt JM, Reichard RW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  toxic shock syndrome.
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N-PSDB; AAT83751.
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Best Local Similarity
Matches 4; Conserv
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Misc-difference 34
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                                                                                                                                                                                                                                                                    1 VAEF 4
                                                                                                                                                               Sequence 35 AA;
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produce specific antibodies with antibacterial action. These vaccines and antibodies would protect a host against invasion by S. aureus, and conditions relating to Staphylococcal infection, e.g. Staphylococcal food poisoning, scaled skin syndrome, and toxic shock syndrome
                                                                                                                                                                                                                                                                                                               Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antihafammatory; anti-HV; antibacterial; vulnerary; antiparkinsonian; antiaickling; antianaemic; antiarchritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiparaemic; antidiabetic; antilonalismi; antiparaemic; anticonvulsant; antiquagal; antiparaemic; cardiant; immune discorder; cardiovaecular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine;
                                                                                                           Gaps
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                                                                                  Length 36;
                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                        Human excretory related polypeptide SEQ ID NO 570.
                                                                                 Score 19; DB 2; I
Pred. No. 4.8e+02;
Mismatches 0;
                                                                                                                                                                                                                  AAM99833 standard; protein; 37 AA.
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0
                                                                                  100.0%;
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2000US-0190076P.
2000US-0198123P.
2000US-0209467P.
2000US-0209467P.
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2000US-0220964P.
2000US-0224518P.
2000US-0224519P.
2000US-0225213P.
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2000US-0216647P.
2000US-0216880P.
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2000US-0217496P.
2000US-0218290P.
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2000US-0184664P.
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                                                                                                                                                                                                                                                                 (first entry)
                                                                                                           4; Conservative
                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                    excretory system.
                                                                                                                                 1 VAEF 4
                                                                                                                                                        3 VAEF 6
                                                           Sequence 36 AA;
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                                                                                                                                                                                                                                           AAM99833;
                                                                                  Query Match
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Matches
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The invention relates to novel excretory system related human polynucleotides (AA199567-AA199503) and the encoded proteins (AAM99594-AA199503) and the encoded proteins (AAM99594-AA199503) and the encoded proteins (AAM99594-CAAM9913) useful for perventing, treating or ameliorating medical conditions e.g. by protein or gene therapy, especially disorders related to the excretory system. The genes are isolated from a range of human tissues disclosed in the specification. The mucleic caids, proteins, cantibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal track, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, cheumatoid attritis and ulcerative colitis; (c) cardiovascular disorders such as wrocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases cuch as viral, bacterial, fungal and parasitic infections. Once: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fig. at ftp.wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated nucleic acid molecule encoding excretory system antigen is used in preventing, treating or ameliorating a medical condition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; SEQ ID NO 570; 574pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rosen CA, Barash SC, Ruben SM
08-NOV-2000; 2000US-0246613P.
17-NOV-2000; 2000US-024920P.
17-NOV-2000; 2000US-024920BP.
17-NOV-2000; 2000US-0249210P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-024921P.
17-NOV-2000; 2000US-024929P.
17-NOV-2000; 2000US-024929P.
17-NOV-2000; 2000US-024939P.
17-NOV-2000; 2000US-025198P.
17-NOV-2000; 2000US-025198P.
17-NOV-2000; 2000US-025198P.
18-DEC-2000; 2000US-025198P.
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N-PSDB; AAI98806.
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Gaps .

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14 VAEF 17

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PR 06-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231241B.
PR 08-SEP-2000; 2000US-023129B.
PR 14-SEP-2000; 2000US-023229BP.
PR 14-SEP-2000; 2000US-023239P.
PR 14-SEP-2000; 2000US-023239P.
PR 14-SEP-2000; 2000US-023239P.
PR 14-SEP-2000; 2000US-023239P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233063P.
PR 25-SEP-2000; 2000US-023666P.
PR 26-SEP-2000; 2000US-024661P.
PR 27-SEP-2000; 2000US-024661P.
PR 27-SEP-20
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Peptide #3978 encoded by probe for measuring cervical gene expression.

Probe; human; microarray; gene expression; cervical epithelial cell;

cervical cancer.

WO200157278-A2

09-AUG-2001.

Homo sapiens

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The invention relates to novel kidney related polynucleotides (AAM52971-AAM5691) and the encoded polypeptides (AAM2417-AAM4691) collectively known as kidney antigens and the use of such kidney antigens for known as kidney antigens and the use of such kidney antigens for cancer metastases. The polynucleotides and proteins are also useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are useful from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (art) agonists are useful in the diagnosis, treatment and prevention of (a) (a) cancer, e.g. breast and ovarian cancer, and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urgepenital, (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anneamia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid archartis and ulcerative collitis; (c) cardiovascular disorders such as mycardial ischaemias; (d) wound healing, (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, battent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the virule of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acids and polypeptides, useful for diagnosing, treating and/or preventing human diseases and disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11; SEQ ID NO 517; 564pp + Sequence Listing; English.
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17-NOV-2000, 2000US-0249287F.

17-NOV-2000, 2000US-0249299F.

17-NOV-2000, 2000US-0249300F.

01-DEC-2000, 2000US-0250160P.

05-DEC-2000, 2000US-0251030F.

05-DEC-2000, 2000US-0251030F.

05-DEC-2000, 2000US-0251198F.

06-DEC-2000, 2000US-025149F.

06-DEC-2000, 2000US-025149F.

08-DEC-2000, 2000US-025186F.

08-DEC-2000, 2000US-025186F.
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Best Local Similarity 100.
Matches 4; Conservative
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Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.

Chen W, Rank DR;

Hanzel DK,

Penn SG,

WPI; 2001-488901/53

(MOLE-) MOLECULAR DYNAMICS INC

26-MAY-2000; 2000US-0207456P. 30-UUN-2000; 2000US-00608408. 03-AUG-2000; 2000US-00532366. 21-SEP-2000; 2000US-0234687P. 27-SEP-2000; 2000US-0234587P. 04-OCT-2000; 2000GB-00024263.

30-JAN-2001; 2001WO-US000670

Claim 27; SEQ ID NO 22370; 487pp; English

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The present invention relates to human single exon nucleic acid probes (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human Hela calls. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; microarray; single exon probe; gene expression; breast; disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide #4013 encoded by breast cell single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 100.0%; Score 19; DB 4; Length 43; Local Similarity 100.0%; Pred. No. 5.9e+02; nes 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB31362 standard; peptide; 43 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40 VAEF 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 VAEF 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 43 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loc
Matches
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Gaps

AAM17544 standard; protein; 43 AA.

ESULT 43 AM17544

14 VAEF 17

1 VAEF 4

(first entry)

12-OCT-2001

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30-JAN-2001; 2001WO-US000662

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Lucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from many of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for verifying the reseast disease. Gene expression analysis is useful for session of the toxicity of chemical agents on cells. The microarray of chancel the expression analysis is useful for this invention presents af ar grader diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed sequence. The present sequence is a peptide specification, but was obtained in electronic format directly from WIPO at the vivo int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                     New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein #3903 encoded by probe for measuring heart cell gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a spatially-addressable set of single exon
                                                                                                                                                                                                                                                                                                                                                                                                   Claim 27; SEQ ID NO 14330; 327pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; gene expression; heart; microarray; vascular system; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 19; DB 4; Length 43; 100.0%; Pred. No. 5.9e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                               Chen W, Rank DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB21904 standard; protein; 43 AA.
                                                                     26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
27-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-023659P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                          (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Conservative
                                                                                                                                                                                                                                             Hanzel DK,
                                                                                                                                                                                                                                                                                    WPI; 2001-496933/54.
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 43 AA;
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ABB21904
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Gaps

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The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see BAZ1353-BAZ41305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hopertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the prince specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Single exon nucleic acid probes for analyzing gene expression in human hearts.
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                                                                                26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-023468PP.
27-SEP-2000; 2000US-0234539P.
04-OCT-2000; 2000GB-00024263.
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, 2000US-0207456P.
, 2000US-00608168.
, 2000US-00632366.
, 2000US-0234687P.
, 2000US-0234687P.
                                                                                                                                                                                                                                                                                                    (MOLE-) MOLECULAR DYNAMICS INC
30-JAN-2001; 2001WO-US000666.
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                                                         2000US-0180312P
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                                                                                                                                                                                                                                                                                                                                                          Penn SG, Hanzel DK,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 4; Conserv
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26-MAY-2000; 2
30-JUN-2000; 2
03-AUG-2000; 2
21-SEP-2000; 2
27-SEP-2000; 2
04-OCT-2000; 2
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ABG51414
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Peptide #3896 encoded by probe for measuring breast gene expression.
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                                                                                                                                                                                                                                                    WO200157270-A2.
                                                                                                                     Sequence 43 AA;
                                                                                                                                                                                             AAM05214;
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Penn SG,
                                                                                                                                        Matches
                                                                                                                                                                          ESULT 47
                                                                                                                                                                              AM05214
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The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver. Comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis.

C hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG47348-ABG5930 represent human liver single exon encoded peptides of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at ttp.wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                               Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 27; SEQ ID NO 30062; 658pp; English
                                                                                                   Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                   gene expression in human adult liver.
(MOLE-) MOLECULAR DYNAMICS INC.
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100.0%; Score 19; DB 4; Length 43; 100.0%; Pred. No. 5.9e+02;
                         0; Indels
                           0; Mismatches
                            4; Conservative
Query Match
Best Local Similarity
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AAM05214 standard; protein; 43 AA.

(first entry) 09-OCT-2001 Probe; human; breast disease; breast cancer; development disorder; inflammatory disease; proliferative breast disease; non-carcinoma tumour.

Homo sapiens

09-AUG-2001

04-FEB-2000; 2000US-0180312P. 26-MAY-2000; 2000US-0207456P. 30-UNN-2000; 2000US-05068408. 03-AUG-2000; 2000US-00532866. 21-SEP-2000; 2000US-0234687P.

27-SEP-2000; 2000US-0236359P. 04-OCT-2000; 2000GB-00024263.

(MOLE-) MOLECULAR DYNAMICS INC

Chen W, Rank DR; Hanzel DK,

WPI; 2001-476286/51

Novel single exon nucleic acid probe used to measuring gene expression in a human breast

Claim 27; SEQ ID NO 13954; 322pp; English

The present invention relates to novel single exon nucleic acid probes (see AA100010-AA110067). The present sequence is a peptide encoded by one auch probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosting, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic actiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences 

Sequence 43 AA;

Gaps ö 100.0%; Score 19; DB 4; Length 43; 100.0%; Pred. No. 5.9e+02; ive 0; Mismatches 0; Indels Query Match Best Local Similarity 100.

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ò g RESULT 48 AAB27178

AAB27178 standard; protein; 47 AA. AAB27178; 

(first entry) 27-FEB-2001

RSV partial protein sequence SEQ ID NO: 26.

Negative stranded RNA virus; vaccine; attenuated virus; RSV; PIV; measles; respiratory syncytial virus; parainfluenza virus.

Respiratory syncytial virus.

WO200061737-A2

19-0CT-2000

12-APR-2000; 2000WO-US009695.

99US-0129006P. 13-APR-1999; USSH ) US DEPT HEALTH & HUMAN SERVICES

Murphy BR, Collins PL, Durbin AP, Skiadopoulos MH;

WPI; 2000-687044/67.

Producing attenuated negative stranded RNA virus vaccines from cloned sequences, useful for immunizing against e.g. respiratory syncytial virus, human parainfluenza virus, Sendai virus Newcastle disease virus, mumps virus and measles virus.

Example 1; Page 62; 137pp; English.

The present invention is concerned with producing vaccines against negative stranded RNA viruses. These viruses include measles, respiratory syncytial virus (RSV) and parainfluenza virus (PIV) in particular. The method of the invention comprises the production of a mutated form of the virus which attenuates the strain and enables it to be used as a vaccine. The present sequence comprises a partial viral protein sequence

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RESULT 49 AAM18541

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Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide #5033 encoded by probe for measuring placental gene expression.
                                                                                                                                                                                        Human; foetal liver; gene expression; single exon nucleic acid probe.
                                                                                                                                                   Peptide #5084 encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 27; SEQ ID NO 30213; 639pp + Sequence Listing; English.
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hes 0; Indels
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100.0%; Pred. No. 6.6e+02.
iive 0; Mismatches 0
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                                       ABB37578 standard; peptide; 48 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                      20-UTN-2000; 2000US-0060B40B.
03-AUG-2000; 2000US-0063D366.
21-SEP-2000; 2000US-023A6FP.
27-SEP-2000; 2000US-023A5559F.
04-OCT-2000; 2000GB-00024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-483447/52
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genetic disorder
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 48 AA;
                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                04-FEB-2002
                                                                                                                                                                                                                                                                                                        09-AUG-2001
                                                                          ABB37578;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.
                                                                                                                                                                                                                                                                                                                                                                    Peptide #4975 encoded by probe for measuring cervical gene expression.
                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                            human; microarray; gene expression; cervical epithelial cell;
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                                       Length 47;
                                                                          Indels
                                     100.0%; Score 19; DB 3; L. 100.0%; Pred. No. 6.4e+02; ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen W, Rank DR,
                                                                                                                                                                                                                                                  AAM18541 standard; protein; 48 AA
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30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-003266.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234587P.
04-OCT-2000; 2000GB-00024263.
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                  Query Match
Best Local Similarity luv.
4; Conservative
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Best Local Similarity 100.
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-488901/53.
                                                                                                                                                   34 VAEF 37
                                                                                                                1 VAEF 4
                                                                                                                                                                                                                                                                                                                                                                                                                                cervical cancer.
Sequence 47 AA;
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                                                                                                                                                                                                                                                                                          AAM18541;
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Gaps

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Homo sapiens

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Length 48;

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The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see PRAZ1352-ARA41305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fip.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow.
                                                                                                                                  Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; bone marrow expressed exon; gene expression analysis; probe;
microarray; cancer; leukaemia; lymphoma; myeloma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 19; DB 4; Length 48; Best Local Similarity 100.0%; Pred. No. 6.6e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                            Claim 15; SEQ ID NO 24638; 530pp; English.
                                                        DR;
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                                                        Rank
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                (MOLE-) MOLECULAR DYNAMICS INC.
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                                                        Chen W,
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30-UUN-2000; 2000US-0060B408.
20-AUG-2000; 2000US-0053366.
21-SEP-2000; 2000US-023468PP.
27-SEP-2000; 2000US-0235359P.
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                                                        Hanzel DK,
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                                                                                            WPI; 2001-488899/53
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                                                        Penn SG,
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                                                                                                                                                                                                                                                                                                                                                                                                              Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to single exon nucleic acid probes (SENP: see AA131315-AA157546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 27; SEQ ID NO 31265; 654pp; English.
                                                                                                                                                                                                                                                                                                                                 Rank DR;
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                                                                                                                           04-FEB-2000; 2000US-0180312P.
26-MY-2000; 2000US-0207456P.
30-UIN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-023468PP.
27-SEP-2000; 2000US-023468PP.
04-OCT-2000; 2000GB-00024263.
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26-MAY-2000; 2000US-0201456P.
30-UTN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00532366.
21-SEP-2000; 2000US-023468TP.
27-SEP-2000; 2000US-023468TP.
04-OCT-2000; 2000GB-00224283.
                                                                                                                                                                                                                                                                                                                                 Chen W,
                                                                                                                                                                                                                                                                                           (MOLE-) MOLECULAR DYNAMICS INC
                                                                                        30-JAN-2001; 2001WO-US000663
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Best Local Similarity
Matches 4; Conserv
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              WO200157272-A2
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04-FEB-2000; 2000US-0180312P.
26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-060840B.
33-AUG-2000; 2000US-00632366.
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21-SEP-2000; 2000US-0234687P.
-2EP-2000; 2000US-0233595.
04-OCT-2000; 2000GB-00024263.
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                                                                                                                                       25-FEB-2003 (first entry)
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                                                  Sequence 48 AA;
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                                                                                          VAEF
                                                                                1 VAEF
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                                                                                                                              ABG52389;
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The present invention relates to novel single exon nucleic acid probes (see AA100010-AA110067). The present sequence is a peptide encoded by one auch probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing predicting, diagnosing, grading, staging, monitoring and prognosing actiolarly those diseases with polygenic actiolarly. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fip. wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel single exon nucleic acid probe used to measuring gene expression in a human breast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide #4789 encoded by probe for measuring breast gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Probe; human; breast disease; breast cancer; development disorder; inflammatory disease; proliferative breast disease; non-carcinoma
but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                   Length 48;
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Larity 100.0%; Pred. No. 6.6e+02;
Conservative 0; Mismatches 0; Indels
                                                                                                                                                           0; Indels
                                                                                                            100.0%; Score 19; DB 4; I
Similarity 100.0%; Pred. No. 6.6e+02;
4; Conservative 0; Mismatches 0;
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; 2000US-00608408.
; 2000US-00632366.
; 2000US-0234687P.
; 2000US-0236359P.
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Best Local Similarity
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                                                                    Sequence 48 AA;
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                                                                                                                                                                                                         1 VAEF
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27-SEP-2000;
04-OCT-2000;
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Matches
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ID AAM0
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                                                           probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved disgnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention
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                                                                                                                                                                                                                                                                                                                             Gaps
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                        Example 4; SEQ ID NO 30993; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                 4; Length 48;
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Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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(first entry)
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                                                                                                                                                                                           WO200164835-A2.
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AAO05247;
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Matches
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 SXXXXXXXXXXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to human polymucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferentiation or which may induce production of other cytokines in other cell differentiation or which may induce polymucleotides and polymetides are useful in gene therapy, vaccines or e.g. stem cell growth factor activity, hematopoissis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                                    Human, cytokine; cell proliferation, cell differentiation, gene therapy, vaccine, peptide therapy, stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory, cancer, leukaemia; nervous system disorders; arthritis; inflammation.
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                                                                                                                                                                                                         Human polypeptide SEQ ID NO 24457.
                                                                                                                  AAO10565 standard; protein; 53 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drmanac RT;
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18-MAY-2000; 2000US-00577409.
                                                                                                                                                                             (first entry)
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Best Local Similarity luv...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-514838/56.
N-PSDB; AAI90496.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tang YT, Liu C,
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                                                                                                                                                                                                                                                                                                                                            WO200164835-A2
              1 VAEF
                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                           06-NOV-2001
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                                                                                                                                               AA010565;
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AO05247
D AAO05:
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                                                                                     ESULT 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to sytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haemstoppiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format
                                                                           Human, cytokine, cell proliferation, cell differentiation, gene therapy, vaccine, peptidde therapy, stem cell growth factor, haematopoiesis; tissue growth factor, immunomchilatory; cancer, leukaemia; nervous system disorders; arthritis; inflammation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; SEQ ID NO 19139; 1399pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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Human polypeptide SEQ ID NO 19139.
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18-MAY-2000; 2000US-00577409.
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31-JAN-2000; 2000US-0179065P.

24-FEB-2000; 2000US-018652B.

24-FEB-2000; 2000US-018656P.

22-MAR-2000; 2000US-0186350P.

15-MAR-2000; 2000US-0186350P.

16-MAR-2000; 2000US-0189874P.

17-MAR-2000; 2000US-0198123P.

17-MUN-2000; 2000US-0198123P.

17-MUN-2000; 2000US-0198123P.

17-MUN-2000; 2000US-0121486FP.

28-JUN-2000; 2000US-0214887P.

11-JUL-2000; 2000US-021486FP.

26-JUL-2000; 2000US-022556FP.

14-AUG-2000; 2000US-022556FP.

14-AUG-2000; 2000US-022556FP.

14-AUG-2000; 2000US-022556FP.

14-AUG-2000; 2000US-022556FP.

14-AUG-2000; 2000US-022556FP.

14-AUG-2000; 2000US-022514FP.

14-AUG-2000; 2000US-022556FP.

14-AUG-2000; 2000US-022556FP.

14-AUG-2000; 2000US-022556FP.

14-AUG-2000; 2000US-022556FP.

14-AUG-2000; 2000US-022556FP.

14-AUG-2000; 2000US-022557FP.

14-AUG-2000; 2000US-022557FP.

14-AUG-2000; 2000US-022557FP.

14-AUG-2000; 2000US-022557FP.

14-AUG-2000; 2000US-02257FP.

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                                                                      17-JAN-2001; 2001WO-US001354
            WO200157182-A2
                                         09-AUG-2001
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2000US-0235835P 2000US-0236327P 2000US-0236368P 2000US-0237378P 2000US-0237378P 2000US-0237378P 2000US-023738P 2000US-0237038P 2000US-0237038P 2000US-0237038P 2000US-0237038P 2000US-0237038P 2000US-0237038P 2000US-0237038P 2000US-0237038P 2000US-0237038P 2000US-024178FP 2000US-024178PP 2000US-024178PP 2000US-024178PP 2000US-024178PP 2000US-024178PP 2000US-024178PP 2000US-0246474P 2000US-0246474PP 2000US-024921PP 2000US-024921PP 2000US-0249244PP 2000US-024924PP 2000US-024924PP 2000US-025924PP 2000US-0251988PP 2000US-0251988PP 2000US-0251988PP 2000US-0251988PP 2000US-0251989PP 2000US-0251989PP 2000US-0251989PP 2000US-0251989PP 29-SBP-2000;
29-SBP-2000;
29-SBP-2000;
29-SBP-2000;
29-SBP-2000;
20-CGT-2000;
20-CG 

(HUMA-) HUMAN GENOME SCI INC

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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polymucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by pressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inscring the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; matrix metalloproteinase; MMP; anticancer; wound healing; matrix metalloproteinase inhibitor; antitumour; antiangiogenic; cardiant; vascular endothelial growth factor inhibitor; VEGF inhibitor; Orfostatic; vulnerary; cerebroprotective; antidiabetic; ophthalmological; tumour; dermarological; metastatic; non-metastatic; vascularised; heart disease; non-vascularised; surgical incision; chronic wound; stroke; anglogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein. (I) proteins and polymucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                              Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
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                                                                                                                                                                                                                                                                                                                        Claim 11; SEQ ID NO 14983; 3071pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 19; DB 4; Length 56; 100.0%; Pred. No. 7.8e+02; ive 0; Mismatches 0; Indels
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Ruben SM
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21-DEC-2001; 2001US-00032376.
21-MAY-2002; 2002US-00153185.
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    Barash SC,
                                                                              WPI; 2001-483426/52
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Best Local Similarity
Matches 4; Conserv
                                                                                                                     N-PSDB; AAK60171
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    Rosen CA,
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BP97126
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The present invention describes an anti-angiogenic composition (I) for inhibiting expression of vascular endothelial growth factor (VEGF). (I) compities an effective amount of a peptide inhibitor of matrix metalloproceinase (WMP), where the peptide can inhibit the expression of VEGF. (I) has cytostatic, vulnerary, cardiant, cerebroprotective, candidabetic, ophthalmological and dermaciological activities. (I) can be used for inhibiting expression of VEGF and so can be used for inhibiting expression of VEGF and so can be used for inhibiting crowth of tumours and diminishing tumours size. The tumour can be metastatic, non-metastatic, vacularised, non-vascularised, hard or soft.

(I) is also useful for treating injuries including wounds, surgical incisions, chronic wounds, heart diseases and stroke. (I) is also useful for treating disorders characterised by excessive angiogenesis e.g. macular degeneration and diabetic retinopathy. The present sequence represents a human MMP cleavage region poptide, which is used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; peptide inhibitor; matrix metalloproteinase-7; PMP-7; cleavage region; proenzyme form; cellular proliferation; fibroblast; keratinocyte; healthy skin development; wound healing; scarring; skin tone; wrinkle; anti-aging; vulnerary.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                            Anti-angiogenic composition comprising peptide inhibitor of matrix metalloproteinase, useful for decreasing the expression of vascular endothelial growth factor and treating cancers and tissue injuries.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 19; DB 6; Length 56; 100.0%; Pred. No. 7.8e+02;
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                                                                                                            Claim 17; Page 15; 103pp; English
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21-DEC-2001; 2001US-00032376.
21-MAY-2002; 2002US-00153185.
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Best Local Similarity 100.
Matches 4; Conservative
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WPI; 2003-381408/36.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VAEF 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 56 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 60
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Gaps ö

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The present invention relates to peptide inhibitors of metalloproteinases (MMPS), particularly metalloproteinase-2 (MMP-2). The inhibitors have peptide sequences related to the cleavage regions of the proenzyme forms of the MMPS. The peptide inhibitors are useful for stimulating cellular proliferation of fibroblasts or keratinocytes, promoting healthy skin development, treating wounds, preventing scarring, improving skin tone, reducing wrinkling and for simulating the development of smooth, healthy skin. The peptide inhibitors are useful as anti-aging and wound healing compounds. ABG76309-ABG76321 represent peptide inhibitors of MMPs

Sequence 56 AA;

Gaps ö Length 56; 100.0%; Score 19; DB 6; Length 56 100.0%; Pred. No. 7.8e+02; iive 0; Mismatches 0; Indels Conservative Ouery Match Best Local Similarity Matches 4; Conserv

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AAW55888

AAW55888 standard; protein; 58 AA 

AAW55888;

(first entry) 22-JUL-1998

Rat PC12.

Rat; telomerase; human; cancer; screening; inhibitor; elucidation; detection; probe; diagnosis; cell growth; ageing.

Rattus sp.

WO9807838-A1

26-FEB-1998

97WO-JP002904 21-AUG-1997;

96JP-00219761. 97JP-00018878. 97JP-00031807 21-AUG-1996; 17-FEB-1997; 31-JAN-1997

(MITU ) MITSUBISHI CHEM CORP.

Ishikawa F, Nakamura H, Takahashi K, Fujino Y, Harada N;

WPI; 1998-169149/15. N-PSDB; AAV25990.

Telomerase protein of higher animals and humans and gene encoding it for use in diagnosis of cancer, screening of telomerase inhibitors and elucidation of biological control mechanisms.

Example 1; Page 69-70; 106pp; Japanese.

The present sequence represents rat PC12 which is used in an example of the present invention which describes protein components of telomerase. The DNA or RNA encoding the telomerase protein component or its fragments can be used as a nucleotide probe for the detection of cancer cells and for diagnosis of cancer. Potential telomerase inhibitors can be screened by measuring their effect on the assay of the active form in cells or tissues. The polypeptide and DNA coding for it can be used in the elucidation of biological control mechanisms of, e.g. cell growth or ageing and of the mechanisms of cancer development

58 AA;

Query Match

DB 2; Score 19; 100.0%;

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         Gaps
         ..
0
         Indels
8.1e+02;
hes 0;
Pred. No. 8.
Mismatches
 100.08;
           4; Conservative
Best Local Similarity
Matches 4; Conserv
                                           49 VAEF 52
                           1 VAEF 4
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                                         셤
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RESULT

ABP04854 standard; protein; 58 AA

ABP04854;

(first entry) 24-JUN-2002

Human ORFX protein sequence SEQ ID NO:9690.

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Human, open reading frame, ORFX, gene therapy, cancer; cirrhosis; hyperproliferative disorder; psortiasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diaberes mellitus; systemic lupus erythematosus; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune datorder; infectious disease; autoimmune dasorder; rheumatosid arthritis; autoimmune thyroiditis; myasthenia gravis.

Homo sapiens.

WO200192523-A2.

06-DEC-2001

29-MAY-2001; 2001WO-US010836.

10-MAY-2000; 2000US-0206132P.

29-AUG-2000; 2000US-0228716P.

(CURA-) CURAGEN CORP.

Shimkets RA, Leach MD;

WPI; 2002-106308/14. N-PSDB; ABN20606

Novel human polypeptides and polymucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders.

Disclosure; SEQ ID NO 9690; 1037pp; English.

in the specification). ABN15762 to ABN27252 encode the human ORFX in the specification). ABN15762 to ABN27252 encode the human ORFX in the specification). ABN15762 to ABN27252 encode the human ORFX in the specification). ABN15762 to ABN27252 encode the human ORFX in the specification of the specification of a specification of the specification present invention describes substantially purified human proteins

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9908-01347324P-
9908-0138034P-
9908-0138453P-
9908-0139453P-
9908-0139453P-
9908-0139453P-
9908-0139453P-
9908-0139453P-
9908-0139453P-
9908-0139453P-
9908-0139453P-
9908-0139453P-
9908-014039P-
9908-014232P-
9908-014232P-
9908-014232P-
9908-014232P-
9908-014232P-
9908-014232P-
9908-014232P-
9908-014232P-
9908-0144086P-
9908-0144086P-
9908-0144086P-
9908-0144333P-
9908-014433P-
9908-014433P-
9908-014532P-
9908-014532P-
9908-0145318P-
9908-0145318P-
9908-0145318P-
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990S-0147204P.
990S-0147302P.
990S-0147192P.
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99US-0146388P.
99US-0146389P.
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09 - 70L - 1999;
12 - 70L - 1999;
13 - 70L - 1999;
15 - 70L - 1999;
16 - 70L - 1999;
16 - 70L - 1999;
19 - 70L - 1999;
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23-JUL-1999;
23-JUL-1999;
26-JUL-1999;
27-JUL-1999;
04-7UN-1999;
07-7UN-1999;
10-7UN-1999;
11-7UN-1999;
                                                                                                                                                                                                                                                                                                01-JUL-1999;
02-JUL-1999;
06-JUL-1999;
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20-JUL-1999;
20-JUL-1999;
20-JUL-1999;
21-JUL-1999;
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02-AUG-1999;
02-AUG-1999;
   ö
                                                                                                                                                                                                                                       Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
   form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                      Gaps
                                                                      .
0
                                                 Query Match
100.0%; Score 19; DB 5; Length 58;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                       Arabidopsis thaliana protéin fragment SEQ ID NO: 77787.
                                                                                                                                                              AAG60085 standard; protein; 59 AA.
                                                                                                                                                                                                                                                                                                                                                            990S-0121825P.
990S-0123180P.
990S-0125788P.
990S-0126264P.
990S-012624F.
990S-0127462P.
990S-0127462P.
990S-0130891P.
990S-0130891P.
990S-0130891P.
990S-0132484P.
990S-0134219P.
                                                                                                                                                                                                                                                                                                                                         25-FEB-2000; 2000EP-00301439
                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                 Arabidopsis thaliana
                                                                                                           30 VAEF 33
                                                                                         1 VAEF 4
                               Sequence 58 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-MAY-1999;
11-MAY-1999;
14-MAY-1999;
14-MAY-1999;
14-MAY-1999;
18-MAY-1999;
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05-MAR-1999;
23-MAR-1999;
25-MAR-1999;
26-APR-1999;
06-APR-1999;
06-APR-1999;
16-APR-1999;
23-APR-1999;
23-APR-1999;
30-APR-1999;
30-APR-1999;
30-APR-1999;
30-APR-1999;
30-APR-1999;
30-APR-1999;
30-APR-1999;
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                                                                                                                                           ESULT 63
                                                                                                                                                     4G60085
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0; Gaps

Indels

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0; Mismatches

4; Conservative

Matches

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RR 06-MUG-1999, 99US-0147302P.
RR 06-MUG-1999, 99US-0147302P.
RR 06-MUG-1999, 99US-0147146P.
RR 10-MUG-1999, 99US-0147146P.
RR 11-MUG-1999, 99US-0147146P.
RR 11-MUG-1999, 99US-014841P.
RR 11-MUG-1999, 99US-014841P.
RR 11-MUG-1999, 99US-014865SP.
RR 21-MUG-1999, 99US-014865SP.
RR 22-MUG-1999, 99US-014865SP.
RR 22-MUG-1999, 99US-014865SP.
RR 23-MUG-1999, 99US-014865SP.
RR 23-MUG-1999, 99US-014865SP.
RR 23-MUG-1999, 99US-014863SP.
RR 23-MUG-1999, 99US-014863SP.
RR 23-MUG-1999, 99US-014863SP.
RR 23-MUG-1999, 99US-014863SP.
RR 23-MUG-1999, 99US-014864SP.
RR
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                           Arabidopsis thaliana protein fragment SEQ ID NO: 78631.
                                                  AAG60683 standard; protein; 59 AA.
                                                                                                                                                                                                9908-0121825P.
9908-0123180P.
9908-0125788P.
9908-0126784P.
9908-01267462P.
9908-01267442P.
9908-01287144-
9908-01287144-
9908-0138814P.
9908-0132481P.
9908-0132481P.
9908-0132481P.
9908-0132481P.
9908-01324821P.
9908-013421P.
9908-013421P.
9908-013421P.
9908-013421P.
9908-0134228P.
9908-013421P.
9908-0134228P.
9908-0134228P.
9908-0134228P.
9908-0134228P.
9908-0134228P.
9908-0134228P.
9908-013428P.
9908-013428P.
9908-0136782P.
9908-0136782P.
                                                                                                                                                                                   2000EP-00301439
                                                                               18-OCT-2000 (first entry)
                                                                                                                                        Arabidopsis thaliana
             45 VAEF 48
1 VAEF 4
                                                                                                                                                                                  25-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-JUN-1999;
14-JUN-1999;
16-JUN-1999;
                                                                                                                                                                                                               09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
01-APR-1999;
06-APR-1999;
16-APR-1999;
116-APR-1999;
119-APR-1999;
23-APR-1999;
23-APR-1999;
23-APR-1999;
30-APR-1999;
30-APR-1999;
30-APR-1999;
                                                                                                                                                       EP1033405-A2
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06-MAY-1999;
06-MAY-1999;
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04-JUN-1999;
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                                                                AAG60683;
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UUS-01394537 UUS-01394557 UUS-01394557 UUS-013945678 UUS-01394518 UUS-01394518 UUS-01394518 UUS-01394518 UUS-01394518 UUS-01394518 UUS-01394518 UUS-01394518 UUS-01394518 UUS-01397518 UUS-0140658 UUS-014184218 UUS-014184218 UUS-014184218 UUS-014184218 UUS-0142184218 UUS-014410858	990S-0144331P 990S-0144331P 990S-0144332P 990S-0144332P 990S-0144332P 990S-0144332P 990S-0144632P 990S-0144632P 990S-0144632P 990S-0144632P 990S-0145088P 990S-0145088P 990S-0145089P 990S-0145192P 990S-0145192P 990S-0145192P 990S-0145193P 990S-0145218P 990S-0145218P 990S-0145218P 990S-0145218P 990S-0145313P 990S-0145313P 990S-0147303P 990S-0147303P 990S-0147303P 990S-0147303P 990S-0147303P 990S-0147303P 990S-0147303P 990S-0147416P 990S-014741935P 990S-01474193P 990S-01474193P
2. CON 1999 2. CON 1999 3. CON	R 19-UUL-1999; R 19-UUL-1999; R 19-UUL-1999; R 20-UUL-1999; R 20-AUG-1999; R 20-A

RR 13-AMC-1999; 99US-0149368P.

RR 10-AMC-1999; 99US-014937EP.

RR 10-AMC-1999; 99US-014932EP.

RR 20-AMC-1999; 99US-014992EP.

RR 10-AMC-1999; 99US-014992EP.

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0; Gaps

1 VAEF

WO200157272-A2

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide #9883 encoded by probe for measuring placental gene expression.
                                                                                                                                   foetal liver; gene expression; single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                       Peptide #9550 encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 27; SEQ ID NO 34679; 639pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Probe, microarray, human; placenta, antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 19; DB 4; 100.0%; Pred. No. 8.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene expression in human fetal liver.
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                        ABB42044 standard; peptide; 60 AA
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                                                                                                                                                                                                                                                                                      26-MAY-2000; 2000US-0207456P.
30-UUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-0033468P.
21-SEP-2000; 2000US-023468PP.
27-SEP-2000; 2000US-0234589P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                      (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                              30-JAN-2001; 2001WO-US000669
                                                                                                                                                                                                                                                                         2000US-0180312P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-OCT-2001 (first entry)
                                                                                (first entry)
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Best Local Similarity luv.
                                                                                                                                                                                                                                                                                                                                                                                                                Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-483447/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genetic disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 VAEF 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4,
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                                                                                                                                                                                          WO200157277-A2
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                                                                                                                                                                Homo sapiens
                                                                                04-FEB-2002
                                                                                                                                                                                                                                                                          04-FEB-2000;
                                                     ABB42044;
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RESULT 65
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Homo sapiens

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Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                            The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenca. The probes are useful for antenatal diagnosis of human genetic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; bone marrow expressed exon; gene expression analysis; probe;
microarray; cancer; leukaemia; lymphoma; myeloma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human bone marrow expressed probe encoded protein SEQ ID NO: 36043.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 19; DB 4; Lv
100.0%; Pred. No. 8.4e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                         Claim 27; SEQ ID NO 36115; 654pp; English.
                                                                                                                                                                                          Chen W, Rank DR;
                                                                                                                                                                                                                                                   gene expression in human placenta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM75737 standard; protein; 60 AA.
                                                                         , 2000US-0180312P.
2000US-0204468P.
2000US-00603408.
2000US-023468PP.
2000US-023468PP.
2000US-0234559P.
                                                                                                                                                                    (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0060B408.
2000US-00632366.
2000US-0234687P.
2000US-0236359P.
2000GB-00024263.
                                                     30-JAN-2001; 2001WO-US000663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JAN-2001; 2001WO-US000668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                         4; Conservative
                                                                                                                                                                                          Hanzel DK,
                                                                                                                                                                                                                 WPI; 2001-488897/53
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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30-JUN-2000; 2
03-AUG-2000; 2
21-SEP-2000; 2
27-SEP-2000; 2
                                                                                                                       21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                      26-MAY-2000;
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                                                                            04-FEB-2000;
                                                                                                             03-AUG-2000;
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                             09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM75737;
                                                                                                                                                                                           Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Gaps

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The invention relates to a single exon nucleic acid probe (SENP) (1) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridiess at high stringency to a nucleic acid molecule expressed in the human adult liver. (1) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG193910 represent human liver single exon encoded peptides of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at
diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, liver, cirrhosis; hyperlipoproteinaemia, hyperlipidaemia; hypercholesterolaemia; coronary heart disease.
                                                                                                                                   100.0%; Score 19; DB 4; Length 60; 100.0%; Pred. No. 8.4e+02; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rank
                                                                                                                                                                                                                                                                                                                                                                                 ABG57475 standard; peptide; 60 AA.
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2000US-00608408.
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21-SEP-2000; 2000US-0234687P
27-SEP-2000; 2000US-0236359P
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                                                                                                                                                                                 4; Conservative
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                                                                                                                                     Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                        1
                                                                                                                                                                                                                            1 VAEF 4
                                                                                           Sequence 60 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                           ABG57475;
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                                                                                                                                                                                                                                              The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention
                                                                                                                                   Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, brain expressed exon, gene expression analysis, probe, microarray, Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy, cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human brain expressed single exon probe encoded protein SEQ ID NO: 35030.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Single exon nucleic acid probes for analyzing gene expression in human brains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                         Example 4; SEQ ID NO 36043; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 19; DB 4; Length 60; 100.0%; Pred. No. 8.4e+02; tive 0; Mismatches 0; Indele
                                                   Rank DR
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       (MOLE-) MOLECULAR DYNAMICS INC
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                                                 Chen W,
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21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-023559P.
04-OCT-2000; 2000GB-00024263.
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
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Best Local Similarity 100...
4; Conservative
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                                                   Penn SG, Hanzel DK,
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                                                                                           WPI; 2001-488900/53
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                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 60 AA;
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05-NOV-2001

AAM62925;

SULT 68 M62925 09-AUG-2001

Length

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WO200157182-A2.
                          Homo sapiens.
                                                                        09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a human ORF polypeptide, a substrate for extracellular signal-regulated Kinase, ERK-6. Substances that modulate the activity of the ORF polypeptide can be used to treat diseases selected from dermatomyositis, polymyositis, inclusion body myositis, ascoold myopathy, AZT myopathy, myocardial infarction, and ischaemia/reperfusion. The probes and antibodies can be used to detect the presence of ORF in a sample
                                                                                                                                                                                                                                           ORF polypeptide; dermatomyositis; polymyositis; inclusion body myositis; sarcoid myopathy; AZT myopathy; myocardial infarction; ischaemia; ERK-6; extracellular signal-regulated kinase; reperfusion.
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                         Gaps
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                      Indels
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        Pred. No. 8.4e+02;
; Mismatches 0;
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100.0%; Pred. No. 8.7e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid encoding ORF polypeptide.
                                                                                                                                      AAY17262 standard; peptide; 62 AA.
                                                                                                                                                                                                                 HLH domain of drosophila E-spl m5
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100.08; Pre
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                                                                                                                                                                                          09-AUG-1999 (first entry)
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Best Local Similarity 100.
        Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                Drosophila melanogaster
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                                                                     8 VAEF 11
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                                               1 VAEF 4
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2000US-0217496P.
2000US-0218290P.
2000US-0220963P.
2000US-0220964P.
2000US-0224513P.
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2000US-0225757P.
2000US-0225758P.
2000US-0225759P.
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2000US-0227182P.
2000US-0227009P.
2000US-022924P.
2000US-022937P.
2000US-0229342P.
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2000US-0230438P.
2000US-0231242P.
2000US-0231243P.
2000US-0231413P.
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17-JAN-2001; 2001WO-US001354
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R 27-SEP-2000; 2000US-0235834F; 27-SEP-2000; 2000US-0235837F; 27-SEP-2000; 2000US-0235837F; 28-SEP-2000; 2000US-0235837F; 28-SEP-2000; 2000US-0235837F; 28-SEP-2000; 2000US-0235837F; 28-SEP-2000; 2000US-0235837F; 28-SEP-2000; 2000US-0235837F; 28-SEP-2000; 2000US-0236369F; 28-SEP-2000; 2000US-0236369F; 28-SEP-2000; 2000US-0236369F; 20-CCT-2000; 2000US-0237039F; 20-CCT-2000; 2000US-0237039F; 20-CCT-2000; 2000US-0231703F; 20-CCT-2000; 2000US-0231703F; 20-CCT-2000; 2000US-024178F; 20-CCT-2000; 2000US-0246474F; 20-CCT-2000; 2000US-0246474F; 20-CCT-2000; 2000US-0246474F; 20-CCT-2000; 2000US-0246477F; 20-CCT-2000; 2000US-0246477F; 20-CCT-2000; 2000US-0246477F; 20-CCT-2000; 2000US-0246477F; 20-CCT-2000; 2000US-0246278F; 20-CCT-2000; 2000US-0249209F; 20-CCT-2000; 2000US-0249217F; 20-CCT-2000; 2000US-0249299F; 20-CCT-2000; 2
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AAKS4951 to AAK64702 encode the human immune/haematopoietic antigen (I) and acid sequences given in AAM92170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polymucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat discorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to cupplement the patients own production of (I). Additionally, (I) to polymucleorides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the nucleic acids into a host cell and culturing the cell to express the diagnose and treat immune/haematopoietic-related diseases, sepecially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK67694 represent human immune/haematopoietic antigen genomic companies from the present invention. AAK64942 to AAK6490 and AAM92169 crepresent sequences used in the exemplification of the present invention
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                                                                                                                        Nucleic acida encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Maisonneuve JL;
Jones R, Carter D;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Acne vulgaris; antiseborrhoeic; dermatological; antibacterial; immunostimulant; immune response; vaccine; immunogenic.
                                                                                                                                                                             Claim 11; SEQ ID NO 18840; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 19; DB 4; Length 62; 100.0%; Pred. No. 8.7e+02; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mitcham JL, Skeiky YAW, Persing DH, Bhatia A,
Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR,
Barth B, Vallieve-Douglass J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABM65667 standard; protein; 62 AA.
                                     Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L1-OCT-2002; 2002WO-US032727.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-OCT-2001; 2001US-00978825.
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Best Local Similarity 100.0
---nhes 4; Conservative
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                                   Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-381789/36.
                                                                       WPI; 2001-483426/52
                                                                                        N-PSDB; AAK64028
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                                   Rosen CA,
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us-09-594-978a-2.rag

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The invention relates to an isolated polynucleotide (ACF64415-ACF64733)

encoding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polynuclectides (ARM35624-ARM65365) and to immunogenic fragments of P. acnes polypeptides. The invention action of the invention, antipodies against polypeptides of the invention, and properties of the invention, and proteins comprising a polypeptide of the invention; a nethod for stimulating an immune response specific for a P. acnes to polypeptide and an isolated T cell population comprising P. acnes polypeptides, this method; a vaccine composition (comprising P. acnes polypeptides, to polypeptide and an isolated T cell population of the invention; a tria method; a vaccine composition (comprising P. acnes polypeptides, polymucleotides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the polypeptides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the polympeptides are useful for diagnosting, preventing or treating acne polypeptides are useful for diagnosting, preventing or treating acne protein. The polymucleotides and immune response specific for a P. acnes protein. The polymucleotides can also be used as probes or primers for nucleic acid hybridisation. The vaccine composition is useful for the sequence represents a specifically claimed P. acnes polypeptide which is the tis useful form parforming a diagnostic assay. The present contain an immunogenic region. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, cytokine, cell proliferation, cell differentiation, gene therapy, vaccine, peptide therapy, stem cell growth factor, haematopoiesis, tissue growth factor; immunomodulatory; cancer; leukaemia, nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 19; DB 6; Length 62;
100.0%; Pred. No. 8.7e+02;
ive 0; Mismatches 0; Indels
                                                             Claim 7; SEQ ID NO 30343; 1481pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human polypeptide SEQ ID NO 23409.
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18-MAY-2000; 2000US-00577409.
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Best Local Similarity 100.
Matches 4; Conservative
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                                                                                                                                              The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polyneptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomodulatory activities activity, tissue growth factor activity, immunomodulatory activity and activity, insue growth factor activity, immunomodulatory activity and activity, insue growth factor activity, immunomodulatory activity and activity in seven system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                              Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid expressed at high level in normal prostatic tissue and encoded polypeptides, used to treat cancer and screen for therapeutic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Expressed sequence tag; EST; prostate; tumor; treatment, gene therapy; cancer; tissue specificity; human.
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                                                                                                                 Claim 20; SEQ ID NO 23409; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 64;
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             WPI; 2001-514838/56.
N-PSDB; AAI89448.
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Gaps ö

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prostatic cancer and (b) for therapy of prostate cancer, optionally where expressed by gene therapy methods. (a) is also used to isolate full-length genes (for gene therapy) and for recombinant production of (I), which can be used to raise specific antibodies. (A) are identified by expressed sequence tags) before these are analyzed for expression pattern (tissue specificity). This approach eliminates many of the false results, as regards tissue specificity, associated with known methods that use single (usually short) ESTS. ANY88304-Y48456 represent peptides encoded by the expressed sequence tags described in the method of the invention
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Sequence 67 AA;

ô Length 67; 0; Indels 100.0%; Score 19; DB 2; L 100.0%; Pred. No. 9.4e+02; cive 0; Mismatches 0; Query Match Best Local Similarity luv... 4; Conservative 1 VAEF 4

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Gaps

18 VAEF 21

ESULT 75

ABP31047 standard; protein; 68 AA.

ABP31047;

(first entry) 08-JUL-2002 Human ORF20 protein, SEQ ID NO:40.

Human; ORF; open reading frame; ORFX; drug screening; diagnosis; disease monitoring; cytokine; cell proliferation; cell differentiation; lamenacopoiseis regulation; lassue growth; angiogenesis; activin; inhibin; chemotactic; chemokinetic; haemostatic; thrombolytic; tumour inhibition; bodily characteristic; fertility; behaviour; cancer; proliferative disorder; neurological disorder; cardiovascular disease; immune system disorder; organ transplantation; tissue growth disorder; tissue regeneration disorder; diabetes mellitus; hypothyroidism; cholesterol ester storage disease; infection; vulnerary; vasotropic; antipsoriatic; antidabetic; cycostatic; nootropic; antipsoriatic; antidabetic; cycostatic; nootropic; cardiant; hypotensive; antitherosclerotic; anticolamatory; immunomodulator; dermatological; analgesic; virucide; antibacterial; fungicide.

WO200190366-A2.

29-NOV-2001,

24-MAY-2001; 2001WO-US017076.

24-MAY-2000; 2000US-0206690P.

(CURA-) CURAGEN CORP.

Leach MD, Shimkets RA;

WPI; 2002-106200/14. N-PSDB; ABN75073. Novel human polypeptides and polynuclectides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and disorders related to organ transplantation

Claim 10; Page 280; 2508pp; English.

Sequences ABP31028-ABP35561 represent 4534 novel human proteins designated ORF (open reading frame) 1-4534, and sequences ABN75054-ABN79587 represent cDNAs encoding them. The invention also encompasses 

polypeptides at least 80% identical to the ORFI-ORF4534 (collectively referred to as ORFX) proteins, polymucleotides at least 85% identical to the ORFX uncleorides at least 85% identical to the ORFX mucleorides, the recombinant production of ORFX proteins, antibodies and polymucleotides, the recombinant production of ORFX proteins, antibodies and polymucleotides, the recombinant production of ORFX proteins, antibodies and polympeptides, methods of screening for modulators of ORFX expression or activity, and methods of screening individuals for a predisposition to an company of polympeptides activities, such as cytokine, cell proliferation, immune modulation, harmatopoiesis regulation, change of biological activities, such as cytokine, cell proliferation, chemokinetic activity, harmane modulation activity, thrombolytic activity, receptor/ligand, antiinfammatory activity, thrombolytic activity, chemokactic/conduction antiinfammatory activity, thrombolytic activity, and may also be involved in the determination of bodily characteristics, fertility and behaviour. ORRY proteins, other proliferative disorders such as psoriasis and antibodies may be used in the treatment of cancers, nucleic acids and antibodies may be used in the treatment of cancers, corber proliferative disorders such as sporiasis and antisporteins, corper proliferative disorders such as psoriasis and antisporteins, diseases, immune system disorders, disorders related to organ ransphantation, disorders of tissue growth and regeneration, diseases such as epilepsy and Alzheimer's disease, corpers, activity, and may also be used as a source of primers and probes, in the detection of ORFX genomic sequences; in genetic diagnosis, and in frue screening, and in drug screening, the function and/or activity of ORFX protein, and in drug screening, the ORFX proteins may also be used as municogns to generate specific and monitoring of ORFX-sesociated diseases cancer and monitoring of ORFX proteins are useful for studying the function are activity of ORFX protei Sequence 68 AA; 888888888888888888888888888888888888

ö 100.0%; Score 19; DB 5; Length 68; 100.0%; Pred. No. 9.6e+02; 0; Indels 0; Mismatches 

1 VAEF 4 3 VAEF 6 Š 셤 Search completed: May 24, 2004, 17:38:06 Job time : 42.4286 secs

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GenCore version 5.1.6
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M protein - protein search, using sw model

May 24, 2004, 17:32:13 ; Search time 10 Seconds (without alignments) 38.477 Million cell updates/sec

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US-09-594-978A-2 19

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ost-processing: Minimum Match 0% Maximum Match 100% Listing first 1000 summaries

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1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* atabase :

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C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: B85745
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
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Cipecies: Bacillus brevis
Cipaces 10-741-1992 #sequence_revision 10-741-1992 #text_change 15-Oct-1999
Cipacesion: Aga375; 139873
B;Ito, K.; Udaka, S.; Yamagata, H.
J. Bacteriol, 174, 2281-2287, 1992
J. Bacteriol, 174, 2281-2287, 1992
A;Ttle: Cloning, characterization, and inactivation of the Bacillus brevis lon gene.
A;Reference number: A42375; MUID:92202157; PMID:1551846
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C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
C;Accession: E64618
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-52 <ITO>
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 18-Feb-1994 #sequence_revision 19-Apr-1996 #text_change 16-Feb-1997
C;Accession: 539049
R;Lutz, F.; Mohr, M.; Grimmig, M.; Leidolf, R.; Linder, D.
R;Lutz, F.; Mohr, M.; Grimmig, M.; Leidolf, R.; Linder, D.
A;Title: Pseudomonas aeruginosa cytotoxin-binding protein in rabbit erythrocyte membrane
A;Reference number: 539049; MUID:94039134; PMID:7693466
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"Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999

"JAccession: 664625

"Jaccession: 67, Periavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.

Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne

"Jaccession, S.; Loftus, B.; Richardson, D.; Weidman, J.M.; Fujil, C.; Bowman, C.; Watthey, L.

"Atuthors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.

"Atuthors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.

"Atuthors: Wallin, E.; Mayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.

"Atuthors: Preliminary; nucleic acid sequence not shown; translation not shown

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"Attenduss. 1-30 -TOM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 19; DB 2; Length 20; 100.0%; Pred. No. 52; cive 0; Mismatches 0; Indels
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88;
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4; Conservative

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Query Match Best Local Similarity Matches 4; Conserv

4,Status: preliminary 4,Molecule type: protein 4,Residues: 1-20 <LUT>

Score 19; Pred. No.

100.0%;

Query Match Best Local Similarity

**ALIGNMENTS** 

T05838 G71308 A69312

T13048 S31816 G96498

A10147 A91038 AF0808 A87516 D85882

B85045 Z2BPA4 S52990 G84787

T04187 TVHUMB S23457

**T25551** 

100.

549849 H65013

7755 7759 7763 7768 7768 7778

H82367

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R.Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.P.; Kerlavage, A.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodsk, A.; Kelley, J.M.; Weidman, J.D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, C.A; Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, C.A; Reference number: Actoon mullipsisson and assembly of Haemophilus influenzae Rd. A;Accession: G64007
A;Accession: G70007
A;Accession:
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C;Species: Salmo salar (Atlantic salmon)
C;Species: Salmo salar (Atlantic salmon)
C;Actession: 151350
C;Accession: 151350
R;Kvingedal, A.M.
Gene 150, 335-339, 1994
A;Title: Characterization of the 5' region of the Atlantic salmon (Salmo salar) transferm
A;Reference number: 151350; WID:95121925; PMID:7821802
A;Accession: 151350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:U32728; GB:L42023; NID:g1573425; PIDN:AAC22109.1; PID:g1573437; T1
                                                                                                                                                                                                                                                                            C;Species: Streptomyces sp.
C;Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 20-Sep-1999
C;Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 20-Sep-1999
C;Accession: JG4002
R;Arisawa, A.; Tsunekawa, H.; Okamura, K.; Okamoto, R.
R;Arisawa, A.; Tsunekawa, H.; Okamura, K.; Okamoto, R.
R;Arisawa, A.; Tsunekawa, H.; Okamura, R.; Okamoto, R.
A;Title: Nucleotide sequence analysis of the carbomycin biosynthetic genes including the A;Reference number: JC4001; MJID:95290751; PMID:7772821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cassette homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Readidues: 1-63 ARIL>
A;Cross-references: DDB:D30759; NID:G551628; PIDN:BAA06419.1; PID:d1006989;
A;Note: the source was designated as Streptomyces thermotolerans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein HI0451 - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999
C;Accession: 664007
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Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 19; DB 2; Length 63; 100.0%; Pred. No. 1.7e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;1-55/Domain: ATP-binding cassette homology (fragment) <ABC2>
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Matches 4; Conservative
12 VAEF 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Keywords: ATP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C, Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Klenk, H.P.; Claycon, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F. 3lode, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Ature 390, 364-370, 1997. Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Ath, H.O.; Woese, C.R.; Venter, J.C. Triand, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Ath, H.O.; Woese, C.R.; Venter, J.C. Triand, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Ath, H.O.; Woese, C.R.; Venter, J.C. Triand, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Attence number: A69250; WuID:98049343; PMID:9389475
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Fraser, C.M.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin Son, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDc ason, D.; Weidman, J.; Smith, H.O.; Venter, J.C.

Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.

Reference number: A71250; WUID:98332770; PMID:9665876
                                                                                    ;Cross-references: GB:AE005174; NID:g12515374; PIDN:AAG56425.1; GSPDB:GN00145; UMGP:Z23
;Experimental source: strain O157:H7, substrain BDL933
;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cross-references: GB:AE001028; GB:AE000782; NID:g2689351; PIDN:AAB90157.1; PID:g26495d
Superfamily: Methanococcus jannaschii hypothetical protein MJ0975
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Experimental source: strain Nichols
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nnserved hypothetical protein AF1090 - Archaeoglobus fulgidus
Species: Archaeoglobus fulgidus
Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 11-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  robable preprotein translocase subunit (secE) - syphilis spirochete; Species: Treponema pallidum subsp. pallidum (syphilis spirochete); Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                            Gapa
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100.0%; Score 19; DB 2; Length 59;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                         100.0%; Score 19; DB 2; Length 54; 100.0%; Pred. No. 1.5e+02; ive 0; Mismatches 0; Indels
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100.0%; Score 19; DB 2; Length 59;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 4; Conservative
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Molecule type: DNA
Residues: 1-54 <STO>
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Residues: 1-59 <CO
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Gene: TP0235
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hypothetical protein BH2182 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: F83922
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res 28, 4317-4313, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
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C.Spsciese: Caenorhabditis elegans
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C.Accession: T27605
                                                                                                                                                                                                                            C;Species: Chlorella virus PBCV-1
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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A;Experimental source: specific host Chlorella strain NC64A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cross-references: EMBL:U40802; PIDN:AAA81506.1; CESP:ZC477.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ribu, Z. submitted to the EMBL Data Library, November 1995 A;Description: The sequence of C. elegans cosmid ZC477. A;Reference number: Z20392 A;Reference number: Z20392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 19; DB 2; I 100.0%; Pred. No. 2.2e+02; ive 0; Mismatches 0;
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100.0%; Pred. No. 2.2e+02;
                                                                                                                                                                                              hypothetical protein A532L - Chlorella virus PBCV-1
                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-79 <GRA>
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A;Molecule type: DNA
A;Residues: 1-79 <DUZ>
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                                                                                                                                                                                                                                                                   C.Accession: T18034
R.Graves, M.V.; Van Etten, J.L.
submitted to the EMEL Data Library, May 1999
A.Reference number: Z18806
A.Accession: T18034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0
Matches 4; Conservative
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Matches 4; Conservative
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A;Molecule type: DNA
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Gene: CESP:ZC477.6
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                                            5 VAEF
     1 VAEF
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Nacession: D97045

Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, in Dally, M.J.; Bennett, G.N.; Xoonin, E.V.; Smith, D.R.

Bacteriol. 183, 4833-4838, 2001

NTitle: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A:Reference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         );Species: phage 186
);Date: 28-May-1993 #sequence_revision 28-May-1993 #text_change 17-Mar-1999
);Date: 28-May-1993 #sequence_revision 28-May-1993 #text_change 17-Mar-1999
);Kacession: S07277; S25273
);Kalionis, B.; Dodd, I.B.; Egan, J.B.
);Kalionis, B.; Dodd, I.B.; Egan, J.B.
);Kalionis, B.; Lonton 20, Egene expression in the P2-related template coliphages. III. DNA sequiper: S07277; MUID:87112711; PMID:3806670
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ol. Microbiol. 6, 2643-26560, 1992
filtle: Control of gene expression in the temperate coliphage 186. X. The cl repressor; Reference number: S25273; MUID:93078618; PMID:1447973
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4,Molecule type: DNA
4,Residues: 1-74 «KUR»
4,Cross-references: GB.AE001437; PIDN:AAK79151.1; PID:g15024100; GSPDB:GN00168
4,Experimental source: Clostridium acetobutylicum ATCC824
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                                                                                                                                                                                                                                                                                  Gaps
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A;Residues: 1-64 <KVI>
A;Cross-references: GB:L26909; NID:g598395; PIDN:AAC42221.1; PID:g598396
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ypothetical protein CAC1179 [imported] - Clostridium acetobutylicum; Species: Clostridium acetobutylicum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h Similarity 100.0%; Score 19; DB 2; Length 75; Similarity 100.0%; Pred. No. 2.1e+02; 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                         Length 64;
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                                                                                                                                      A;Introns: 14/1
C;Superfamily: transferrin; transferrin repeat homology
                                                                                                                                                                                                                      Query Match
100.0%; Score 19; DB 2; I
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0;
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Best Local Similarity
Matches 4; Conserv
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Residues: 1-75 <KAL>
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Residues: 1-75 <DIB>
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                                                                                                           A;Gene: Tf
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ransferrin - sheep (fragments)

SCULT 16

38 VAĖF 41

1 VAEF 4

Gene: BH2182

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hypothetical protein ypjB [imported] - Lactococcus lactis subsp. lactis (strain IL1403) C;Species: Lactococcus lactis subsp. lactis C,Species: Lactococcus lactis subsp. lactis C,Date: 32-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001 C;Accession: F86818 R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlic Genome Res. 11, 731-753, 2001 A;Atille: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss; A;Reference number: A86625; MUID:21235186; PMID:11337471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Yersinia pestis
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T15018
C;Accession: T15018
R;Lindler, L.B.; Plano, G.V.; Burland, V.; Mayhew, G.F.; Blattner, F.R.
Infect. Immun. 66, 5731-5742, 1998
A;Title: Complete DNA sequence and detailed analysis of the Yersinia pestis KIMS plasmid
A;Reference number: Z18268; WUID:99043898; PMID:9826348
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C;Genetics:
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A;Experimental source: strain IL1403
                                          Gaps
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                                          Indels
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100.0%; Score 19; DB 2; I
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0;
       100.0%; Pred. No. 2.5e+02; iive 0; Mismatches 0;
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       Best Local Similarity 100.
Matches 4; Conservative
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Matches 4; Conserv
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A;Molecule type: DNA
A;Residues: 1-89 <STO>
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                                                                                                                                                      12 VAEF 15
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                                                                                                         1 VAEF 4
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Superfamily: Escherichia coli ribosomal protein S15; eubacterial ribosomal protein S15
23-89/Domain: eubacterial ribosomal protein S15 homology <ES15>
;Residues: 1-84 <STO>
;Cross-references: GB:AP001514; GB:BA000004; NID:g10174613; PIDN:BAB05901.1; GSPDB:GN00
;Experimental source: strain C-125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ibosomal protein S15 - Haemophilus influenzae (strain Rd KW20)
Species: Haemophilus influenzae
Date: 10-Sep-1999 #text_change 10-Sep-1999
Accession: H64116; E64126
F10-Sep-1999
F1eischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchmann, J.L.; Geoghagen, N.S.M.; Sience 269, 496-512, 1995
Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
Accession: H64116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cross-references: GB:U32812, GB:L42023; NID:91574784; PIDN:AAC22973.1; PID:91574788; Note: named as homolog to a protein from Escherichia coli Accession: E64125
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Cross-references: GB:U32825; GB:L42023; NID:g1574307; PIDN:AAC23117.1; PID:g1574309;
Note: named by homology to a protein from Escherichia coli
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'Date: 20-Sep-1991 #sequence_revision 20-Sep-1991 #text_change 05-Dec-1997
'Addession: A38725,
'Biol. Chem. 266, 6201-6208, 1991
'Title: The distribution of cerebral expression of the transferrin gene is 'Afecression: A38725, MUID:91177867; PMID:1848850
'Status: preliminary
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Residues: 1-89 <TIG1>
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                                                                                                                                                                                                    Length 84;
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                                                                                                                                                                                                                                                                0; Indels
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.Superfamily: transferrin; transferrin repeat homology
.Keywords: duplication
                                                                                                                                                                                             Query Match
100.0%; Score 19; DB 2; L
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0;
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4; Conservative

VAEF 16

13

Molecule type: DNA

Query Match

1 VAEF 4

Query Match Best Local Similarity

Molecule type: mRNA Residues: 1-87 <TUA>

Gaps

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RESULT 25
C64490
hypothetical protein MJ1524 - Methanococcus jannaschii
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A, Experimental source: strain PAO1
C,Genetics:
A,Gene: PA3202
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Matches 4; Conservative
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Best Local Similarity
Matches 4; Conserv
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A Molecule type: DNA
A Residues: 1-101 < KUR>
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4;Molecule type: DNA
4;Residues: 1-99 <STO>
4;Cross-references: GB:AE004744; GB:AE004091; NID:g9949317; PIDN:AAG06590.1; GSPDB:GN001
Science 294, 2317-2323, 2001
A,Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         conserved hypothetical protein lmo2579 [imported] - Listeria monocytogenes (strain EGD-
                                                                   ster, E.W.
Ayfille: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AB3053
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4,Experimental source: strain EGD-e
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A;Experimental source: strain C58 (Dupont)
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Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity
Matches 4; Conserv
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1, Molecule type: DNA
1, Residues: 1-97 <GLA>
                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-96 <KUR>
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C;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Accession: H90297
S;She, O, Singh, R.K.; Confalontir, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chandon, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
A;Bescription: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: H90297
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C;Species: Methanococcus maripaludis
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
C;Date: 20-Sep-1999 #sequence_revision 3.7. Leigh, J.A.
B;Ressler, P.S.; McLarnan, J.; Leigh, J.A.
J. Bacteriol. 179, S41-543, 1997
A;Title: Nitrogenase phylogeny and the molybdenum dependence of nitrogen fixation in Met
A;Reference number: Z16944, MUID:97144542; PMID:8990309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: GB: AE006641; NID: 913814625; PIDN: AAK41639.1; GSPDB: GN00155
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-106 <-KES>
A;Cross-references: EMBL:U75887; NID:g1666882; PIDN:AAC45519.1; PID:g1666890
A;Experimental source: strain JJ
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   Length 99;
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Query Match
100.0%; Score 19; DB 2; I
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 2.8e+02;
iive 0; Mismatches 0;
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Gaps

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Gaps

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Page 13

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A;Experimental source: specific host Chlorella strain NC64
C;Genetics:
A;Gene: A92L
C;Superfamily: Chlorella virus PBCV-1 hypothetical protein A92L
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;Experimental source: strain H37Rv
    'Defection of the control of contr
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; Cole, S. T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S. (Cole, S. T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S. (Cone, S. T.; Brosch, R.; Peulin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. ature 393, 537-544, 1998

ature 393, 537-544, 1998

Authoris: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

fAuthoris: Gares, R.; Sulston, G. Mycobacterium tuberculosis from the complete genome increase on muber: A70500; MUID:98295987; PMID:9634230

fAccession: E70949

scatus: preliminary; nucleic acid sequence not shown; translation not shown

Molecule type: DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cross-references: GB:U67593; GB:L77117; NID:g2826427; PIDN:AAB99550.1; PID:g1592154;
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Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ypochetical protein A92L - Chlorella virus PBCV-1; Species: Chlorella virus PBCV-1; Species: Chlorella virus PBCV-1; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000; Accession: T175B Etten, J.L.; Graves, M.V.; Van Etten, J.L.
ubmitted to the EMBL Data Library, May 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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;Residues: 1-111 <GRA>
;Cross-references: EMBL:U42580; NID:g4028896; PIDN:AAC96460.1
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Superfamily: uncharacterized conserved protein MJ1524
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Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity
Matches 4; Conserva
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Cjaccesion: B83431
Ristover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br Addan, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, i. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Tile: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathon A;Reference number: A82950; MUD:20437337; PMID:10984043
A;Accession: B83431
A;Accession: B83431
A;Accession: preliminary
A;Accellering type: DNA
A;Residues: 1-112 < GTO>
A;Cross-references: GB:AE004598; GB:AE004091; NID:g9947687; PIDN:AAG05111.1; GSPDB:GN001
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R;Hofstead, S.J.; Matson, J.A.; Malacko, A.R.; Marquardt, H.
A. Antibiot. 45, 1250-1254, 1992
A;Fitle: Kedarcidin, a new chromoprotein antitumor antibiotic. II. Isolation, purification, A;Reference number: A55872; MUID:93015257; PMID:1399845
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Submitted to the Brookhaven Protein Data Bank, June 1994

A;Reference number: A52519; PDB:1AkP

A;Concents: annotation; conformation and disulfide bond assignments by (1)H-NMR, residues

A;Concents: annotation; conformation and disulfide bond assignments by (1)H-NMR, residues

R;Zein, N; Csaszza, A,W.; Doyle, T.W.; Leet, J.E.; Schroeder, D.R.; Solomon, W.; Nadler,

Proc. Natl. Acad. Sci. U.S.A. 90, 8009-8012, 1993

A;Title: Selective proteolytic activity of the antitumor agent kedarcidin.

A;Reference number: A58601; MUID:93376732; PMID:8367457

A;Concents: annotation; protein activity

C;Superfamily: macromomycin
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A;Residues: 1-114 4GDF.
A;Note: sequence extracted from NCBI backbone (NCBIP:118354)
R;Constantine, K.L.; Colson, K.L.; Wittekind, M.; Friedrichs, M.S.; Zein, N.; Tuttle, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: pscI; PA1722
C;Superfamily: Yersinia enterocolitica plasmid pYV virC-region hypothetical protein yscI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  type III export protein PscI PA1722 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
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C.Species: Streptoalloteichus sp.
A.Yariety: strain LSBS-6 (ATCC 53650)
C.Date: 21-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 15-Sep-2000
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Length 111;
Query Match 100.0%; Score 19; DB 2; Length 11 Best Local Similarity 100.0%; Pred. No. 3.1e+02; Matches 4; Conservative 0; Mismatches 0; Indels
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C;Accession: F95327
R;Barnett, M.J; Fisher. R.F; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows
; Kanlan, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C
proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A;Aftle: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot
A;Reference number: A95262; MUID:21396509; PMID:11481432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lypothetical protein SMa0974 [imported] - Sinorhizobium meliloti (strain 1021) magaplasm
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A;Experimental source: strain 1021, megaplasmid pSymA
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
                               C,Accession: A01608
R;Hobart, P.M.; Shen, L.P.; Crawford, R.; Pictet, R.L.; Rutter, W.J.
Science 210, 1360-1363, 1980
A;Title: Comparison of the nucleic acid sequence of anglerfish and mammalian insulin mR1
A;Reference number: A94254; MUID:81056434; PMID:7001633
                                                                                                                                                                                               A; Accession. A01608
A; Molecule type: mRNA
A; Molecule type: mlsulin
C; Superfamily: insulin
C; Superfamily: predicted <SIG>
C; Superfamily: insulin chain B #status predicted <BCH>
F; 25-54, Domain: signal sequence #status predicted <BCH>
F; 25-54, Domain: onnecting peptide #status predicted <CPEP>
F; 56-93, Domain: insulin chain A #status predicted <APH>
F; 56-116, Domain: insulin chain A #status predicted <APH>
F; 51-102, 44-115, 101-106/Disulfide bonds: #status predicted
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C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-May-2000
C;Accession: T48682
S;Poustka, A.; Wellenreuther, R.; Mewes, H.W.; Weil, B.; Wiemann, S. submitted to the Protein Sequence Database, April 2000
A;Reference number: Z24535
A;Accession: T48682
A;Status: preliminary
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C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
31-Mar-1981 #sequence_revision 31-Mar-1981 #text_change 16-Jul-1999
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100.0%; Pred. No. 3.3e+02;
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A,Residues: 1-118 <AAA>
A,Cross-references: EMBL:AL353932
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Laga 4; Conservative
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Best Local Similarity
Matches 4; Conserv?
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A;Note: DKFZp761N05121.1
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A;Molecule type: DNA
A;Residues: 1-119 <KUR>
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C,Species: Pyrococcus abyssi
C,Species: Pyrococcus abyssi
C,Saccession: D7518
R;anonymous, Genoscope
R;acfarence number: A7501
A;Accession: Profilminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-115 cKAW>
A;Residues: 1-115 cKAW>
A;Cross-references: GB:AJ248283; GB:AL096836; NID:g5457433; PIDN:CAB49195.1; PID:e151508
A;Experimental source: strain Orsay
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Agrocession: D97414  

Agrocession: D97414  

And Interpretation of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A; Reference number: A97359; MUID:2160851; PMID:11743194
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Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0;
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100.0%; Score 19; DB 2; I
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0;
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100.0%; Score 19; DB 2; I
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0;
          C;Keywords: antibiotic; pigment binding F;37-47,88-95/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               insulin precursor - American goosefish
C;Species: Lophius americanus (American goosefish)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: AGR C 804
A;Map position: circular chromosome
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4, Molecule type: DNA
4, Residues: 1-114 < KUR>
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                                                                                                                                                                                                                                                                                                           49 VAEF 52
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". Expecies: Mycobacterium tuberculosis (strain H37RV)
C; Species: Mycobacterium tuberculosis
C; Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C; Accession: D70790
R; Colo. S. T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome & A; Reference number: A70500; MUID:98295987; PMID:9634230
A; Accession: D70790
A; Residues: preliminary; nucleic acid sequence not shown; translation not shown
A; Residues: 1-125 COL>
A; COSB-Infaronon
       ki, S.; Church, G.M.; Daniels, C.J.; Mang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N. Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. A. Bacteriol. 19, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct: A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: B69129
A;Accession: Breliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-125 <MTH>
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A;Experimental source: serotype O2, strain NCTC 11168
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AL022121; GB:AL123456; NID:g3261559; PIDN:CAA17997.1; PID:e1264535
A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R.Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.W.; Churcher, C.; Basham, D.; Chilling C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell Mature 403, 665-668, 2000
A.Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hype A;Reference number: A81250; MUID:20150912; PMID:10688204
                                                                                                                                                                                                                                 A;Cross-references: GB:AE000810; GB:AE000666; NID:g2621277; PIDN:AAB84740.1; PID:g262128:
A;Experimental source: strain Delta H
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C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C;Accession: B81368
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Similarity 100.0%; Score 19; DB 2; I
Similarity 100.0%; Pred. No. 3.5e+02;
4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                A,Gene: MTH234
C,Superfamily: 4-carboxymuconolactone decarboxylase
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A,Gene: Rv3675
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; Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, ebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.; Fitter The composite genome of the legume symbiont Sinorhizobium meliloti.
;Reference number: A96039; MUID:21368234; PMID:11474104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amma-carboxymuconolactone decarboxylase - Methanobacterium thermoautotrophicum;Species: Methanobacterium thermoautotrophicum;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Jun-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              onjugal transfer protein XFa0006 [imported] - Xylella fastidiosa (strain 9a5c)
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;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
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100.0%; Pred. No. 3.4e+02;
.ive 0; Mismatches 0; Indels
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Best Local Similarity 100...
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Best Local Similarity luv...
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R.Crossman, M.W.; Hauft, S.M.; Gordon, J.I.
G. Cell Biol. 126, 1547-1564, 1994
A.Fittle: The mouse ileal lipid-binding protein gene: a model for studying axial patterni A;Reference number: A54797; WUID:94375529; PMID:8089185
A.Accession: A54797
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C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: D72348
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
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A/Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A/Reference number: A72200; MUID:99287316; PMID:10360571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable cathepsin B-like cysteine proteinase (EC 3.4.22.-) T15B16.17b - Arabidopsis tha
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A;Nolecule type: DNA
A;Residues: 1-129 <STO:
A;Cosidues: L-129 <STO:
A;Cosidues: EMBL:AF104919; NID:93859590; PIDN:AAC72873.1; PID:93859607
A;Experimental source: cultivar Columbia
                                                                                         ileal lipid-binding protein - mouse
Species: Mus musculus (house mouse)
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 05-Nov-1999
C;Accession: A54797
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C,Date: 26-Peb-1999 #sequence_revision 26-Peb-1999 #text_change 22-Jun-1999
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A,Molecule type: mRNA
A,Residues: 1-128 <CRC>
A,Residues: GB:U00938; NID:g507143; PIDN:AAC27352.1; PID:g507144
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100.0%; Score 19; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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R;Stoneking, T.; Smith, R.
submitted to the EMBL Data Library, November 1998
A;Pescription: The sequence of A. thaliana T15B16.
A;Reference number: Z14488
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C;Keywords: cysteine proteinase; hydrolase
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A;Introns: 23/1; 81/3; 111/3
C;Superfamily: myelin P2 protein
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Best Local Similarity 100.0
Thes 4; Conservative
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A,Introns: 26/3; 44/3; 71/3
A,Note: T15816.17b
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%;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; May, C.; Schlueter, T.; Simoes, N.; Titerez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Reference number: AB1077; MUID:21537279; PMID:11679669
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A; Reference number: A70500; MUID:98295987; PMID:9634230
A; Residues: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA A; Residues: 1-127 < COL>
A; Residues: 1-127 < COL>
A; Residues: BBAAD22121; GB:AL123456; NID:g3261559; PIDN:CAA18069.1; PID:g296017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lypothetical protein lin2399 [imported] - Listeria innocua (strain Clip11262)
                                                                                                                                                                                                                                                                                                                                                                                                                                    Species: Mycobacterium tuberculosis
| Bate: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Species: Listeria innocua
Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein Rv3747 - Mycobacterium tuberculosis (strain H37RV)
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                                                           100.0%; Score 19; DB 2; Length 126; 100.0%; Pred. No. 3.6e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h. Similarity 100.0%; Score 19; DB 2; Length 127; Similarity 100.0%; Pred. No. 3.6e+02; 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 127;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 19; DB 2; 100.0%; Pred. No. 3.6e+02; iive 0; Mismatches 0;
                                                    Query Match
Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity
Matches 4; Conserv
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4, Molecule type: DNA
4, Residues: 1-127 <GLA>
                                                                                                                                                                                                                                                 83 VAEF 86
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A;Gene: Cj0939c
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conserved hypothetical protein YPO1120 [imported] - Yersinia pestis (strain C092)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C;Date: 01-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C;Date: 02-Nov-2001
C;Date: 03-Nov-2001
C;Dat
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C;Species: Deinococcus radiodurans
C;Species: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C;Accession: H75623
R;White, O.; Esten, J.A.; Heidelberg, J.F.; Hickey, B.K.; Peterson, J.D.; Dodson, R.J.; A.; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma}S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. Dana Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anak A;Reference number: AB1807; WUID:21595285; PMID:11759840
                                                                                                                                                                                                                              hypothetical protein alr1525 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AG1996
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A;Status: preliminary
A;Molecule type: DNA
A;Mosidues: 1-133 «KUR»
A;Cross-references: GB:AL590842; PIDN:CAC89963.1; PID:g15979187; GSPDB:GN00175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-13 <KUS
A;Crosa-references: GB:BA000019; PIDN:BAB77891.1; PID:g17135345; GSPDB:GN00179
A;Experimental source: strain PCC 7120
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Best Local Similarity 100.0%; Score 19; DB 2; Length 132;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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C;Superfamily: 15.5K protein (tolAB operon 5' region)
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A;Gene: alr1525
C;Superfamily: rbcX protein
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     84
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     81 VAEF
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Date: 20-Aug-1999 #text_change 06-Jan-2003

Accession: G75208

Anonymous, Genoscope

Anonymous, Genoscope

Anonymous, Genoscope

Appendix to the EMBL Data Library, July 1999

Bescription: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru-

Reference number: A75001

Accession: G77208

Status: preliminary

Molecule type: DNA

Residues: 1-131 < KAWA

Residues: 1-131 < KAWA

Accession: G75208

Status: Streininary

Accession: G75208

Status: BNA

Accession: G75208

A
Accession: D72348
Status: preliminary
Modelle type: DNA
Modelle type: DNA
Modelle type: DNA
Cross-references: GB:AE001739; GB:AE000512; NID:g4981176; PIDN:AAD35739.1; PID:g498117
Experimental source: strain MSB8
Genetics: TM0655
Superfamily: conserved hypothetical protein MJ0315
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1. Species: Anabaena sp.
1. Date: 28. Aug-1985 #sequence_revision 07-Oct-1994 #text_change 13-Sep-1998
1. Date: 28. Aug-198270
1. Larimer, F.W.; Soper, T.S.
1. Larimer, F.W.; Soper, T.S.
1. Soper, T.S.
1. Soper, T.S.
1. Title: Overproduction of Anabaena 7120 ribulose-bisphosphate carboxylase/oxygenase in Reference number: JQ2270; MUID:93231541; PMID:8472962
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100.0%; Score 19; DB 2; Length 131;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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100.0%; Score 19; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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'Superfamily: uncharacterized conserved protein
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Residues: 1-132 <LAR>
Spesives: references: DDBJ:J01540
Byperimental source: strain 7120
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Cispecies: Escherichia coli

Cipate: 18-Unl-2014 Haequence_revision 18-Unl-2001 #text_change 03-Aug-2001

Cipate: 18-Unl-2001 #aequence_revision 18-Unl-2001 #text_change 03-Aug-2001

Cipate: 18-Unl-2001 #aequence_revision 18-Unl-2001 #text_change 03-Aug-2001

Cipate: 18-Unl-2001 #aequence_revision 18-Unl-2001 #text_change 03-Aug-2001

RiHayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.

Basawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

A;Reference number: A99629; MUID:21156231; PMID:11258796

A;Reference number: A99629; MUID:21156231; PMID:11258796

A;Residue: preliminary

A;Molecule type: DNA

A;Residues: 1-134 <HAY>
A, Actual States and Sequence not shown, translation not shown
A, Molecule type: DNA
A, Molecule type: DNA
A, Molecule type: DNA
A, Molecule type: DNA
A, Residues: 1-134 < RLAT>
A, Experimental source: GB:AB000177, GB:U00096, NID:g1786955, PIDN:AAC73830.1; PID:g1786957;
A, Experimental source: strain K-12, substrain MG1655
C, Comment: This is one of the proteins, encoded by the fii-tolAB gene cluster, that is is Genetics:
A, Gene: ybgC
A, Map position: 17 min
A, Start codon: GTG
C, Superfamily: 15.5K protein (tolAB operon 5' region)
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A;Experimental source: strain 0157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ypothetical protein ybgC [imported] - Escherichia coli (strain 0157:H7, substrain EDL93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross references: GB:BA000007; PIDN:BAB34194.1; PID:g13360230; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
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C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Date: 10-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: D85576
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, lature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 19; DB 2; Length 134; 100.0%; Pred. No. 3.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
100.0%; Score 19; DB 1; 1
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0;
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A;Gene: ECs0771
C;Superfamily: 15.5K protein (tolAB operon 5' region)
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Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129 VAEF 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  129 VAEF 132
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C.Species: Escherichia coli
C.Species: Bscherichia coli
C.Date: 15-Oct-1982 #sequence_revision 30-Jun-1988 #text_change 01-Mar-2002
C.Accession: ASSB0, G64809
B.Sun, T.P.; Webster, R.E.
J. Bacteriol. 169, 2667-2674, 1987
A.Title: Nucleotide sequence of a gene cluster involved in entry of E colicins and single A.Reference number: A91835; MUD:87222192; PMID:3294803
A.Rocession: A25980
A.Rocession: A25980
A.Rocession: A25980
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A.Rocession: A25980
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A; Cross-references: GB:M16489; NID:g148021; PIDN:AAA83918.1; PID:g1128977
A; Cross-reference: GB:M16489; NID:g148021; PIDN:AAA83918.1; PID:g1128977
B; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Coscience, D.G.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A; Title: The complete genome sequence of Escherichia coli K-12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R. No. W. Shukla, H.D.; Lasky, S. P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo Jung, K.H.; Alam, M.; Freitas, T. Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
Proc. Natl. Acad. Sci. Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li A; Itle: Genome sequence of Halobacterium species NRC-1.

A; Reference number: A64160; MUID:20504483; PMID:11016950
                                                                                                                                                                                                                    A;Cross-references: GB:AE001826; NID:g6460827; PIDN:AAF12590.1; PID:g6460886; TIGR:DRB0C
A;Experimental source: strain R1
               Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.; Reference number: A75250; MUID:20036896; PMID:10567266
; Accession: H75623
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|Cross-references: GB:AE004437; NID:g10580221; PIDN:AAG19133.1; GSPDB:GN00138
|Genetics:
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pate: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
Accession: A84221
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A;Reference number: A64720; MUID:97426617; PMID:9278503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 19; DB 2; Lengtn 13. Pred. No. 3.8e+02;
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Best Local Similarity 100.0%;
Matches 4; Conservative 0
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4, Genome: plasmid
4, Note: plasmid MP1
                                                                                                                 A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-133 <WHI>
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D.J.; Mayhew K.; Apodaca,

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Absorbation synthase beta subunit - Methanobacterium thermoautotrophicum (strain Delta H) c.species: Methanobacterium thermoautotrophicum (species: Methanobacterium thermoautotrophicum (species: Methanobacterium thermoautotrophicum (species: Methanobacterium thermoautotrophicum (species: Os-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 05-May-2000 (;Date: Os-Dec-1997 #sec-1997 #sec-1997 #text_change 05-May-2000 R.; Date: 
                                                                                     Rybarkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling C.W.; Quall, M.; Rajandream, M.A.; Rutherford, K.M.; VanVllet, A.; Whitehead, S.; Barrel. Nature 403, 665-668, 2000
Affile: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hypi A;Reference number: A81250; WUID:20150912; PMID:10688204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liagellar basal-body rod protein FlgC VC2199 [imported] - Vibrio cholerae (strain N16961 C;Species: Vibrio cholerae (pate: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001 C;Accession: F82106 C;Accession: F82106 R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P. I. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000 A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A;Reference number: As2035; MUID:20406833; PMID:10952301
                                                                                                                                                                                                                                                                                                                                                                      A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1.137 PARA.
A.Residues: 1.137 PARA.
A.Stross-references: GB:AL139076; GB:AL111168; NID:g6968128; PIDN:CAB73094.1; PID:g696827:
A.Experimental source: serotype O2, strain NCTC 11168
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A;Experimental source: serogroup O1; strain N16961; biotype El Tor
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C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C;Accession: E81355
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ilarity 100.0%; Pred. No. 3.9e+02;
Conservative 0; Mismatches 0;
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100.0%; Score 19; DB 2; I
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0;
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Matches 4; Conserv
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A.Molecule type: DNA
A.Residues: 1-138 <HEI>
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A,Gene: VC2199
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Species: Symechocystis sp.
Species: Synechocystis sp.
Accession: S76416
Scaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
NA Res. 3, 109-136, 1996
Synechocystis
Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;Status: preliminary
;Molecule type: DNA
;Residues: 1-136 «KAN»
;Cross-references: BMBL:D90915; GB:AB001339; NID:g1653604; PIDN:BAA18545.1; PID:g165363
;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, J., T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Garar, P.
sture 413, 848-852, 2001
;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Title: Complete genome sequence of a miltiple drug resistant Salmonella enterica serow; Reference number: AB0502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    onserved hypothetical protein STY0790 [imported] - Salmonella enterica subsp. enterica ;Species: Salmonella enterica subsp. enterica serovar Typhi ;Note: this species has also been called Salmonella typhi ;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 ;Accession: AD0592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81355
ypothetical protein Cj0829c [imported] - Campylobacter jejuni (strain NCTC 11168)
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                      100.0%; Score 19; DB 2; Length 134; 100.0%; Pred. No. 3.8e+02; ive 0; Mismatches 0; Indels
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Best Local Similarity 100.
Matches 4; Conservative
                      Query Match
Best Local Similarity 100.
Matches 4; Conservative
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Molecule type: DNA
Residues: 1-134 <PAR>
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STY0790

Genetics:

Query Match

Best Loca Matches

ESULT 55

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Query Match Best Local Similarity 100.

10 VAEF 13

1 VAEF 4

',Status: preliminary
',Molecule type: DNA

;,Genetics:

., Accession: A83975

Accession: A83975

11 VAEF 14

1 VAEF 4

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Best Loc Matches

65 VAEF 68

1 VAEF 4

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C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 21-Jul-2000
C;Accession: H69515
C;Accession: H69515
C;Accession: H69516
C;Accession: H69516
C;Accession: H69517
C;Accession: H69518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cidate: 30-Sep-1993 #Sequence_revision 20-Aug-1994 #text_change 28-May-1999
CiAccession: 302579
Rivertilnyk, E.; Orr, W.; White, T.C.; Iu, B.; Singh, J.
Plant Physiol. 101, 171-177, 1993
A;Title: Characterization of three related low-temperature-regulated cDNAs from winter E A;Reference number: J02279; MUID:94105287; PMID:7904076
A;Accession: J02279
A;Molecule type: mRNA
A;Residues: 1-142 - WRRA
A;Residues: 1-142 - WRRA
A;Cross-references: GB:S66726; NID:9544693; PIDN:AAB29482.1; PID:9544694
C;Comment: This protein is a low-temperature-related protein.
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C;Superfamily: riboflavin synthase beta chain
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                                                                                            Cow-temperature regulated protein BN115 - rape
;/Species: Brassica napus (rape)
;/Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 28-May-1999
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100.0%; Score 19; DB 2; Length 142;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 4e+02;
tive 0; Mismatches 0; Indels
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Best Local Similarity 100.
Matches 4; Conservative
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A; Residues: 1-143 < KLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 VAEF 128
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';Species: Archaeoglobus fulgidus
';Species: Archaeoglobus fulgidus
';Species: Archaeoglobus fulgidus
';Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 24-Nov-1999
';Accession: B69323
';Accession: B69323
';Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
';Klenk, H.P.; Clayton, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
lature 390, 364-370, 1997
';Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
';Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
';Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec
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A, Residues: 1-140 «KLB»
A, Cross-references: GB.AE001064; GB.AE000782; NID:92689387; PIDN:AAB90658.1; PID:9265004
C. Superfamily: Archaeoglobus fulgidus hypothetical protein AF0586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiralocleic Acids Res. 28, 4317-4331, 2000
Ucleic Acids Res. 28, 4317-4331, 2000
Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , Residues: 1-139 <STO>
,/Residues: 1-139 <STO>
,/Cross-references: GB:AP001516; GB:BA000004; NID:g10175192; PIDN:BAB06320.1; GSPDB:GN00
,/Experimental source: strain C-125
"Cross-references: GB:AE000902; GB:AE000666; NID:g2622500; PIDN:AAE85867.1; PID:g262250; Experimental source: strain Delta H
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i, Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pothetical protein BH2601 [imported] - Bacillus halodurans (strain C-125)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Species: Bacillus halodurans
Date: 01-Dec-2000 #sequence revision 01-Dec-2000 #text_change 15-Jun-2001
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100.0%; Score 19; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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:/Superfamily: Bacillus subtilis hypothetical protein ylbD
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Local Similarity 100.0%; Pred. No. 3.9e+02;
hes 4; Conservative 0; Mismatches 0.
                                                                                                                                                                                               100.0%; Score 19; DB 2; I
100.0%; Pred. No. 3.9e+02;
tive 0; Mismatches 0;
                                                                                                   Gene: MTH1390
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DNA Res. 3, 109-136, 1996
A,Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
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Variety: PCC 6803
Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
Accession: 877043
K.; Okumura, B.; Kotani, H.; Tanaka, A.; Assamizu, B.; Nakamura, Y.; Miyajima, N.; K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cross-references: EMBL:AL109949; PIDN:CAB52892.1; GSPDB:GN00070; SCOEDB:SCJ11.07c
Experimental source: strain A3(2)
Comment: A complete transposase sequence can be assembled from three adjacent orfs (PI
                                                                                                                                                                                                                                                                                              obable transposase, truncated section 1 [imported] - Streptomyces coelicolor (fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Accession: B41715
; Kroemer, W. J., Armid, E. .
. Biol. Chem. 266, 24573-24579, 1991
;Title: Halobacterial S9 operon. Three ribosomal protein genes are cotranscribed with
                                                                                                                                                                                                                                                                                                                                                                                                      Æ.
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Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000
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| Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 14-Apr-2003
                                                             Gaps
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Cross-references: GB:M76567; NID:g148775; PIDN:AAA73097.1; PID:g148777
Superfamily: ribosomal protein L13
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        Length 143;
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     100.0%; Score 19; DB 2; I
100.0%; Pred. No. 4.1e+02;
ive 0; Mismatches 0;
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Molecule type: DNA
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Best Local Similarity 100.
Matches 4; Conservative
        Query Match 100.
Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity
Matches 4; Conserv
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Molecule type: DNA
                                                                                                                                                                   10 VAEF 13
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                                                                                                                   1 VAEF 4
                                                                                                                                                                                                                                                                                                                                                                                Accession: T36978
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                                                                                                                                                                                                                                                 SSULT 63
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Cjacession: C84294
Cjacession: C84294
Cjacession: C84294
Ring W W J; Kennedy, S. P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S. Leithauser, B.; Keller, K.: Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablon Jung, K.H.; Alam, M.; Freites, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
Apturbors: Hou, S.; Danniels, C.J.; Dennis, P.P.; Ower, A.D.; Ebhardt, H.; Lowe, T.M.; Life Apturbors: As a Houle Sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A; Reference number: S74322; MUID:97061201; FMID:8905231
A; Accession: S77043
A; Status: nucleid acid sequence not shown; translation not shown
A; Status: nucleid acid sequence not shown; translation not shown
A; Residues: 1.145 < KAN-
A; Residues: 1.145 < KAN-
A; Residues: Efferences: EMBL:D64005; GB:AB001339; NID:g1001779; PIDN:BAA10735.1; PID:g100658
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C; Superfamily: Synechocystis hypothetical protein sl10678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   conserved hypothetical protein SA0624 [imported] - Staphylococcus aureus (strain N315)
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A;Experimental source: strain N315
C;Genetics:
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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecules: 1-147 <STO>
A;Cross-references: GB:AE004437; NID:g10580903; PIDN:AAG19719.1; GSPDB:GN00138
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C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C,Species: Staphylococcus aureus
C,Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
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100.0%; Score 19; DB 2; Length 145;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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100.0%; Score 19; DB 2; Sest Local Similarity 100.0%; Pred. No. 4.2e+02; Matches 4; Conservative 0; Mismatches 0;
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us-09-594-978a-2.rpr

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C; Superfamily: galactoside O-acetyltransferase
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Best Local S
Matches 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
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);Species: Neisseria meningitidis
);Date: 05-MAY-2000 #sequence_revision 05-MAY-2000 #text_change 02-Feb-2001
);Accession: E81788
(;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel, Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel, Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Jature 404, 502-506, 2000
);Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.
);Accession: E81788
);Accession: E81788
);Accession: E81788
);Accession: E81788
);Accession: E81788
);Accession: E81789
);Accession: E817789
);Accession: E81789
);Accession: E8
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1, Residues: 1-148 <PAR>
1, Cross-references: GB:AL162758, GB:AL157959; NID:97380672; PIDN:CAB85372.1; PID:9738078
1, Experimental source: serogroup A, strain 22491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        yabou street and protein SC2EL.35 - Streptomyces coelicolor 'Species: Streptomyces coelicolor 'Species: Streptomyces coelicolor 'Species: Streptomyces coelicolor 'Jace: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 04-Mar-2000 'Jace: 05-Nov-1999 #text_change 04-Mar-2000 #text_change 04-M
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2;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 18-Jun-1993
2;Accession: S10655
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./Superfamily: Streptomyces coelicolor hypothetical protein SC2E1.35
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Query Match 100.0%; Score 19; DB 2; Length 147; Best Local Similarity 100.0%; Pred. No. 4.2e+02; Matches 4; Conservative 0; Mismatches 0; Indels
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?;\\Superfamily: hypothetical protein ytwl
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ribosphate isomerase homolog lmo0498 [imported] - Listeria monocytogenes (strain c; species: Listeria monocytogenes
C; species: Listeria monocytogenes
C; pate: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C; Accession: AC1137
R; dlaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, Dominguez-Bernal, G.; Duraud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fshi, H. Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maritle: Comparative genomics of Listeria species
A; Reference number: AB1077; MUD:21537279; PMID:11679669
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C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C;Accession: AB2857
C;Accession: AB2857
B;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
R;Wood, D.W.; Setubal, J.C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
Rarp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
Ssichence 294, 2317-2323, 2001
Setupa M.; Rrespan, W.; Perry, M.; Gordon-Kamm,
R;Zwickl, P.; Fabry, S.; Bogedain, C.; Haas, A.; Hensel, R.
J. Bacteriol. 172, 4329-4338, 1990
A;Title: Glyceraldehyde-3-phosphate dehydrogenase from the hyperthermophilic archaebacts scherichia coli.
A;Reference number: S10650; MUID:90330536; PMID:2165475
A;Accession: S10655
A;Molecule type: DNA
A;Residues: 1-148 <2MI>A;Accessiones: 1-148 <2MI>A;Accessiones: Tanaslated the codon GGT for residue 54 as Glu
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Ayitle: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A.Reference number: AB2577; MUID:21608550; PMID:11743193
A.Rocession: AB2857
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A;Molecule type: DNA
A;Residues: 1-149 <GLA>
A;Residues: 1-149 <GLA>
A;Cross-references: GB:NC_001210; PIDN:CAC98577.1; PID:g16409874; GSPDB:GN00177
A;Experimental source: strain EGD-e
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A;Molecule type: DNA
A;Realdues: 1-150 «KNO.
A;Crosa-references: GB:AE008688; PIDN:AAL43272.1; PID:g17740759; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
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100.0%; Score 19; DB 2; Length 148;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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105 VAEF 108
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Sience 294, 849-852, 2001
Shaubners: Kreft, J.; Kuhn, M.; Kunst, P.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mathle: Comparative genomics of Listeria species
FReference number: AB1077; MUID:21537279; PMID:11679669
Status: preliminary
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Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Fsihi, H.; Domiquez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.

cience 294, 849-852, 2001
Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma, C.; C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, Jittle: Comparative genomics of Listeria species.

Reference number: AB1077; MUID:21537279; PMID:11679669
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Cross-references: GB.NC_003210; PIDN:CAC98328.1; PID:g16409472; GSPDB:GN00177
Experimental source: strain EGD-e
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; Gross-references: GB:AL592022; PIDN:CAC95393.1; PID:g16412579; GSPDB:GN00178
; Experimental source: strain Clip11262
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Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
Accession: AB1089
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Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
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Gene: Atu2283
Map position: circular chromosome
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Molecule type: DNA
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hypothetical protein CC0121 [imported] - Caulobacter crescentus
CiSpecies: Caulobacter crescentus
CiSpecies: Caulobacter crescentus
CiSpecies: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
CiAccession: H87263
Ribiterman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.;
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon:
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Dodson, S.J.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proco. Natl. Acad. Sci. U.S.A. 98, 4136-411, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
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A;Molecule type: DNA
A;Residues: 1-151 <STO>
A;Cross-references: GB:AE005673; NID:g13421228; PIDN:AAK22108.1; GSPDB:GN00148
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Best Local Similarity 100.
Matches 4; Conservative
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Gaps ; 0 Н

us-09-594-978a-2.rsp

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P48856 homo sapien
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028439 archaeoglob
015400 homo sapien
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YH89_STRAM
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                                BFLI HUMAN
FRIZ RANCA
RL10 THETN
DSBB PASMU
ESM5 DROME
YB18 ARCFU
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APT HABDU
RETB BOVIN
DNAA WOLSP
UCRI PARDE
NTPA METJA
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09w7r2 verasper mo

1000141 lophius pis

001841 lophius pis

001842 pyrobaculum

02786 sus scrofa

062786 sus scrofa

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   | P74750 synechocyst<br>000999 herbesvirus   | Q91274 petromyzon<br>O75161 homo sapien  | Q92c34 listeria in O8v7c1 listeria mo  | P53049 saccharomyc                      | O88563 rattus conf   | O14146 nome Bapien<br>O15438 home sapien  
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| 2000 TO  | 027552 methanobact 625 19 100.0 2649 1 P285 HUMAN Q9byk8 027552 methanobact 626 19 100.0 2725 1 FLNC HUMAN Q14315 Q34305 gea mays (m 627 19 100.0 2774 1 MAPA_RAT P34926 P10253 homo sapien 628 19 100.0 2805 1 MAPA_HUMAN P778559 | 027552 methanobact 625 19 100.0 2649 1 P288_HUMAN Q9byk8 027552 methanobact 626 19 100.0 2725 1 FLNC_HUMAN Q14315 024315 02755 2ea mays (m 627 19 100.0 2774 1 MAPA_HUMAN P10503 yang papers 629 19 100.0 2412 1 POLG_TBEVS P78559 030 1412 1 POLG_TBEVS P78559 030 1412 1 POLG_TBEVS P78559 030 1414 1 POLG_TBEVS P785937 0415 1 POLG_TBEVS P78593 0415 1 POLG_TBEVS P78593 0415 1 POLG_TBEVS P785937 0415 1 POLG_TBEVS | O27552 methanobact 625 19 100.0 2649 1 P285_HUMAN Q9byk8 02755 methanobact 626 19 100.0 2725 1 FLMC HUMAN Q14315 02755 methanobact 628 19 100.0 2774 1 MAPA_RAT P34315 0253 memoral espien 629 19 100.0 2774 1 MAPA_RAT P78559 0253 mays (m 628 19 100.0 2774 1 MAPA_RAT P78559 0253 memoral espien 629 19 100.0 3412 1 POLG_TBRVS P07720 P71698 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 P7859-P494           P10253 home sapien         623         19         100.0         3412         1         POLG_TBRVS         P047720           Q9kp73 vibrio chol         629         19         100.0         3414         1         POLG_TBRVS         P047720           Q8L645 arabidopsis         631         19         100.0         3414         1         POLG_TBRVS         P047329           Q10737 haemonchus         632         19         100.0         3414         1         POLG_TBRVW         Q04538           Q99189 saccharomyc         633         19         100.0         3415         1         Q04538           Q928B cauliobacter         633         19         100.0         3415         1         POLG_PWNL         Q04538           Q928B cauliobacter         636         19         100.0         5179         1 | Q54617 arabidopsis         625         19         100.0         2649         1         P285-HUMAN         Q394yk8           Q27552 methanobact         626         19         100.0         2725         1         PLWAR         PAP4-1415         PAP4-1415 <td< td=""><td>  O24617 arabidopsis   G25   19   100.0   2649   1   P285 HUMAN   Q9byk8   Q27552 methanobact   G26   19   100.0   2725   FLNC HUMAN   Q14115   Q9xg95   Ame marge (m   G28   19   100.0   2805   MAPA HUMAN   Q14115   P78559   P78659   P78</td><td>  Participation   Participatio</td><td>  Care   Care  </td><td>  March Rayles   Marc</td><td>  Color   Colo</td><td>  Color</td><td>  100.0 2765   19 PLMC HTMANN   0395/NE    </td><td>  2007-15   2007</td><td>  Control of the cont</td><td>  Control of the cont</td><td>0.74617 activity activity         625         19 100.0         2645         19 100.0         2755         1 PRAF, HUMAN         Q04918           0.75627 activity activity         627         19 100.0         274         MAPA, HUMAN         Q04312           2.0562 b home captic chol         629         19 100.0         2414         PDLG_TRRVA         P7859           2.05673 b home captic chol         629         19 100.0         3414         PDLG_TRRVA         P7859           2.0573 b home captic chol         631         19 100.0         3414         PDLG_TRRVA         P7859           2.07518 carchidopater         631         19 100.0         3414         PDLG_TRRVA         P7859           2.07528 cantidomans         631         19 100.0         3414         PDLG_TRRVA         P7859           2.07528 cantidomans         631         19 100.0         3414         PDLG_TRRVA         P7859           2.0852 cantidomans         655         19 100.0         3414         PDLG_TRRVA         P7859           2.0852 cantidomans         656         19 100.0         3414         PDLG_TRRVA         P7859           2.0852 cantidomans         656         19 100.0         3414         PDLG_TRRVA         P7859           2.08</td><td>  Color</td><td>  Color   Colo</td><td>  Coloniary   Colo</td><td>  Participation   Participatio</td><td>  Park Adoption   Park Adoptio</td><td>  October   Color   Co</td><td>  October   Color   Co</td><td>CONSTANT AND ADMINISTRATION OF SEAS IN PRINCE HINNAM         CONSTANT AND ADMINISTRATION OF SEAS IN PRINCE HINNAM</td><td>Option of the control of the</td><td>  Colored   Colo</td><td>  Control of the cont</td></td<> | O24617 arabidopsis   G25   19   100.0   2649   1   P285 HUMAN   Q9byk8   Q27552 methanobact   G26   19   100.0   2725   FLNC HUMAN   Q14115   Q9xg95   Ame marge (m   G28   19   100.0   2805   MAPA HUMAN   Q14115   P78559   P78659   P78  | Participation   Participatio | Care   Care | March Rayles   Marc | Color   Colo | Color                                    | 100.0 2765   19 PLMC HTMANN   0395/NE   | 2007-15   2007 | Control of the cont | Control of the cont | 0.74617 activity activity         625         19 100.0         2645         19 100.0         2755         1 PRAF, HUMAN         Q04918           0.75627 activity activity         627         19 100.0         274         MAPA, HUMAN         Q04312           2.0562 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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Hypothetical UPF0165 protein AF1090.
AF1090.
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STRAIN=VC-16 / DSM 4304 / ATCC 49558;
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Praead H.K., Annapurna P.S.;
Submitted (DEC-1997) to Swiss-Prot.
-!- SIMILARITY: STRONG, TO THE N-TERMINALS OF C.ELEGANS F20A1.4
AND H.INFLUENZAE H10967.
-!- CAUTION: We are unable to find this protein in the translation of the genome of strain H37Rv.

NON TER 19 19 19 SEQÜENCE 19 AA; 2211 MW; ABC1854BFIFF1F70 CRC64;
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Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
NCBI_TaxID=160;
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MEDLINE=98332770; PubMed=9665876;
Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
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15-JUL-1999 (Rel. 38, Last sequence update)
16-JUL-1999 (Rel. 40, Last sequence update)
30 kDa non-secretory protein 2 (Fragment).
Mycobacterium tuberculosis.
Bacteria, Actinobacteria, Actino
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15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
18-OCT-2001 translocase secE subunit.
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Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VAEF 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TREPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NS2 MYCTU
P81136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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SECE TREPA
ID SECE TRE!
AC 083263;
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MEDLINE-98049343; PubMed=9389475;
Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
Kerchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
Peterson S., Reich C.I., Moneil L.K., Badger J.H., Glodek A., Zhou L.,
Overteon M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T., Broband L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S., Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001901; SecE.
InterPro; IPR005807; SecE_bac.
Pfam; PF00584; SecE; 1.
TIGRPAMs; TIGR00964; 3a0501806; 1.
PROSITE; PS01067; SECE_SECGIG; 1.
PROSITE; PS01067; SECE_SECGIG; 1.
Protein transport; Translocation, Transmembrane; Complete protecome.
TRANSMEM 39 59 POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 19; DB 1; Length 59; 100.0%; Pred. No. 1.1e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Archaeea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
NCBI_TaxID=2234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 AA; 6789 MW; 9AC35BA8F48B2A7F CRC64;
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Length 63;

Q

us-09-594-978a-2.rsp

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Query Match
Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                   1 VAEF 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=727;
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                                                                                                                                                                                                                                                                                                                                                          RS15 HAEIN
P44389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INIT MET
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                                                                                                                                                                                                                                                                                            RESULT 5
HABEIN
10 P44389,
DT 01-NOV.
DT 01-
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                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstailonth a butopean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

STRAINEd / KW20 / ATCC 51907;

MEDLINE=95350630; PubMed=7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

Rerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 41, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Hypothetical protein HI0451.
H10451.
Haemophilus influenzae.
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 19; DB 1; Length 59; 100.0%; Pred. No. 1.1e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                            Brial, ASSE, A69386.
TIGR, AF1090; -.
INTERPO, IPRO08203; DUF104.
INTERPO: IPRO08204; DUF104.
Fam, PP01954; DUF104.1.
ProDom; PD005964; DUF104.1.
Hypotherical protein; Complete proteome.
SEQUENCE 59 AA; 6887 MW; B72E847382B2B6B6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; G64007; G64007.
TYGR; H10451; --
Hypotheital protein; Complete proteome.
SEQUENCE. 63 AA; 7047 MW; 36B14E60AC306B67 CRC64;
   SIMILARITY: Belongs to the UPF0165 family.
                                                                                                                                                                                                                                                                                               EMBL; AE001028; AAB90157.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U32728; AAC22109.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 VAEF 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 VAEF 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ESULT 4
451_HAEIN
D Y451_HAEIN
C P43998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=95350630; PubMed=7542800; Patch State C., Clayton R.A., Kirkness E.F., Fleischmann R.D., Adams M.D., White O., Clayton R.A., Merrick J.M., McKenlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutten G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.E., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Pritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 269:496-512(1995).
-!- FUNCTION: This protein is one of the 16S ribosomal RNA binding proteins (By similarity).
-!- SIMILARITY: Belongs to the S15P family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
30S ribosomal protein S1S,
(RPSO-A OR RPSI5-A OR HI1328) AND (RPSO-B OR RPSI5-B OR HI1468)
Haemophilus influenzae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria, Proteobacteria, Gammaproteobacteria, Pasteurellales,
Pasteurellaceae, Haemophilus.
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100.0%; Score 19; DB 1; Length 63 ilarity 100.0%; Pred. No. 1.1e+02; Conservative 0; Mismatches 0; Indels
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TIGROMSITE; PS00362; RIBOSOMAL S15; 1.
Ribosomal protein; rRNA-binding; Complete proteome.
INIT_MET
                                                                                                                                                                                                                                                                                                                                                                                                  88 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 100.0%; Pred. No. 1.6
4; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Interpro; IPR00589; Ribosomal_815.
Interpro; IRR06289; Ribosomal_815_b.
Pfam; PF00312; Ribosomal_815, I.
ProDom; PD157043; RS15_bact; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88 AA; 10064 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, U32812; AAC22973.1; -. EMBL, U32825; AAC23117.1; -. PIR; H64116, H64116. H4SSP, P005766; LA32.
                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 VAEF 14
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ALB2\_METKA

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Archaea; Buryarchaeota; Methanococci; Methanococcales; Methanocaldococcaceae; Methanocaldococcus.
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MEDLINE=93015257; PubMed=1399845;
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                                                                                                              EMBL; U67593; AAB99550.1; -. PIR; C64490; C64490.
  Methanococcus jannaschii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52 VAEF 55
                                                                                  NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VAEF 4
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RA Sleazev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,
RA Sleazev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,
RA Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
RA Natale D.A., Rogozin I.B., Tatusov R.I.,
Mathyth A.G., Koonin E.V., Kozyavkin S.A.,
The complete genome of hyperthermophile Methanopyrus kandleri AV19
RT and monophyly of archanogens."
Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649.

C. --- FUNCTION: Binds double-stranded DNA tightly but without sequence specificity. It is distributed uniformly and abundantly on the chromosome, suggesting a role in chromatin architecture. However, it does not significantly compact DNA (By similarity).

C. --- SUMINT: Homoterraner (By similarity).
C. --- FTM: Acetylated. Deacetylation by the SIR2-homolog deacetylase increases its DNA-binding affinity, thereby repressing represent the archaeal histone-like Alba family.

C. --- SIMILARITY: Belongs to the archaeal histone-like Alba family.

C. --- SIMILARITY: Belongs to the archaeal histone-like Alba family.

C. --- SIMILARITY: Belongs to the archaeal histone-like RMBL outstation between the Swiss Institute of Bioinformatics and the EMBL outstation.

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                                                                                                                                                                                                                                                                                                                        Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
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NA-binding; Acetylation; Complete proteome.

ACETYLATION (BY SIMILARITY).
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                                                                                                                                                   10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
DNA-binding protein Alba 2.
Methanopyrus kandleri.
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(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                           93 AA.
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or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=AV19 / DSM 6324 / JCM 9639;
MEDLINE=21927647; PubMed=11930014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE010398; AAM02302.1; -.
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16-OCT-2001 (Rel. 40, Last s
16-OCT-2001 (Rel. 40, Last a
Hypochetical protein MJ1524.
MJ1524.
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Best Local Similarity
Matches 4; Conserv
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Q58919;
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Q8TWE6;
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YF24\_METUA RESULT 7

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STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

MEDLINE=9633799; PubMed=8688087;

Bult C.J., White O., Oleen G.V., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodoysky M.,

Ricmplete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hofstead S.J., Matson J.A., Malacko A.R., Marquardt H.; "Kedarcidin, a new chromoprotein antitumor antiblotic. II. Isolation, purification and physico-chemical properties."; J. Antiblot. 45:1250-1254 (1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Selomon W., Nadler S.G.;
Selective proteolytic attivity of the antitumor agent kedarcidin.";
Proc. Natl. Acad. Sci. U.S.A. 90:8009-8012(1993).
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales.
NCBI_TaxID=38989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 108;
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Pfam; PF02641; DUF190; 1.

Hypothetical protein; Complete proteome.

SEQUENCE 108 AA; 12398 MW; D3E286AFB9D4AF8B CRC64;
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100.0%; Pred. No. 1.9e+02;
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KEDA ACTSL STANDARD; PRT; 114 AA.

AC P41249;
DT 01-FRE-1995 (Rel. 31, Created)
DT 01-FRE-1995 (Rel. 31, Last sequence update)
DT 01-FRE-2003 (Rel. 41, Last annotation update)
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P01341;
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Best Local
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X MEDLINE-95001846; PubMed-7918358;

A CONStantine K.L., Colson K.L., Wittekind M., Friedrichs M.S.,

CONStantine K.L., Colson K.L., Wittekind M., Friedrichs M.S.,

A Zein N., Tuttle J., Langley D.R., Leet J.E., Schroeder D.R., Lam K.S.,

Raguential 1H, 13C, and 1SN NMR assignments and solution

T conformation of apokedarcidin.,

B biochemistry 33:11438-11452(1994).

- PUNCTION: BINDS NOW-COVALENTY TO AN ENEDIYNE CHROMOPHORE WHICH IS

THE CYTOTOXIC AND WUTAGENIC COMPONENT OF THE ANTHBIOTIC. THE

CHROMOPHORE CLEAVES DUPLEX DNA SITE-SPECIFICALLY IN A SINGLE-
STRANDED MANNER. THE APOPROTEIN CLEAVES PROTEINS SELECTIVELY, IN

PARTICULAR HIGHLY BASIC HISTONES, WITH HI PROTEINS BEING CLEAVED

THE MORE READILY.
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STRANDED ANTIPRARALLEL BETA-BARREL DOMAIN LINKED TO A SUBDOMAIN
COMPOSED OF TWO BETA-HAIRPIN RIBBONS.

-i- SIMILARITY: Belongs to the neocarzinostatin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Pleuronectiformes;
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100.0%; Pred. No. 28+02; V. matches 0; Indels
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16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Insulin precursor.
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NCBI_TaxID=98923;
[1]
                                                                                                                                                                                                                                                                                            Antibiotic, DNA-binding, 3D-structure
DISULFID 37
                                                                                                                                                                                                                                           PDB, 1AKP, 31-AUG-94.
InterPro; IPR002186; Neocarzinostat.
Pfam, PF00960; Neocarzinostat, 1.
ProDom; PD012709; Neocarzinostat; 1.
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               112 :
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Andoh T., Nagasawa H.;
"Two molecular forms of insulin from barfin flounder, Verasper moseri, are derived from a single gene.";
are derived from a single gene.";
2001. Sci. 15:931-937(1998).
-!- FUNCTION: Insulin decreases blood glucose concentration. It increases cell permeability to monosaccharides, amino acids and fatty acids. It accelerates glycolysis, the pentose phosphate cycle, and glycogen sytthesis in liver.
-!- SUBUNIT: Heterodimer of a B chain and an A chain linked by two
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MEDLINE=81056434; PubMed=7001633;
Hobart P.M., Shen L.-P., Crawford R., Pictet R.L., Rutter W.J.;
"Comparison of the nucleic acid sequence of anglerfish and mammalian insulin mRNA's from cloned cDNA's.";
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Pred. No. 2e+02;
; Mismatches 0; Indels
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INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
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HSSP; P01315; IMPJ;
InterPro; IPR00482; Ins/IGF/relax.
Pfam; PF00049; Insulin; 1.
PRINTS; PR00277; INSULINB.
SMRRT; SM0078; IOSF; 1.
PROSITE: PS00262; INSULIN; 1.
INSULIN family; Hormone; Glucose metabolism; Signal.
                                                                                                                                                                                                                                                                 disulfide bonds.
--- SUBCELLULAR LOCATION: Secreted.
--- SIMILARITY: Belongs to the insulin family.
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21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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SEQUENCE OF 25-54 AND 96-116.
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115 AA;
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4; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                piscatorius).";
Hoppe-Seyler's Z. Physiol. Chem. 350:1286-1288(1969).
-I-FUNCTION: Insulin decreases blood glucose concentration. It increases cell permeability to monosaccharides, amino acids and fatty acids. It accelerates glycolysis, the pentose phosphate cycle, and glycogen synthesis in liver.
-I-SUBUNIT: Heterodimer of a B chain and an A chain linked by two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
Adama M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adamatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
SPECIES=L.piscatorius;
MEDLINE=7003620; PLUMG=5389298;
Meumann P.A., 600choof M., Humbel R.E.;
"Amino acid sequence of insulin from the angler fish (Lophius
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).

Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neophera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 19; DB 1; Length 116; 100.0%; Pred. No. 2.1e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116 AA; 12737 MW; C686F8EF8183BEFE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, V00634; CAA23907.1; -.
PIR; A01608; IPAF.
HISSP, P01309; 1LBH.
HISSP, P01309; 1LBH.
FR0049; Insulin; 1.
PRINTS; PR00277; INSULINB.
SMART; SM00079; INSULINB.
PROSTITE; PS00262; INSULINB.
PROSTITE; PS00262; INSULIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11

U279 DROME

AC 0279-DROME STANDARD; PRT; 119 AA.

AC 0208F3;
DT 10-0CT-2003 (Rel. 42, Last sequence update)
DT 10-0CT-2003 (Rel. 42, Last sequence update)
DT 10-0CT-2003 (Rel. 42, Last sequence update)
DE 10-0CT-2003 (Rel. 42, Last amnotation update)
DE 0CT-2003 (Rel. 42, Last amnotation update)
DE 0CT-2009 (Rel. 42, Last amnotation update)
DE 0CT-2003 (Rel. 42, Last amnotation update)
DE 0CT-2003 (Rel. 42, Last update
                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the insulin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INSULIN B CHAIN.
C PEPTIDE.
INSULIN A CHAIN.
INTERCHAIN.
INTERCHAIN.
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Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                      disulfide bonds.
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DISULFID
DISULFID
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PROPEP
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RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Rally Baril J.F., Agbayani A., An H.-J., Andrews-Ffannkoch C., Baldwin D., Ballew R.M., Basua A., Baxendale J.P., Banadari D., Balanakov S. B. Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S. B. Borkova D., Botchan M.R., Bouck J., Broktein P., Brottier P., Borkova D., Botchan M.R., Buller H., Cadieu E., Center A., Chandra I., Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I., R. Cherry J.M., Cawley S., Dahlec C., Davenport L.B., Davies P., Dockon K. Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunkov B.C., Dunbon K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., R. Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Glasser K., Gorger F., Gorrell J.H., Gu Z., Kennison J.R., Houck J., R. Alali M., Kalush F., Karpen G. H., Errandez J.R., Houck J., R. Jalali M., Kalush F., Karpen G. H., Ex, Kerchum K.A., Karpen G. H., Karpen G. H., Karpen G. H., J., Howland T.J., Wall M., Hold M., Mattel B., McIntosh T.C., McLeod M.P., McCherson D., Lai X., Mattel B., McIntosh T.C., McLeod M.P., McCherson D., Lasko D., Lei Y., Leviteky A.A., Liu J.H., Wazny D.M., Nelson D.L., Ra Blazon D.R., Nalson K.A., Nixon K., Nussken D.R., Palazolo J.M., Pitman G.S., Pan S., Pollad J., Puri V., Reese M.G., Ra Blazon D.M., Mulphy B., Murphy L., Murphy D.M., Nelson D.K., Banter K., Samengron R., Simpson M., Skupski M.P., Smith T., Raylon R., Spier B., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"A Drosophila full-length CDNA resource.";
"A Drosophila full-length CDNA resource.";
-i- SIMILARITY: Belongs to the UPF0279 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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100.0%; Pred. No. 2.1e+02;
ive 0; Mismatches 0; Indels
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MEDLINE=22426066; PubMed=12537569;
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EMBL; AY084100; AAL89838.1; -.
FlyBaae; FBGN0034327; CG14505.
Interpro; IPR007967; DUF727.
Pfam; PF05303; DUF727; 1.
SEQUENCE 119 AA; 13534 MW; 8:
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ID GTR2_PIG STANDARD;

AC 065786;

DT 28-FRB-2003 (Rel. 41, Created)
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                                                                                                                                                                                                                                                                                                    Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-IM2 / ATCC 51768 / DSM 7523;
MEDLINE=21664397; PubMed=11792869;
Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
-!- SIMILARITY: Belongs to the L18B family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Pasteurella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 19; DB 1; Length 122; 100.0%; Pred. No. 2.2e+02; ive 0; Mismatches 0; Indels
ryrobaculum aerophilum.
Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
Thermoproteacaea; Pyrobaculum.
NCBI_TaxID=13773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ribosomal protein, Complete proteome.
SEQUENCE 122 AA, 13252 MW, 88F3DB732C4E0394 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein PM0670 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HAMAP; MF_00329; -; 1.
InterPro; IPR001196; Ribosomal_L15.
InterPro; IPR000039; Ribosomal_L18e.
Pfam; PF00256; L15; 1.
PROSITE; PS01106; RIBOSOWAL_L18E; FALSE_NEG.
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PIRSF; PIRSF000029; Cytochrome_b562; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Pm70;
MEDLINE=21145866; PubMed=11248100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pasteurella multocida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                        aerophilum.";
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Y670_PASMU
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                                                                                                                                                                                                                                                                                                                               Canty J.M., Young R.F., Fallavollita J.A.;
Submitted (MAR.1998) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: Facilitative glucose transporter. This isoform likely mediates the bidirectional transfer of glucose across the plasma membrane of hepatocytes and is responsible for uptake of glucose by the beta cells, may comprise part of the glucose-sensing mechanism of the beta cell. May also participate with the Na(+)/glucose cotransporter in the transcellular transport of glucose in the small intestine and kidney (By similarity).

-!- SUBCELLULAR LOCATION: Integral membrane protein.

-!- SIMILARITY: Belongs to the sugar transporter family. Glucose transporter subfamily.
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                       28-FEB-2003 (Rel. 41, Last sequence update)
Solute carrier family 2, facilitated glucose transporter, member 2
Solute carrier family 2, facilitated glucose transporter, member 2
(Glucose transporter type 2, liver) (Fragment).
Suc2A2 OR GLUT2.
Sus scrofa (Fig)
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R InterPro; IPRO05114; MS.
R InterPro; IPRO05114; MS.
R InterPro; IPRO05829; Sug_transporter.
R InterPro; IPRO05829; Sug_transporter.
R InterPro; IPRO05829; Sug_transporter.
R PRONTS; PRO0171; SUGRITANSPORT.
R PROSITE; PS00217; SUGAR_TRANSPORT_1; PARTIAL.
R PROSITE; PS00217; SUGAR_TRANSPORT_2; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13503 MW; D5F73168DBF03203 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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Matches 4; Conservative
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106 1
120 1
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                     NCBI_TaxID=9823;
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DOMAIN
TRANSMEM
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SEQUENCE
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DOMAIN

ESULT 13 18E\_PYRAE

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Gaps

130 AA.

PRT;

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SEQUENCE FROM N.A.
STRAIN=MSB8 / DSM 3109 / ATCC 43589;
MEDLINE=99287316; PubMed=10360571;
Melson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
"Evidence for lateral gene transfer between Archaea and Bacteria from
Mature 399:323-329(1999).
                                                                                                            28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last sequence update)
5-adenosylmethiconne decarboxylase proenzyme (EC 4.1.1.50) (AdoMetDC)
(SamDC) [Contains: S-adenosylmethiconne decarboxylase beta chain; S-adenosylmethiconne decarboxylase alpha chain].
                                                                                                                                                                                                                                                                                              Thermotoga maritima.
Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=2336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SITE
                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BYBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@labsab.ch).
                                                                                                                                                                                                  ö
                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=DBA/2J; TISSUE=Liver;
MEDLINE=9475529; PubMed=8089185;
Crossman M.W., Hauft S.M., Gordon J.I.;
Crossman M.W., Hauft S.M., Gordon J.I.;
The mouse ileal lipid-binding protein gene: a model for studying axial patterning during gut morphogenesis.";
J. Cell Biol. 126:1547-1564 (1994).

-i. FUNCTION: ILEAL PROTEIN WHICH STIMULATES GASTRIC ACID AND PEPSINOGEN SECRETION. SEEMS TO BE ABLE TO BIND TO BILE SALTS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCPL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BILIRUBINS.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to the fatty-acid binding protein (FABP)
                                                                                                                                                                                                  ö
                                                                                                                                       100.0%; Score 19; DB 1; Length 124; 100.0%; Pred. No. 2.2e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 100.0%; Score 19; DB 1; Length 127; Local Similarity 100.0%; Pred. No. 2.2e+02; nes 4; Conservative 0; Mismatches 0; Indels
                                           1 23 POTENTIAL.
24 124 HYPOTHETICAL PROTEIN PM0670.
124 AA, 13746 MW, D7B2B485C7B51B9A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BÝ SIMILARITY.
ACETYLATION (BY SIMILARITY).
0690BBDD0A9CD922 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Gastrotropin (GT) (lleal lipid-binding protein) (ILBP).
FABP6 OR ILLBP.
Mus musculus (Mouse).
Hypothetical protein; Signal; Complete proteome.
SIGNAL 1 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00214; FABP; 1.
Transport; Lipid-binding; Acetylation.
INIT_MET 0 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000463; Fatty acid BP.
InterPro; IPR000566; Lipocin_cytFABP.
Ffam; PF00061; lipocalin; 1.
PRINTS; PR00178; FATTYACIDBP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127 AA; 14355 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U00938; AAC27352.1; -. PIR; A54797; A54797.
                                                                                                                                                                                             4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P10289; 1EAL.
MGD; MGI:96565; Fabp6.
                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                              45 VAEF 48
                                                                                                                                                                                                                                                1 VAEF 4
                                                                                                                                                                                                                                                                                                                                                                                                                           ILBP MOUSE
                                                                                         SEQUENCE
                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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ILBP_MOUSE
                                                                                                                                                                                             Matches
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Matches
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-i - FUNCTION: Decarboxylation of S-adenosylmethionine provides the aminopropyl molety required for spermidine biosynthesis from putrescine (By similarity).
-! - CATALYTIC ACTIVITY: S-adenosyl-L-methionine = (5-deoxy-5-adenosyl) (3-aminopropyl) methylsulfonium salt + CO(2).
-! - COFACTOR: Pyruvoyl group (By similarity).
-! - COFACTOR: Pyruvoyl group (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN (BY SIMILARITY).
S-ADENOSYLMETHIONINE DECARBOXYLASE ALPHA
CHAIN (BY SIMILARITY).
CLEAVAGE (NONHYDROLYTIC) (BY SIMILARITY).
CONVERTED TO A PYRUVOYL GROUP (BY
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S-ADENOSYLMETHIONINE DECARBOXYLASE BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HAMAP; MF_00464; -; 1.
InterPror, IPRO0386; SAMDC.
Pfam; PF02675; AdoMetlD; 1.
Spermidine biosynthesis; Lyase; Decarboxylase; Zymogen; Pyruvate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7659FE20A2019928 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 19; DB 1; I
100.0%; Pred. No. 2.3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE001739; AAD35739.1; -. PIR; D72348; D72348.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 AA; 14785 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62
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ID Y194_PYRAB
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VAEF 94 1 VAEF 4

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YBGC ECOLI
P08999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                     Archaea; Buryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPHRMS;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2003 (Rel. 41, Last annotation update)
6,7-dimethyl-8-ribityllumazine synthase (EC 2.5.1.9) (DMRL synthase)
(Lumazine synthase) (Riboflavin synthase beta chain).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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WEDLINE=22511545; PubMed=12622808;

CODEO G.N., Barbe V., Flament D., Galperin M., Heilig R., Lecompte (
Conen G.N., Barbe V., Flament D., Galperin M., Thierry J.-C.,

Poch O., Prieur D., Querellou J., Ripp R., Thierry J.-C.,

Van der Oost J., Weissenbach J., Zivanovic Y., Forterre P.,

"An integrated analysis of the genome of the hyperthermophilic
archaeon Pyrococcus abyssi.", 2003).

-i- SIMILARITY: Belongs to the UPF0146 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PERM: PF03686; UPF0146; 1.

PIRSF: PIRSF016725; UCP016725; 1.

Probom: PD021130; UPF0146; 1.

Hypothetical protein; Complete proteome.

BEQUENCE 131 AA; 14629 MW, D13F378187F832C3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
                         16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical UPP0146 protein PYRAB01940.
Pyrosoccus abyssi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133 AA.
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NCBI TaxID=64091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AJ248283; CAB49118.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HAMAP; MF_00341; -; 1.
ThterPro; IPR005353; UPF0146.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                       NCBI_TaxID=29292;
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[SB_HALN]
) RISB_HALN1
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Sun T.-P., Webster R.E., nucleotide sequence of a gene cluster involved in entry of E colicins and single-stranded DNA of infecting filamentous bacteriophages into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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SPECIES-E.coli; STRAIN-K12 / MG1655;
SPECIES-E.coli; STRAIN-K12 / MG1655;
MEDLINE-9426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
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YBGC OR B0736 OR C0815 OR Z0904 OR EC80771 OR SF0561 OR S0574.
Escherichia coli,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 19; DB 1; Length 133; 100.0%; Pred. No. 2.4e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; O66529; 1HQK.
HRAMAP, MF 00178; -; 1.
InterPro; IRR02180; DMRL synthase.
Pfam; PF00885; DMRL synthase; 1.
ProDom; PD003664; DMRL synthase; 1.
Riboflavin biosynthesis; Transferaes; Complete proteome.
SEQUENCE 133 AA; 13719 MW; B9724DC24660D6CD CRC64;
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01-NOV-1988 (Rel. 09, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enterobacteriaceae; Escherichia.
NCBI_TaxID=562, 217992, 83334, 623;
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Escherichia coli 0157:H7, and
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A Gregor J., Davis N.W., Kirkpatrick H.M., Goeden M.A., Rose D.J.,

Myll B., Shoo Y.,

"The complete genome sequence of Escherichia coll K-12.";

Science 277.1455-1474(1597).

Remoto X., Tada T., Tada T., Tada T., Tada T., Kanal K., Kada K., Manikov K.,

Remoto K., Tada T., Tada T., Toh T., Walhare M., Kanal K., Mashimoto K.,

Remoto K., Tada T., Tada T., Toh T., Walhare M., Kanal K., Mashimoto K.,

Remoto K., Tada T., Tada T., Tada T., Tada T., Takana K., Manikov W.,

Remoto K., Tada T., Tada T., Tada T., Tada T., Takana K., Manikov W.,

Remoto K., Tada T., Tada T., Tada T., Takana K., Manikov W.,

Remoto K., Tada T., Tada T., Tada T., Takana K., Manikov W.,

Sampel G., Sell Y., Tadami H., Takanoto K., Wada C., Yamanoto Y.,

Rand M., Manikow Remona K., Walama K., Manikov W.,

Remoto K., Manikow R., Manikow W.,

Remoto K., Manikow W., Walama W., Wala K., Manikov W.,

Remoto K., Manikow R., Manikow W., Wala K., Manikow W.,

Remoto K., Manikow R., Manikow W., Manikow W.,

Remoto K., Manikow R., Manikow W., Manikow W.,

Remoto K., Manikow W., Manikow W., Manikow W.,

Remoto K., Manikow W., Manikow W., Manikow W.,

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Fountoulakis M., Takacs M.-F., Berridt P., Langen H., Takacs B.;
Fourtoulakis M., Takacs M.-F., Berridt P., Langen H., Takacs B.;
"Enrichment of low abundance proteins of Escherichia coli by
hydroxyapatite chromatography.";
Blectrophoreais 20:2181-2195(1999).
-!-SIMILARITY: BELONGS TO THE 4-HYDROXYBENZOYL-COA THIOESTERASE
-PAMILY: STRONG, TO H.INFLUENZAE H10386.
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SPECIES=S.flexneri; STRAIN=2457T / ATCC 700930 / Serotype 2a; MBDINE=22590274; PubMed=12704152; MEDINE=22590274; PubMed=12704152; Medi J.; Goldberg M.B., Burland V., Venkatesan M.M., Deng W., Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling P. Mau B., Perna M.T., Payre S.M., Runyen-Janecky L.J., Zhou S., Schwartz D.C., Blattner F.B., "Complete genome sequence and comparative genomics of Shigella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae; Methanothermobacter.
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16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
6,7-dimethyl-8-ribityllumazine synthase (BC 2.5.1.9)
(Lumazine synthase) (Riboflavin synthase beta chain).
RIBH OR WIH1390.
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EMBL, ABOU552; AAA019288.1; --
EMBL, ABOU552; AAA55072.1; ---
EMBL, ABOU552; AAA55072.1; ---
EMBL, ABOU552; AAA74398.1; ---
EMBL, ABOL5086; AAA4298.1; ---
EMBL, ABOL5086; AAA4298.1; ---
EMBL, ABOL5099; AAA8205.1; ---
INT A2590; WHECJS, 4HBCOA_thiost_AS.
INT EFFO; IPRO08684; 4HBCOA_thiostER.
FIGH, FROMOSE1; 1.
FIGREPAS; TIGRO0051; 1.
PROSITE; PS01228; 4HBCOA_THIOSTERASE; 1.
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Infect. Immun. 71:2775-2786(2003).
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EMBL; AE000177; AAC73830.1; -
EMBL; D90713; BAA35402.1; -.
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027443;
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                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAIN=VC-16 / DSM 4304 / ATCC 49558;
MEDLINE=98049343; PubMed=9389475;
MEDLINE=98049340; PubMed=9780475;
Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 19; DB 1; Length 139; 100.0%; Pred. No. 2.5e+02; ive 0; Mismatches 0; Indels
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein AF0586.
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HSSP, P11989; IRVO.
HAMAP, MF 00178; -; 1.
INTERPRO; IPR002180; DWRL synthase.
Pfam; PR00885; DWRL synthase; 1.
ProDom; P000364; DWRL synthase; 1.
TIGRFAMS; TIGR00114; rIDH; 1.
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Matches 4; Conservative
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  NCBI_TaxID=187420
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029669;
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STRAIN=VC-16 / DSM 4304 / ATCC 49558;

MIDDINIPS-960494313; Pubbed=9389475;

MEDLINES-960494313; Pubbed=9389475;

MEDLINES-960494313; Pubbed=9389475;

METCHAN H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,

Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,

Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,

Richardson D.L., Kerlavage A.R., McKenney K., Adams M.D., Loftus B.,

Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,

Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,

Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,

Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,

Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,

Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
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Nature 390:364-370(1997).
-!- FUNCTION: Riboflavin synthase is a bifunctional enzyme complex catalyzing the formation of riboflavin from 5-amino-6-(1'-D)-ribityl-amino-2,4(1H,3H)-pyrimidinedione and L-3,4-dihydrohy-2-butanone-4-phosphate via 6,7-dimethyl-8-lumazine. The beta subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-PED-2003 (Rel. 41, Last annotation update)
6.7-dimethyl-8-ribityllumazine synthase (EC 2.5.1.9) (DWRL synthase)
6.7-dimethyl-8-ribityllumazine synthase beta chain).
RIBH OR RIBE OR AF2128.
Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D., Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C., Felsefachmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S., Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou Joverbeek K., Gocayne J.D., Weldman J.F., McDonald L., Utterback T., Cotton M.D., Spriggs T., Arriach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujil C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The complete genome sequence of the hyperthermophilic, sulphate-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein; Complete proteome.
SEGUENCE 140 AA: 16175 MW; D3B1FE3A62A05901 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Archaea; Buryarchãeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE001064; AAB90658.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR, B69323; B69323.
TIGR; AF0586; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 24
CLM4_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
DDT TDD TTD DDT TTD TTD TT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
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               2,4(1H,3H)-pyrimidinedione with L-3,4-dihydrohy-2-butanone-4-phosphate yielding 6,7-dimethyl-8-lumazine (By similarity).
-!- CAPALYTIC ACTIVITY: 2 6,7-dimethyl-8-(1-D-ribityl)lumazine = riboflavin + 4-(1-D-ribitylamino)-5-amino-2,6-dihydroxypyrimidine.
-!- PATHMAY: Riboflavin blosynthesis; last step.
-!- SIMILARITY: Belongs to the DMRL synthase family.
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Science 289:905-920(2000).
-!- SIMILARITY: Belongs to the L13P family of ribosomal proteins.
catalyzes the condensation of 5-amino-6-(1'-D)-ribityl-amino-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ban N., Nissen P., Hansen J., Moore P.B., Steitz T.A., "The complete atomic structure of the large ribosomal subunit at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EXECUTION TO A SEQUENCE FROM N.A. MEDIJINE=92105119; PubMed=1840597; Kroemer W.J., Arndt E.; Kroemer W.J., Arndt E.; Arlalobacterial S9 operon. Three ribosomal protein genes are cortaniscribed with genes encoding a tRNA(Leu), the enolase, putative membrane protein in the archaebacterium Haloarcula (Halobacterium) marismortula.; Halobacterium) marismortula.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 19; DB 1; Length 143; Best Local Similarity 100.0%; Pred. No. 2.5e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Riboflavin biosynthesis; Transferase; Complete proteome.
SEQUENCE 143 AA; 15645 MW; BBA3141206905410 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haloarcula marismortui (Halobacterium marismortui).
Archaea, Euryarchaecta, Halobacteria, Halobacteriales,
Halobacteriaceae, Haloarcula.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
50S ribosomal protein L13P (Hmal13).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biol. Chem. 266:24573-24579(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00885; DWRL synthase; 1.
ProDom; PD003664; DWRL synthase; 1.
TIGRFAMS; TIGR00114; ribH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAMAP; MF 00178; -; 1.
InterPro; IPR002180; DMRL synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=ATCC 43049;
MEDLINE=20396344; PubMed=10937989;
                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE000957; AAB89124.1; -. PIR; H69515; H69515.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P11998; 1RVV.
TIGR; AF2128; -.
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ID RL13 HALMA
AC P29198;
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=21085660; PubMed=11217851;

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Kawai J., Shinagawa A., Shibata K., Xomo H., Adachi J., Fukuda S.,

A Arakawa T., Hara A., Fukulishi Y., Komo H., Adaukawa T., Saito N.,

A Arakawa T., Jawa M., Nishi K., Xiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casawant T.,

Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

Rushi P., Lewis S., Matsuo M., Nikaido I., Pesole G., Quackenbush J.,

Rushi P., Lewis S., Matsuo M., Aono H., Baldarelli R., Barsh G.,

Schriml L.M., Staubii F., Suzuki R., Tomita M., Wagner L., Washio T.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Lyons P., Ring B., Ringwald M., Rodriguez I., Sakamico N.,

Sasaki H., Satoo K., Schoenbach C., Seya T., Shibata Y., Storch K.F.,

Ruzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Havsehizaki A., Yoshida K., Hasegawa Y., Kawaji H., Rohtsuki S.,

Havsehizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .i. FUNCTION: Implicated in the early stage of ectopic ossification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fayashizaki Y.;
rPunctional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 19; DB 1; Length 145; 100.0%; Pred. No. 2.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         069CE666662AE3BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLM4_MOUSE STANDARD; PRT; 148 AA. 69JM83; 09CR31; 09DLE9; 16-CT-2001 (Rel. 40, Created) 16-CT-2001 (Rel. 40, Last sequence update) 28-FFB-2003 (Rel. 41, Last annotation update) Calmodulin 4 (Calcium-binding protein Dd112). CALM4 OR DD112.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                 EMBL; M7656; AAA73097.1; -..
PTR; B41715; B4775.
PDB; IRPK; C6.SEP-01.
PDB; IRPK; 19-UTL-02.
PDB; IXD1; 19-UTL-02.
PDB; IXD1; 19-UTL-02.
PDB; IXD1; 19-UTL-02.
PDB; IXD1; 23-AUG-02.
PDB; IMX; 113-AUG-02.
PDB; IXD1; 13-AUG-02.
PEACSTER; PS00572; Ribosomal_L13; 1.
TIGREAMs; TIGRO1077; L13, AE; 1.
PROSITE; PS00783; RIBOSOMAL_L13; 1.
Ribosomal protein; 3D-structure.
SEQUENCE 145 AA; 16228 MW; 069CE66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L13e/a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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115 VAEF 118
                                                                              RISB_PYRAE
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Matches
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                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its mes by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=90330536; PubMed=2165475;
Zwiczl P., Fabry S., Bogedain C., Haas A., Hensel R.;
Zwiczl P., Fabry S., Bogedain C., Haas A., Hensel R.;
"Glyceraldehyde-3-phosphate dehydrogenase from the hyperthermophilic archaebacterium Pyrococcus woesei: characterization of the enzyme, cloning and sequencing of the gene, and expression in Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pyrococcus woesei.
Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                          EF-HAND 1 (POTENTIAL).
EF-HAND 2 (POTENTIAL).
E-HAND 3 (POTENTIAL).
E -> V (IN REF. 2; BAB22914).
M -> V (IN REF. 2; BAB22914).
VEN -> I (IN REF. 1).
VEN -> I (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 19; DB 1; Length 148; 100.0%; Pred. No. 2.6e+02;
SIMILARITY: Contains 3 EF-hand calcium-binding domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein in GAPDH 3'region (ORF X) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         148 AA; 15256 MW; 8C7E51A072DF5D50 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Bacteriol. 172:4329-4338(1990).
PIR, S10655, S10655.
Hypothetical protein.
NON TER
SEQUENCE 149 AA; 15256 MW; 8C7
                                                                                                                                                          EMBL, AB036744; BAA95412.1; --
EMBL, AK009956; BAB26608.1; --
EMBL, AK00964; BAB26425.1; --
EMBL, AK009648; BAB2914.1; --
HSSP; P02593; 1CDM.
MGD, MGI:1991464; Calm4.
                                                                                                                                                                                                                                                                                                       FIGURE 5. PROUSES, ELECTORERIN.
PRODOM; PROUSES, ERCOVERIN.
PROSTER; PROUSES, EF, 4.
PROSTER; PROUSES, EF, 4.
PROSTER; PROUSES, EF, 4.
CASIND 21 87. F. HAND; 3.
CASIND 21 82. EF.
CASIND 57 68 EF.
CASIND 93 104 EF.
CASIND 93 104 EF.
CONFLICT 124 124 M.
CONFLICT 124 124 WED
                                                                                                                                                                                                                                                           InterPro; IPR002048; BF-hand.
InterPro; IPR001125; Recoverin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                              Pfam; PF00036; efhand; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148 AA;
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 VAEF 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pyrococcus.
NCBI_TaxID=2262;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PYRWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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P20298;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).

-Invorton: Acad. Sci. U.S.A. 99:984-989(2002).

-I FUNCTION: Riboflavin synthase is a bifunctional enzyme complex catalyzing the formation of riboflavin from 5-amino-6 (1'-D) ribity1-amino-2,4(1H,3H)-pyrimidinedione and L-3,4-dihydrohy-2-butanone-4-phosphate via 6,7-dimethy1-8-lumazine. The beta subunit catalyzes the condensation of 5-amino-6 (1'-D) ribity1-amino-2,4(1H,3H)-pyrimidinedione with L-3,4-dihydrohy-2-butanone-4-phosphate yielding 6,7-dimethy1-8-lumazine (By similarity).

-I CATALYTIC ACTIVITY: 2 6,7-dimethy1-8-(1-D ribity1) lumazine = riboflavin biosynthesis; last step.

-I PATHWAY: Riboflavin biosynthesis; last step.
-I SIMILARITY: Belongs to the DMRL synthase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                            10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
61-OCT-2003 (Rel. 42, Last annotation update)
67-dimethyl-8-ribityllumazine synthase (EC 2.5.1.9) (DWRL synthase)
61.00 (Lumazine synthase) (Riboflavin synthase beta chain).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=IM2 / ATCC 51768 / DSM 7523;
MEDLINE=21664397; PubMed=11792869;
Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
Miller J.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prodom; PD003664; DWRL synthase; 1.
TIGRRAMs; TIGR00114; ribH; 1.
Riboflavin biosynthesis; Transferase; Complete proteome.
SEQUENCE 150 AA; 16474 MW; 73751C1363A8ADBD CRC64;
                                                                                                                                                                                                                                                                 Pyrobaculum aerophilum.
Archaea, Crenarchaeota, Thermoprotei, Thermoproteales,
Thermoproteaceae, Pyrobaculum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
150 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HAMAP; MF_00178; -; 1.
InterPro; IPR002180; DMRL_synthase.
Pfam; PF00885; DMRL_synthase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE009923; AAL64819.1; -.
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Local 4; Conservative
STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=13773;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aerophilum.";
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P11418;
RISB_PYRAE
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                                   Q8ZTE3;
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SODC_PRIGL
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HAEIN
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PCP_HABIN
셤
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                                                                                                                                                                                                                                                                                                                                                                                               responsible to the control of the co
                                                                                                                                                                                                                              MEDLINE=89290012; PubMed=2500367; Calabrese L., Polticelli F., O'Neill P., Galtieri A., Barra D., Calabrese L., Polticelli F., O'Neill P., Galtieri A., Barra D., Schinina M.E., Bossa F.; "Substitution of arginine for lysine 134 alters electrostatic parameters of the active site in shark Cu, Zn superoxide dismutase."; FEBS Lett. 250:49-52(1989):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gapa
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10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
6,7-dimethyl-8-ribityllumazine synthase (RC 2.5.1.9) (DMRL synthase)
(Lumazine synthase) (Riboflavin synthase beta chain)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

STRAIN=ATCC 35092 / DSM 1617 / P2;

STRAIN=ATCC 35092 / DSM 1617 / P2;

STRAIN=2133226; PubMed=11427726;

She O., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,

Awayaz M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,

De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,

De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,

Theixamp-de Jong I., Jeffris A.C., Kozera C.J., Medina N., Peng X.,

Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,

Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland I.,
                         Prionace glauca (Blue shark).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Chondrichthyes,
Elasmobranchii, Galeomorphii, Galeoidea, Carcharhiniformes,
Carcharhinidae, Prionace
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sulfolobus solfataricus.
Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZINC.
COPPER.
BY SIMILARITY.
; 661764234F23C5AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COPPER.
COPPER AND ZINC.
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Superoxide dismutase [Cu-Zn] (EC 1.15.1.1)
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Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=2287;
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                                                                                                                                          NCBI_TaxID=7815;
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                                                                                                                                                                                                            SEQUENCE
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Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;

"The complete genome of the crenarchaeon Sulfolobus solfataricus P2.",
Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).

-!- FUNCTION: Riboflavin synthase is a bifunctional enzyme complex
catalyzing the formation of riboflavin from 5-amino-6-(1'-D)-
ribityl-amino-2,4(1H,3H)-pyrimidinedione and L-3,4-dihydrohy-2-
butanome-4-phosphate via 6,7-dimethyl-8-lumazine. The beta subunit
catalyzes the condensation of 5-amino-6-(1'-D)-ribityl-
amino-2,4(1H,3H)-pyrimidinedione with L-3,4-dihydrohy-2-
butanome-4-phosphate yielding 6,7-dimethyl-8-lumazine (By
                                                                                                                                                                                                                                                                                                                                                                                                                      -| CATALYTIC ACTIVITY: 2 6,7-dimethyl-8-(1-D-ribityl)lumazine = riboflavin + 4-(1-D-ribitylamino)-5-amino-2,6-dihydroxypyrimidine.
-| PATHWAY: Riboflavin biosynthesis; last step.
-| SIMILARITY: Belongs to the DWRL synthase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIJNE-88115138; PubMed=2828309; Deich R.A., Metcalf B.J., Finn C.W., Farley J.E., Green B.A.; Deich R.A., Metcalf B.J., Finn C.W., Farley J.E., Green B.A.; Cloning of genes encoding a 15,000-dalton peptidoglycan-associated outer membrane lipoprotein and an antigenically related 15,000-dalton J. Bacteriol. 170:489-498(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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STRAINERA ( FW20 / ARCC 51907;
STRAINERA ( FW20 / PLDMeda~7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
Kerlavage A.R., Bult C.J., Tromb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-1989 (Rel. 10, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Outer membrane lipoprotein PCP precursor (15 kDa lipoprotein) (PAL cross-reacting lipoprotein).
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Pasteurellaceae, Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 154;
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SEQUENCE 154 AA; 17247 MW; ADFA9E6A2C723210 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 19; DB 1; I 100.0%; Pred. No. 2.7e+02;
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InterPro; IPR00128; -; 1.
InterPro; IPR00128; DMRL_synthase.
ProDom; PD003664; DMRL_synthase; 1.
TIGREAMS; TIGR00114; rlbH; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; B90184; B90184.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 VABF 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb.ch/announce/or send an email to license@isb.ch).
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0
Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Geoglagen N.S.M., Gnehn C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Wenter J.C., "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
Taraxacum officinale (Common dandelion).
Fukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
campanulids; Asterales; Asteraceae; Cichorioideae; Cichorieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                         Science 269:496-512(1995).
-!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000437; Prok lipoprot S.
PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.
Outer membrane; Lipoprotein; Signal; Complete proteome; Palmitate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-palmitoyl cysteine.
S-diacylglycerol cysteine.
S-GLVAERVF - VAGRRVRI (IN REF. 1)
D7880327FCF0C985 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OUTER MEMBRANE LIPOPROTEIN PCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 19; DB 1; Length 155; 100.0%; Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xu X.-Y., Bewley J.D., Greenwood J.S.;
Submitted (DEC-1997) to the EMBL/GenBarnk/DDBJ databases.
-!- ALLERGEN: Causes an allergic reaction in human.
-!- SIMILARITY: Belongs to the BetVI family.
                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: TO E.COLI AND S.TYPHIMURIUM SLYB AND TO Y.ENTEROCOLITICA PCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 157 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 155 OUT
19 19 N-F
19 19 S-d
135 143 CSL
155 AA; 15425 MW; L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M18877; AAA24938.1; -.
EMBL; U32832; AAC23228.1; -.
PIR; 164130; 164130.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           138 VAEF 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=50225;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGR; HI1579;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Root;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RAP_TAROF
049065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Paraxacum.
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CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: Riboflavin synthase is a bifunctional enzyme complex catalyzing the formation of riboflavin from 5-amino-6-(1'-D)-ribityl-amino-2,4(1H,3H)-pyrimidinedione and L-3,4-dihydrohy-2-butanone-4-phosphate via 6,7-dimethyl-8-lumazine. The beta subunit catalyzes the condensation of 5-amino-6-(1'-D)-ribityl-amino-2,4(1H,3H)-pyrimidinedione with L-3,4-dihydrohy-2-butanone-4-phosphate yielding 6,7-dimethyl-8-lumazine (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21456156; PubMed=11572479; Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M., Kawarabayasi Y., Hino Y., Horikawa H., Jon-no K., Takahi S., Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S., Nagai Y., Nishijima K., Otsua R., Nakazawa H., Takamiya M., Kato Y., Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A., Oshima T., Kikuchi H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- CATALYTIC ACTIVITY: 2 6,7-dimethyl-8-(1-D-ribityl)lumazine = riboflavin + 4-(1-D-ribitylamino)-5-amino-2,6-dihydroxypyrimidine-
-!- PATHWAY: Riboflavin biosynthesis; last step.
-!- SIMILARITY: Belongs to the DWRL synthase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
6,7-dimethyl-8-ribityllumazine synthase (EC 2.5.1.9) (DMRL synthase)
(Lumazine synthase) (Riboflavin synthase beta chain).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                 100.0%; Score 19; DB 1; Length 157; 100.0%; Pred. No. 2.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete genome sequence of an aerobic thermoacidophilic
Crenarchaeon, Sulfolobus tokodaii strain7.";
DNA Res. 8:123-140(2001).
                                                                                                                                                                                                                                        0; Indels
                                                                                            PRINTS; PRO0634; BETALLERGEN.
PROSITE; PS00451; PATHOGRNESIS BETVI; 1.
Allergen, Plant defense; Pathogenesis-related protein.
SEQUENCE 157 AA; 17040 MW; 5892AB8593A8A7E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                   157 AA.
                                                                                                                                                                                                                                          0, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, AP000982; BAB65375.1; -.
HAMAP; MF 00178; -; 1.
InterPro; IPR002180; DMRL_synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00885; DMRL synthase; 1.
ProDom; PD003664; DWRL synthase; 1.
                 EMBL; AF036931; AAB92255.1; --
HSSP; O24248; 1E09.
InterPro; IPR000916; Bet_v_I.
Pfam; PF00407; Bet_v_I; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ProDom; PD003664; DMRL syntha
TIGRFAMS; TIGR00114; ribH; 1.
                                                                                                                                                                                                                                               4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=JCM 10545 / 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sulfolobus tokodaii.
                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                    1 VAEF 4
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us-09-594-978a-2.rsp

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YEAST
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P32630;
                                                                                                             Signal
                                                                                                                                                                                                         RESULT 33
UTR5_YEAST
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                                  Gaps
                                                                                                                                                                                            STRAIN=Oregon-R;
MEDLINE=87086754; PubMed=3098981;
Shore E.M., Guild G.M.;
"Larval salivary gland secretion proteins in Drosophila structural analysis of the Sgs-5 gene.";
J. Mol. Biol. 190:149-158(1986).
                                  ;
                                                                                                                                  Drosophila melanogaster (Fruit fly).

Eukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Bphydroidea; Drosophilidae; Drosophila.
                     Length 157;
                                 0; Indels
Riboflavin biosynthesis; Transferase; Complete proteome. SEQUENCE 157 AA; 17501 MW; 5295580775164A18 CRC64;
                    Score 19; DB 1; L
Pred. No. 2.8e+02;
                                                                                              SGSS_DROME STANDARD; PRT; 163 AA. P07701; Q9VEIS; 107. Created) 01-ARR-1988 (Rel. 07, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) 2GIVARY glue protein Sgs-5 precursor. GSS OR CG7596.
                                  0; Mismatches
                    Query Match
Best Local Similarity 100.0%;
Matches 4; Conservative 0
                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                             14 VAEF 17
                                                1 VAEF 4
                                                                                 RESULT 32
3GS5_DROME
 3 %
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                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the "EMBL outstation the buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"The gene clusters ARC and COR on chromosomes 5 and 10, respectively, of Saccharomyces cerevisiae share a common ancestry.";
J. Mol. Biol. 233:372-388(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Eukaryota, Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 18 POTENTIAL.
19 163 SALIVARY GLUE PROTEIN SGS-5.
163 AA, 18821 MW, 3A476FID3B06D864 CRC64;
                                                            Drosophila melanogaster.";
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., "The genome sequence of Drosophila melanogaster."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
110-OCT-2003 (Rel. 22, Last annotation update)
UTRS protein (Unknown transcript 5 protein)
UTRS OR YEL035C OR SYGP-ORF27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               166 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE003718; AAF55436.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X04269; CAA27820.1; -.
                                                                                                                                Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A24504; A24504.
FlyBase; FBgn0003375; Sgs5.
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STANDARD;
                     BFL1 MOUSE
Q07440;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           strain 1.";
Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
-!- FUNCTION: This protein is essential for replication of the chromosome. It is also involved in DNA recombination and repair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PS9932. Q7UXV3;

15-MAR-2004 (Rel. 43, Created)

15-MAR-2004 (Rel. 43, Last sequence update)

15-MAR-2004 (Rel. 43, Last sequence update)

15-MAR-2004 (Rel. 43, Last annocation update)

Single-strand binding protein (SSB) (Helix-destabilizing protein).

SSB OR RB9917.

Rhodopirellula baltica.

Bacteria, Planctomycetes; Planctomycetacia; Planctomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete genome sequence of the marine planctomycete Pirellula sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
Schlesner H., Amann R., Reinhardt R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 19; DB 1; Length 169; 100.0%; Pred. No. 38+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE, PS50935, SSB, 1.
DNA-binding; DNA repair; DNA replication; Complete proteome
                                                                                                                                                                                                                                                                              100.0%; Score 19; DB 1; Length 166; 100.0%; Pred. No. 2.9e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 POLY-GLY.
18108 MW; AA8F93E0FA51F287 CRC64;
                                                                                                                                                                                                     RGNTTIN (IN REF. 1).
166 AA; 19335 MW; ASBEBBDOFAGD3DEA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              169 AA.
                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -! - SIMILARITY: Contains 1 SSB domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22735913; PubMed=12835416;
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EMBL; L22173; AAA34936.1; -.
EMBL; S65964; AAD13970.1; -.
EMBL; S6620; AAB28442.1; -.
EMBL; U18779; AAB5507.1; -.
PIR; S50509; S50509.
GGTOOTILINE; 139039; -.
SGD; S000761; UTES.
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Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                      4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               169 AA;
                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                   92 VAEF 95
                                                                                                                                                                                                                                                                                                                                                                                   1 VAEF 4
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28 VAEF 31

ESULT 35

1 VAEF 4

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                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                             MEDLINE-33346743; PubMed:83345191;
Lin E.Y., Orlofsky A., Berger M.S., Prystowsky M.B.;
"Characterization of Al, a novel hemopoietic-specific early-response
gene with sequence similarity to bcl-2.";
J. Immunol. 151:1979-1988(1993).
                                      01-FEB-1995 (Rel. 31, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Bcl-2-related protein Al (BFL-1 protein) (Hemopoietic-specific early
                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                      MEDIJNE-98307518; PubMed-9645611;
Hatakeyama S., Hamasaki A., Negishi I., Loh D.Y., Sendo F.,
Nakayama K., Nakayama K.-I.;
"Multiple gene duplication and expression of mouse bcl-2-related
genes, Al.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 19; DB 1; Length 172; 100.0%; Pred. No. 3e+02; cive 0; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37AD35818E756488 CRC64;
172 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALA/PRO-RICH.
BH1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; L16462; AAA16886.1; -.
EMBL; U23774; AAB97953.1; -.
EMBL; U23773; AAB97953.1; JOINED.
PIR; 149449; 149449.
HSSP; QO7817; INAZ.
MGD; MGI:102687; BC12ala.
InterPro; IPR004475; BC12_Emily.
PRT;
                                                                                                                                                              [1]
SEQUENCE FROM N.A.
""""THE GRA/J; TISSUE=Bone marrow;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART, SM00337, BCL, 1.
SMOSITE, PSS0062, BCL2 FAMILY, 1.
PROSITE, PS01080, BH1; 1.
PROSITE, PS01258, BH2; 1.
                                                                            response protein) (A1-A).
BCL2A1 OR BCL2A1A OR BFL1 OR A1.
Mus musculus (Mouse),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19914 MW;
                         01-FEB-1995 (Rel. 31, Created)
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=129/Sv; TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24
77
132 1
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Matches 4; Conserv
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CONFLICT
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DDTTCOOC OCT STANKER S
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MEDLINE-22388257; PubMed=12477932,

RISILENE, 2288257; PubMed=12477932,

RISILENE, 2011ins F.S., Wagner L., Sheamen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetcow K.H., Scheefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetcow K.H., Scheefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetcow K.H., Scheefer C.F., Bhat N.K.,

Batchench C., Marusina K., Farmer A.A., Rubin G.M., Hang L.,

Brachercon M., Scares M.B., Bonaldo M.F., Casavant T.L., Scheefer T.E.,

Bras S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bras S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bras S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gibs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gargues S., Sanchez A.

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Graen B.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Marra M.A.,

Rodriguez A.C., Grimwood J., Schmutz J., Marra M.A.,

Rodriguez A.C., Grimwood J., Schmutz J., Marra M.A.,

Roderstein and mouse cDNA sequences "; Sen M. Marra M.A.;

Froc. Natl. Acads apoptosis induced by IL-3 deprivation. May

Froc. Natl. Acads apoptosis induced by IL-3 deprivation. May

Frim In maintaining endothelial survival during infection (By

similarity.)
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"GRS, a novel member of the Bcl-2 gene family, is highly expressed in multiple cancer cell lines and in normal leukocytes.";
Oncogene 14:997-1001(1997).
                                                                                                                                                                                BFL1 HUMAN STANDARD; PRT; 175 AA.
Q16548; Q95524;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-2014 (Rel. 43, Last annotation update)
BCl-2-related protein Al (BFL-1 protein) (Hemopoietic-specific early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Choi S.S., Park I.-C., Yun J.W., Sung Y.C., Hong S.-I., Shin H.-S., "A novel Bcl-2 related gene, Bfl-1, is overexpressed in stomach cancer and preferentially expressed in bone marrow."; Oncogene 11:1693-1698(1995).
                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Umbilical vein,
MEDLINE=96184764; PubMed=8605321;
Karsan A., Yee E., Kaushansky K., Harlan J.M.;
"Cloning of hwan Bcl-2 homologue: inflammatory cytokines induce human A1 in cultured endothelial cells.";
Blood 87:3089-3096(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97203281; PubMed=9050999;
Kenny J.J., Knobloch T.J., Augustus M., Carter K.C., Rosen C.A.,
Lang J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMITATION: Intracellular.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Liver;
MEDLINE=96068895; PubMed=7478596;
                                                                                                                                                                                                                                                                                                                                             response protein) (GRS protein). BCL2A1 OR BFL1 OR GRS OR BCL2L5.
                                                                                                                                                                                                                                                                                                                                                                                                 (Human)
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TISSUE=T-cell;
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                                                    122 VAEF 125
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-i- TISSUE SPECIFICITY: Seems to be restricted to the hematopoietic compartment. Expressed in peripheral blood, spleen, and bone marrow, at moderate levels in lung, small intestine and testis, a minimal levels in other tissues. Also found in vascular smooth muscle cells and hematopoietic malignancies.
-i- INDUCTION: By phorbol ester and inflammatory cytokines, such as TNF-alpha, or IL-1-beta, but not by growth factors.
-i- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
-i- SIMILARITY: Belongs to the Bcl-2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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MEDLINE=87222424; PubMed=3495534;
Dickey L.F., Sreedharan S., Theil B.C., Didebury J.R., Wang Y.-H.,
Kaufman R.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
10-OCT-2003 (Rel. 42, Last annocation update)
10-OCT-2003 (Rel. 42, Last annocation update)
Ferritiin, middle subunit (Ferritin M) (Ferritin X) (Ferritin H').
Rana catesbelana (Bull frog).
Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota, Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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100.0%; Score 19; DB 1; Length 175;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MIM; 601056; --
GO: 0008189; F: apoptosis inhibitor activity; TAS.
GO: GO: 000816; F: apoptosis inhibitor activity; TAS.
GO: GO: 000816; F: anti-apoptosis; TAS.
InterPro; IPR000712; BC12_BH.
InterPro; IPR000475; BC12_Emily.
PFAM; PR00452; BC12; 1.
PROSTIE; PS01086; BC1; 1.
PROSTIE; PS01080; BH1; 1.
PROSTIE; PS01080; BH1; 1.
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Q -> H (IN REF. 3).
; 329D98AF2BE07A0D CRC64;
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BH1.
BH2.
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97 BB
147 BB
72 N
107 Q
20132 MW;
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EMBL, U27467; AAC50288.1; --
EMBL, Y09397; CAA70566.1; --
EMBL, BC016281, AAH16281.1; --
PIK, I39055; I39055.
HSSP, P53563; IAF3.
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77
132
12
107
105 AA;
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Last sequence update) Last annotation update)

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                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=MB4 / JCM 11007;
MEDLINE=21992816; Pubmed=11997336;
Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
Chen Y., Xue Y., Xu Y., Lian X., Huang L., Dong X., Ma Y., Ling L.,
Tan H., Chen R., Wang J., Yu J., Yang H.,
Tan H., Chen R., Wang J., Yu J., Yang H.,
Tan H., Complete sequence of T. tengcongensis genome.";
Genome Res. 12:689-700(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: Belongs to the L10P family of ribosomal proteins.
                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HAMAP; MF 00362; -; 1.
InterPro; IPR001790; Ribosomal_L10.
InterPro; IPR00263; Ribosomal_L10eub.
Pfam; PF00466; Ribosomal_L10; I.
PROSITE; PS01109; RIBOSOMAL_L10; FALSE_NEG.
Ribosomal_protein; Complete_proteome.
SEQUENCE 177 AA; 19591 MW; SODDCF896EF6i
                                                                                                                                                                                                                                  Thermoanaerobacter tengcongensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE013173; AAM25445.1; -.
                                                                                                                                                      508 ribosomal protein L10.
                                 (Rel. 41, (Rel. 41, 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                        RPLJ OR TTE2304
                             28-FEB-2003 (
28-FEB-2003 (
28-FEB-2003 (
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Matches
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SOW WENT THE COURT OF THE COURT
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                                                                                                                                                                                        Ha Y., Shi D., Small G.W., Theil E.C., Allewell N.M.;
"Crystal structure of bullfrog M ferritin at 2.8 A resolution:
"Crystal structure of bullfrog M ferritin at 2.8 A resolution:
analysis of subunit interactions and the binuclear metal center.";
J. Biol. Inorg. Chem. 4:243-256(1999).
-!- FUNCTION: Ferritin is an intracellular molecule that stores iron in a soluble, nontoxic, readily available form. The functional molecule, which is composed of 24 chains, is roughly spherical and contains a central cavity into which the polymeric ferric iron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MISCELLANEOUS: THERE ARE THREE TYPES OF PERRITIN SUBUNITS: L, M AND H CHAINS IN AMPHIBIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, J02724; .-

EMBL, J02724; .-

PIR, C27805, C7805.

PDB; IMFR, 22-UUN-99.

InterPro; IPR001519; Ferritin.

InterPro; IPR001519; Ferritin. Dps.

InterPro; IPR001040; Ferritin. Ilke.

ProDom; PD0000971; Ferritin; 1.

PROSITE; PS00200; FERRITIN. 1; 1.

PROSITE; PS50905; FERRITIN. Ilke.

Iron storade; Iron; Metal-Einding; 3D-structure.

Iron storade; Iron; Metal-Einding; 3D-structure.

Iron Storade; Iron (BY SIMILARITY).

FERRITIN. Ilke.

IRON (BY SIMILARITY).

IRON (BY SIMILARITY).

IRON (BY SIMILARITY).

IRON (BY SIMILARITY).

IRON (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: Belongs to the ferritin family. SIMILARITY: Contains 1 ferritin-like diiron domain.
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                                                                                                                 X-RAY CRYSTALLCGRAPHY (2.8 ANGSTROMS).
MEDLINE-99367924; Pubmed=10439069;
the first processed in amphibia."; J. Biol. Chem. 262:7901-7907(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           core is deposited
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176 AA;
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Matches 4; Conserv
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Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.; "Complete genomic sequence of Pasteurella multocida Pm70."; Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
                                  ö
                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Pasteurella.
                                                                                                                                                                                         DSBB PASMU STANDARD; PRT; 178 AA.
Q9L6B3; P57804;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Disulfide bond formation protein B (Disulfide oxidoreductase)
                                                                                                                                                                                                                                                                                                                                                                                                                 Fuller T.E., Kennedy M.J., Lowery D.E.;
"Identification of Pasteurella multocida virulence genes in a
septicemic mouse model using signature-tagged mutagenesis.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                  Indels
100.0%; Score 19; DB 1; L
100.0%; Pred. No. 3.1e+02;
.ive 0; Mismatches 0;
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MEDLINE=21145866; PubMed=11248100;
                                    4; Conservative
                                                                                                                                                                                                                                                                                                                 Pasteurella multocida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                     1 VAEF 4
                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=747;
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Gaps

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Conservative

51

1 VAEF 4 48 VAEF 177 AA.

STANDARD;

ESULT 38 L10\_THETN D \_RL10\_THETN

; 0

Length 177;

19591 MW; 50DDCF896EF6F4E8 CRC64;

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                                                                                                                                                                                                                                                                                                                                     Gaps
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Klaembt C., Knust E., Tietze K., Campos-Ortega J.A.;
Closely related transcripts encoded by the neurogenic gene complex
enhancer of split of Drosophila melanogaster.";
EMBO J. 8:203-210(1989).
                                                                   similarity)
-!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N. Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DROWE STANDARD; PRT; 178 AA.

P13056; Q9VB18;

1 0.1-3AN-1990 (Rel. 13, Created)

1 15-MAR-2004 (Rel. 13, Last sequence update)

T 15-MAR-2004 (Rel. 43, Last annotation update)

Exhancer of split m5 protein (E(spl)m5).

HLMM OR CG6096.

Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Doptephydroidea; Dorsophilade, Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
FUNCTION: Required for disulfide bond formation in some periplasmic proteins. Acts by oxidizing the dsbA protein (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PERIPLASMIC (POTENTIAL).
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                                                                                                               (By similarity).
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MEDLINE=20196006; PubMed=10731132;
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1es 4; Conservative
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178 AA;
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Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Abril J.F., Adjavani A., An H.-J., Andrews-Peannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Ballew R.M., Basu B.P., Barman B.P., Brandari D., Bolshakov S., Barkordan M.R., Bouck J., Broketein P., Brotter P., Charles P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davemport L.B., Davies P., Cherry J.M., Cawley S., Dahlke C., Davemport L.B., Davies P., Brotter M., Chandra I., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Borlein M.J., Branqelista C.C., Ferraz C., Ferriara S., Fleischmann W., Rosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Classer K., Glock A., Gonrell J.H., Gu Z., Guan P., Harris M.L., Earvey D.A., Heiman T.J., Wei M.-H., Ibegwam C., Jalail M., Kalush F., Karpen G.H., Re. Y., Kraft C., Liang Y., Lin X., Lisko P., Lei Y., Levitsky A.A., Li M., Li Z., Liang Y., Lin X., Martei B., McIntosh T.C., McLeod M.P., McPherson D., Mount S.M., Muy M., Muydhy B., Murphy D.M., Nelson D.M., Nelson D.M., Nelson D.K., Nelson K., Staplech T., Rorner E., Wang A.H., Wang X., Shue B.C., Siden-Kiamos I., Staplech M., Sturng R., Sun R., Shen H., Mang X., Shen R., Spier B., Spier B., Spradling A.C., Staplech M., Sturng R., Sun R., Mang S., Wang S., Zhu X., Smith H.O., R. Andrews B.M., Moodage T., Worley C., Mang G., Zhao M., Zhou X., Zhu X., Zhu X., Smith H.O., Albergen D. R., Albergen B.M., Zhou K., Zhu M., Zhou X., Zhu X., Smith H.O., Albergen B.M., Whore E., Wang S., Zhao M., Zhou X., Zhu M., Zhou X., Zhu X., Zhu X., Smith H.O., Steinece 287:2185-2195(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --- FUNCTION: Participates in the control of cell fate choice by uncommitted neurodectodermal cells in the embryo. Transcriptional repression moifse: 5'-CACNAG-3'.

--- SUBJURIT: Transcription repression requires formation of a complex with a co-repressor protein (Groucho). Forms homodimers.

--- SUBSILIULAR LOCATION: Nuclear (Probable).

--- SUBSILIULAR LOCATION: Nuclear (Probable).

--- DEVELOPMENTAL STAGE: Expressed at the time when separation of neural and epidermal precursors cells occurs. Mesectodermal expression appears shortly before the onset of gastrulation.

--- DOMAIN: The orange domain and the basic helix-loop-helix motific mediate prepression of specific transcriptional activators, such as basic helix-loop-helix protein dimers.

--- DOMAIN: The C-terminal WEWFW motifies a transcriptional repression domain necessary for the interaction with Groucho, a transcriptional co-repressor recruited to specific target DNA by Hairy-related proteins.

--- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIINE=95094252; PubMed=8001118; Paroush Z., Finley R.L. Ur., Kidd T., Wainwright S.M., Ingham P.W., Paroush Z., Finley R.L. Or., Kidd T., Wainwright S.M., Ingham P.W., Isb-Horowicz D.; Rish-Horowicz D.; "Groucho is required Dr. Drosophila neurogenesis, segmentation, and sex determination and interacts directly with hairy-related bHLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X16552; CAA34552.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       proteins.";
cell 79:805-815(1994)
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EMBL; AB003754; AAF56552.1; -. PIR; S03629; S03629.

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SEQUENCE
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Ketchum K.A., Dodson R.J., Gwinn M., Hickey B.K., Peterson J.D.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Pleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.D.,
Peterson S., Reich C.I., McKenlu L.K., Badger J.H., Glodek A., Zhou L.,
Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Nature 390:364-370(1997).
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                                                             GO; GO: 0005634, C: nucleus; IDA.
GO; GO: 0005634, C: nucleus; IDA.
GO; GO: 0003677; F: DNA binding; IDA.
GO; GO: 0003677; F: DNA binding; IDA.
InterPro; IPR001092; HLH; basic.
Ffam; PF00010; HLH; 1.
SMART; SW00353; HLH; 1.
SWART; SW00511; ORANGE; 1.
PROSITE; PS50888; HLH; 1.
Differentiation; Neurogenesis; Nuclear protein; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 19; DB 1; Length 178; 100.0%; Pred. No. 3.1e+02; tive 0; Mismatches 0; Indels
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FIGR; AF1118; -- Signal; Complete proteome.

Hypothetical protein; Signal; Complete proteome.

SIGNAL

178 HYPOTHETICAL PROTEIN AF1118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORANGE.
WRPW MOTIF.
19363D0F6043C84F CRC64;
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Archaeoglobaceae; Archaeoglobus.
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HELIX-LOOP-HELIX MOTIF.
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(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
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STRAIN=VC-16 / DSM 4304 / ATCC 49558;
MEDLINE=98049343; PubMed=9389475;
                                                                                                                                                                                                                                                                                                                                                                              Transcription regulation; Repressor.
DNA_BIND 19 33 BASIC D
DOMAIN 34 74 HELIX-L
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                                FBgn0002631; HLHm5
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Archaeoglobus fulgidus.
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129
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Best Local Similarity
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B18 ARCFU
D YB18 ARCFU
C 029147;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-0CT-2001
       TRANSFAC; FlyBase; Fi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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CTRAIN=3500HP / ATCC 700724;
Munson R.S. Jr., Ray W.C., Mahairas G., Sabo P., Mungur R.,
Munson R.S. Jr., Ray W.C., Mahairas G., Sabo P., Mungur R.,
Annoson L., Nguyen D., Wang J., Forst C., Hood L.;
In "The complete genome sequence of Haemophilus ducrey!.";
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
I. FUNCTION: Catalyzes a salvage reaction resulting in the formation of AMP, that is energically less costly than de novo synthesis.
C. !- CATALYTIC ACTIVITY: AMP + diphosphate = adenine + 5-phospho-alpha-D-ribosos 1-diphosphate.
C. I. CATALYTIC HOMOdimer (By similarity).
C. !- PATHWAY: Purine salvage.
C. !- SUBUNIT: Homodimer (By similarity).
C. !- SUBCATION: Cytoplasmic.
C. !- SUBCATION: Belongs to the purine/pyrimidine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its wase by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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HAMAP; MF 00004; -; 1.

InterPro; IPR002375; Pr/py_rp transf.

InterPro; IPR000375; Pr/py_rp transf.

InterPro; IPR000186; PRTransferase.

PRam; PR00186; Pribosyltran; 1.

TIGGRAMs; TIGR01090; apt; 1.

TIGGRAMs; TIGR01090; apt; 1.

TIGGRAMs; TIGR01090; pW PW RTANSFER; 1.

TRANSFERSE; Glycosyltransferase; Purine salvage; Complete proteome.

Transferase; Glycosyltransferase; Purine salvage; TRANSFER; 1.

Transferase; Glycosyltransferase; Purine salvage; TRANSFER; 1.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haemophilus ducreyi.
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
                                                      100.0%; Score 19; DB 1; Length 178; 100.0%; Pred. No. 3.1e+02; ive 0; Mismatches 0; Indels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
19319 MW; 378A4F200240D924 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-MAR-2004 (Rel. 43, Last Sequence update)
Adenine phosphoribosyltransferase (SC 2.4.2.7) (APRT).
APT OR HD1918.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 19; DB 1; L
100.0%; Pred. No. 3.1e+02;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Q7VXQ4;
15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last seq
15-MAR-2004 (Rel. 43, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE017156; AAP96568.1; -.
                            Query Match
Best Local Similarity 100...
4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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   178 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                              155 VAEF 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VAEF 48
                                                                                                                                                                               1 VAEF 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=730;
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RETB BOVIN
ID RETB BOVIN
AC P18902;
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Kidney glomerul.

Kidney glomerul.

Sorceted.

Sorceted.

Soluzina Locarion Secreted.

Soluzina Locarion Secreted.

Soluzina Locarion Secreted.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).

MEDLINE=93266508; PubMed=8496140;
Zanotti G., Berni R., Monaco H.L.;
Zanotti G., Berni R., Monaco H.L.;
Crystal structure of liganded and unliganded forms of bovine plasma retinol-binding protein.";
J. Biol. Chem. 268:10728-10738 (1993)
J. FUNCTION: Delivers retinol from the liver stores to the peripheral tissues. In plasma, the RBP-retinol complex interacts with transchyretin, this prevents its loss by filtration through the
                                                                                                                                                                                                                                                                   Zanotti G.; "If a settinol-binding protein. Amino acid sequence, "The bovine plasma retinol-binding protein. Amino acid sequence, interaction with transthyretin, crystallization and preliminary X-ray
                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Expression and cellular localization of retinol-binding protein messenger ribonucleic acid in bovine blastocysts and extraembryonic
                                                                                                  Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY.
MEDLINS-92322903; PubMed=1623143;
Monaco H.L., Zanotti G.
"Three-dimensional structure and active site of three hydrophobic molecule-binding proteins with significant amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-93385352; PubMed-8373966;
Liu K.H., Dore J.J. Jr., Roberts M.P., Krishnan R., Hopkins F.M.,
Godkin J.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0179; LIPOCALIN.
PROSITE; PS00213; LIPOCALIN; 1.
Plasma; Vitamin A; Retinol-binding; Transport; Liver; Lipocalin;
                                                                                                                                                                                                                              MEDLINE=91006139; PubMed=2209607;
Berni R., Stoppini M., Zapponi M.C., Meloni M.L., Monaco H.L.,
Zanotti G.;
01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
02-FEB-2003 (Rel. 41, Last annotation update)
Plasma retinol-binding protein (PRBP) (RBP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PDB; 1HBP; 31-JAN-94.
PDB; 1HBQ; 31-JAN-94.
PDB; 1FEL; 01-NOV-94.
PDB; 1FEN; 01-NOV-94.
PDB; 1FEN; 01-NOV-94.
InterPro; 1FR002345; Lipocalin.
InterPro; 1FR002345; Lipocalin.
                                                                                                                                                                                                                                                                                                                                               Eur. J. Biochem. 192:507-513(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3iol. Reprod. 49:393-400(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  iopolymers 32:457-465(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00061; lipocalin; 1.
                                                                                                                                                                                                                                                                                                                                                                        [2]
SEQUENCE OF 52-183 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, S65585, AAB28336.1;
PIR, 146955, 146955.
PIR, S13186, S13186.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1ERB; 31-JAN-94.
1HBP; 31-JAN-94.
1HBQ; 31-JAN-94.
1FEL; 01-NOV-94.
                                                                                                Bos taurus (Bovine).
                                                                                                                                                                   NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similarity."
                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wolbachia sp.
Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales;
Rickettsiaceae; Wolbachieae; Wolbachieae;
NCBI_TaxID=956;
                                                                                                                                                                                                                                                                   100.0%; Score 19; DB 1; Length 183; 100.0%; Pred. No. 3.2e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
28-FEB-2003 (Rel. 41, Last amotation update)
Chromosomal replication initiator protein dnaA (Fragment)
                                                                                                                                                                                                                                                   21068 MW; D6BA064CB9E67C09 CRC64;
          BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                        186 AA
                                                                                                                                                                                                                                                                                       4; Conservative
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            183 AA;
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Matches 4; Conserv
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3D-structure.
DISULFID
DISULFID
DISULFID 17
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P35907;
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                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDILINE-88007612; PubMed=2820981; MEDILINE-88007612; PubMed=2820981; Kurowski B., Ludwig B.; Kurowski B., Ludwig B.; "The genes of the Paracoccus denitrificans bc1 complex. Nucleotide sequence and homologies between bacterial and mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
01-NAX-2004 (Rel. 43, Last annotation update)
Ubiquinol-cytochrome C reductase iron-sulfur subunit (EC 1.10.2.2)
(Rieske iron-sulfur protein) (RISP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gubunits.",
J. Biol. Chem. 262:13805-13811(1987).
-!-FUNCTION: Component of the ubiquinol-cytochrome c reductase
complex (complex III or cytochrome b-c1 complex), which is a
respiratory chain that generates an electrochemical potential
coupled to ATP synthesis.
-!-CATALYTIC ACTIVITY: QH(2) + 2 ferricytochrome c = Q + 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ferrocytochrome c.
-!- COFACTOR: Binds 1 2Fe-28 iron sulfur cluster per subunit (By
                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Paracoccus denitrificans.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
Rhodobacteraceae; Paracoccus.
                                                                                                                                                                                                                                                                                                                                               h Similarity 100.0%; Score 19; DB 1; Length 186; Similarity 100.0%; Pred. No. 3.3e+02; 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                  186 AA; 21283 MW; C423C06CEFFB0459 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein.
SIMILARITY: Belongs to the Rieske family.
EMBL, Z28981; CAA82285.1; -.
PIR; S39317; S39317.
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HAMAP, MF_00377; -; 1.
INTERFO; IPR001957; Bac_DnaA.
PENTYS; PR000051; DNAA.
PRINTS; PR000051; DNAA.
DNA replication; DNAA, PARTIAL.
NON TER 1 1
NON TER 186 186
SEQUENCE 186 AA; 21283 MW; C423C06CEFFB0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interprof. 1PR005805; Rieske.
InterProf. 1PR005806; Rieske dom.
InterProf. 1PR006317; Rieske_proteo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M17522; AAA25571.1; -. EMBL; X05799; CAA29243.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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HSSP; P13272; 1RIE.
                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               134 VAEF 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 VAEF 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ESULT 45
CRI PARDE
D UCRI PARDE
C P05417;
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-!- FUNCTION: CAN EFFICIENTLY HYDROLYZE NONSTANDARD NUCLEOTIDES SUCH
AS XTP TO XMP OR ITP TO IMP, BUT NOT THE STANDARD NUCLEOTIDES. XTP
IS THE BEST SUBSTRATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=JAL-I DSW 2661 / ATCC 43067;
MEDLINE=96337999; PubMed=8688087;
MEDLINE=96337999; PubMed=8688087;
MEDLINE=96337999; PubMed=8688087;
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D., Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D., Rerlavage A.R., Doughberty B.A., Tomb J.-F., Adams M.D., Reich C.I., Gocaphagen N.S.M., Weidman J.F., Fuhrmann J.L., Glodek A., Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D., Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.M., Banna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C., "Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
MEDLINE=9932061; PubMed=1040428;
MHANDG W.Y., Chung J.H., Kim S.-H., Han Y.S., Cho Y.;
"Ştructure-based identification of a novel NTPase from Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                         (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Nucleoside-triphosphatase (EC 3.6.1.15) (Nucleoside triphosphate
phosphohydrolase) (NTPase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 100.0%; Score 19; DB 1; Length 190; Local Similarity 100.0%; Pred. No. 3.38+02; hes 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   F83F5D9A9C1FBEE4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Archaea; Buryarchaeota; Methanococci; Methanococcales; Methanocaldococcaceae; Methanocaldococcus. NGBI_TaxID=2190;
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                                                                                                                                                                                                                                                                                         IRON-SULFUR (2FE-2S) (IRON-SULFUR (2FE-2S) (IRON-SULFUR (2FE-2S) (IRON-SULFUR (2FE-2S) (BY SIMILARITY.

    -!- SUBUNIT: Homodimer.
    -!- SIMILARITY: Belongs to the HAM1 NTPase family.

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InterPro; IPR006311; Tat
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152
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137
137
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NTPA METJA
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"Complete genome sequence of the alkaliphilic bacterium Bacillus
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P05823;
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SEQUENCE PROM N.A.
SEQUENCE PROM N.A.
MEDLINE-C-125 / JCM 9153;
MEDLINE-20512582; PubMed=11058132;
MEDLINE-20512582; PubMed=11058132;
MEDLINE-20512582; PubMed=11058132;
MEDLINE-20512582; PubMed=11058132;
MEDLINE-11: H., NakaBone K., Takaki Y., Maeno G., Sasaki R., Masui N., Horikoshi K.;
Horikoshi K.;
                                                                                                                                                                                                                                                                        TIGR; MJ0226; -. HAMD: 1. MF 01405; 
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Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=86665;
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
HAM1 protein homolog 2.
                                                                                                                                                                     EMBL; U67478; AAB98211.1; -
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PDB; 1B78; 28-JAN-00.
PDB; ZMJP; 28-JAN-00.
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Best Local Similarity
Matches 4; Conserv
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09K8D9;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENBL outstation the Buropean Bioinformatics in Statement of Broomers are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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halodurans and genomic sequence comparison with Bacillus subtilis.";
Nucleic Acids Res. 28:4317-4331(2000).
-!- SIMILARITY: Belongs to the HAM1 NTPase family.
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MICHIGLS T., Cornellis G., Ellis K., Grinsted J.;
Michiels T., Cornellis G., Ellis K., Grinsted J.;
Michiels T., Cornellis G., Ellis K., Grinsted J.;
Michiels T., Cornellis G., Ellis K., Grinsted J.;
of a new category of class II transposable elements.";
J. Bacteriol, 16:5424-631(1987).
-i. FUNCTION: RESOLVASE CATALYZES THE RESOLUTION (A SITE-SPECIFIC RECOMBINATION) OF THE COINTEGRATED REPLICON TO YIELD THE FINAL TRANSPOSITION PRODUCTS.
-I. MISCELLANEOUS: TN2501 IS A CRYPTIC CLASS II TRANSPOSON FOUND AS PART OF THE LACTOSE TRANSPOSON TWS51.
-I. SIMILARITY: Belongs to the site-specific recombinase resolvase
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Enterobacteriaceae, Escherichia.
NCBI_TaxID=562;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hydrolase, Complete proteome.
SEQUENCE 194 AA, 21868 MW, BBC5A0C4F19A04B3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match
Local Similarity 100.0%; Pred. No. 3.4e+02; les 4; Conservative 0; Mismatches 0;
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01-NOV-1988 (Rel. 09, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Transposon Th2501 resolvase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AP001517; BAB06786.1; -.
PIR; C84033.
RASP; OS7679; 1B78.
HAWAR; MF_01405; -; 1.
InterPro; IPR002637; Hamlp_like.
Pfan; PP01725; Hamlp_like; 1.
ProDom; PD004952; Hamlp_like; 1.
PIGRFAMS; TIGRO0042; TIGRO0042; 1.
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SEQUENCE
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R Fam; PF02796; HTH 7; 1.

R Pfam; PF02796; HTH 7; 1.

R PROSTIE; PS00397; RECOMBINASES 1; 1.

R PROSTIE; PS00398; RECOMBINASES 2; 1.

R PRANSIE COVALENT LINKAGE TO DNA DURING STRAND CLEAVAGE AND REJOINING STRAND CLEAVAGE TO NA DURING STRAND CLEAVAGE TO NA DURING HT STRAND CLEAVAGE AND REJOINING STRAND CLEAVAGE AND REJOINING HT STRAND CLEAVAGE AND REJOINING STRAND CLEAVAGE TO NA DURING STRAND CLEAV
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MEDLINE-9745617; PubMed-9278503;
MEDLINE-97456617; PubMed-9278503;
MEDLINE-97456617; PubMed-9278503;
Blatther F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregort J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2003 (Rel. 41, Last annotation update)
Purative DNA invertase from lambdoid prophage Qin.
PINQ OR B1545.
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PINQ ECOLI
P77170;
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EMBL; AE000252; AAC74618.1; -. BMBL; D90798; BAAL5249.1; -. PIR; D64909; D64909. HSSP; P03012; 2RSL.

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InterPro; IPR006119; Recombinase.
InterPro; IPR006119; Recombinase.
InterPro; IPR006119; resolvase_N.
Pfam; PF02705; HTH 7.
Pfam; PF02705; HTH 7.
PROSITE; PS00399; RECOMBINASES_1; FALSE_NEG.
PROSITE; PS00399; RECOMBINASES_2; 1.
Hypotherical protein; DNA recombination; DNA integration; DNA-binding; DNA invertase; Complete proteome.
ACT_SITE 11 11 TRANSIENT COVALENT LINKAGE TO DNA DURING
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STRAND CLEAYAGE AND REJOINING
(BY SIMILARITY),
7 7CF47F6D88DBD497 CRC64;
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STRAIN=06.41 / CFT013 / ATCC 700928;
MEDLINE=22386234; PubMed=12471157;
MEDLINE=22386234; PubMed=12471157;
MEDLINE=22386234; PubMed=12471157;
MEDLINE=22386234; PubMed=12471157;
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D., Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence of uropathogenic Escherichia coli,"; Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
-1- SIMILARITY: Belongs to the site-specific recombinase resolvase
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SEQUENCE FROM N.A.
MEDLINES97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Blattner F.R., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden C.K., Mayhew G.F.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 19; DB 1; Length 196; Best Local Similarity 100.0%; Pred. No. 3.4e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2003 (Rel. 41, Last annotation update)
18-EEB-2003 (Rel. 41, Last annotation update)
18-EEB-2003 (Rel. 41, Last annotation update)
18-EEB-2003 (Rel. 41, Last annotation update)
18-Cherichia coli, and
18-Cherichia coli, and
18-Cherichia coli 06.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            196 AA; 21852 MW;
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MEDLINE=93315143; PubMed=7686882;
    CCCCCCCCCLTTTPPPPRCTTTPPPPPRCTTTTPPPPPRCTTTTPPPPRCTTTTPPPPRCTTTTPPPRCTTTTPPPRCTTTTPPRCTTTTPP
                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF02796; HTH 7; 1.
Pfam; PF00239; resolvase; 1.
PROSTIE; PS00397; RECOMBINASES 1; FALSE NEG.
PROSTIE; PS00398; RECOMBINASES 2; 1.
Hypothetical protein; DNA recombination; DNA integration; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TEAMSIENT COVALENT LINKAGE TO DNA DURING STRAND CLEAVAGE AND REJOINING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shigella flexneri.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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01-UUL-1989 (Rel. 11, Last sequence update)
10-OCT-2003 (Rel. 42, Last amortation update)
11-Anneriptional regulatory protein uhpA.
UHPA OR B3669 OR C4553 OR Z5159 OR BCS4606 OR SF3792 OR S3976.
Escherichia coli,
Escherichia coli 06,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              region of Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 19; DB 1; Length 196; 100.0%; Pred. No. 3.4e+02; ive 0; Mismatches 0; Indels
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SPECIES=E.coli; STRAIN=K12 / MG1655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enterobacteriaceae; Escherichia.
NCBI_TaxID=562, 217992, 83334, 623;
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"Nucleotide sequence of the uhp r.
J. Bacteriol. 169:3556-3563(1987)
                                                                                                                                                                                                                                                                            PIR; A64888; A64888.

HSSP; P03012; ZRSL.

EcoGene; E013372; pinR.

InterPro; IPR006120; HTH 7.

InterPro; IPR006118; Recombinase.

InterPro; IPR006119; resolvase_N.
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MEDLINE=87279903; PubMed=3301805;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invertase; Complete proteome.
                                                                                                                                                                                                             EMBL; AE000234; AAC74456.1; -.
EMBL; D90775; BAA14979.1; -.
EMBL; AE016764; AAN81596.1; -.
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nes 4; Conservative
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    family
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P10940;
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PRINTING WOD, PRINCET G. II. Dainish D. D. Balther F.R.;

This section of analysis of 116 kilobases of the Eschrichia coli for the condition of replication.";

Reconsists organizational symmetry around the origin of replication.";

RESOURCE FROM N. ANANCO: MI / CFU73 / ArcC 70928;

RESOURCE FROM N. ANANCO: MI / CFU73 / ArcC 70928;

RESOURCE FROM N. ANANCO: MI / CFU73 / ArcC 70928;

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RESOURCE FROM N. ANANCO: MI / CFU73 / ArcC 70928;

RESOURCE FROM N. ANANCO: MI / CFU73 / ArcC 70928;

RESOURCE FROM N. ANANCO: MI / CFU73 / ArcC 70927;

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RESOURCE FROM N. ANANCO: MI / CFU73 / ArcC 70927;

RESOURCE FROM N. ANANCO: MI / Arc P R. ArcC ARC MI / CFU73 / ArcC 70927;

RESOURCE FROM N. ANANCO: MI / Arc P R. ArcC ARC MI / CFU73 / Arc P R. ArcC ARC MI / Arc P R. Arc P R
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-AUG-1992 (Rel. 21, Last sequence update)
01-AUG-1992 (Rel. 21, Last sequence update)
28-FBB-2003 (Rel. 41, Last amotation update)
Transcriptional regulatory protein uhpA.
Transcriptional regulatory protein uhpA.
Salmonella typhimurium.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PROUDIS; HERPLUIS.
PRINTS; PROUDIS; HTH LUXR; 1.
ProDom; PD000307; HTH LUXR; 1.
ProDom; PD000309; Response reg; 1.
SMART; SM00421; HTH LUXR; 1.
SMART; SM00448; REC; HTH LUXR; 1.
SMART; SM00448; REC; HTH LUXR FAMILY; 1.
PROSITE; PS00101; RESPONSE REGULATORY; 1.
Sensory transduction; Phosphorylation; Transcription regulation; DNA-binding; Activator; Sugar transport; Complete proteome.
DNA-binding; Activator; Sugar transport; Complete proteome.
DNA-binding; Activator; Sugar transport; Complete proteome.
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"Structure and function of the uhp genes for the sugar phosphate
transport system in Escherichia coli and Salmonella typhimurium.'
J. Bacteriol. 174:2754-2762(1992).
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H-T-H MOTIF (BY SIMILARITY).
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                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
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MEDLINE=92234930; PubMed=1569007;
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NCBI_TaxID=602;
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155 174 H
196 AA; 20889 MW;
                                                                                                                                      EMBL; M17102; AAA24720.1; -.
EMBL; M89479; AAA24724.1; -.
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Best Local Similarity
Matches 4; Conserv
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HPA_SALTY
O_UHPA_SALTY
C_P27667;
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MOD RES
DNA_BIND
SEQUENCE
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Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D. Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- FUNCTION: APPEARS TO BE THE POSITIVE ACTIVATOR OF UHPT
TRANSCRIPTION.
-!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-!- PTM: PHOSPHORYLATED BY UHPB (PROBABLE).
-!- PTM: PHOSPHORYLATED BY UHPB (PROBABLE).
-!- SIMILARITY: Contains 1 response regulatory domain.
-!- SIMILARITY: BELONGS TO THE LUXR/UHPR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=99303612; PubMed=10373455;
Muramatsu M., Sankaranand V.S., Anant S., Sugai M., Kinoshita K.,
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Activation-induced cytidine deaminase (EC 3.5.4.5) (Cytidine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 19; DB 1; Length 196; 100.0%; Pred. No. 3.48+02; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          198 AA
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                                                                                                                                                 Nature 413:852-856(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity
Matches 4; Conserv
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Q9WVE0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQÜENCE
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RETB HORSE
Q28369;
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ACT_SITE
SEQUENCE
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RETB_HORSE
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                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBJ outstation the business institute of Bioinformatics and the EMBJ outstation institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                         for efficient antibody responses.
-!- CATALYTIC ACTIVITY: Cytidine + H(2)O = uridine + NH(3).
-!- COFACTOR: Zinc (By similarity).
-!- SIMILARITY: Belongs to the cytidine and deoxycytidylate deaminases
                                                                                            J. Biol. Chem. 274:18470-18476(1999).
-I- FUNCTION: RNA-editing deaminase involved in somatic hypermutation, gene conversion, and Class-switch recombination. Required for several crucial steps of B-cell terminal differentiation necessary
Davidson N.O., Honjo T.; "Specific expression of activation-induced cytidine deaminase (AID), a "Specific expression of activation-induced cytidine deaminase (AID), a novel member of the RNA-editing deaminase family in germinal center B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=ATCC 35092 / DSM 1617 / P2;
MEDLINE=20165489; PubMed=10701121;
MEDLINE=20165489; PubMed=1.0701121;
Charlebois R.L., Singh R.K., Chan-Weiher C.C.-Y., Allard G., Chow C.,
Confalonieri F., Curtis B., Duguet M., Erauso G., Faguy D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Imidazole glycerol phosphate synthase subunit hisH (EC 2.4.2.-) (IGP synthase glutamine amidotransferase subunit) (IGP synthase subunit hisH) (IMGP synthase subunit hisH) (IMGP synthase subunit hisH) (IGPS subunit hisH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae; Sulfolobus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEGUENCE FROM N.A.
SETALTH-ATCC 35092 / DSM 1617 / P2;
STRAINE-97C35708; PubMed=9209067;
Charlebois R.L., Sensen C.W., Doclittle W.F., Brown J.R.;
"Evolutionary analysis of the hiscGABGFDEHI gene cluster from the archaeon Sulfolobus solfataricus P2.";
J. Bacteriol 179:4429-4432 (1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 19; DB 1; Length 198; 100.0%; Pred. No. 3.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18A3BA10CA54BEB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, AF132979; AAD41793.1; -.

MGD; MGI:1142279; Aicda.

GO; GO:004126; F:cytldine deaminase activity; IDA.

GO; GO:004126; F:cytldine deaminase activity; IDA.

InterPro; IPR002125; dCMP/cyt_deam.

Pfam; PF05240; APOBEC_C; 1.

PROSITE; P$001903; CYT_DCMP_DEAMINASES; 1.

MENA processing; Hydrolase; Zinc.

METAL

87 ZINC (BY SIMILARITY).

METAL

90 90 ZINC (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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Best Local Similarity 100.0%;
Matches 4; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sulfolobus solfataricus.
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                                                                                                                                                                                                                                                                                                 family.
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HISS SULSO
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                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE 35092 / DSM 1617 / P2;

MEDLINE-2132295; PubMed=11427726;

Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,

Awayez M.J., Chan-Weiher C.C.-Y., Gordon P.M. K.,

Heikamp-de Jong I., Jeffries A.C., Kocza C.J., Medina N., Peng X.,

Heikamp-de Jong I., Jeffries M.E., Theriault C., Tolstrup N.,

Aralebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,

Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,

Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.,

The complete genome of the crenarchaeon Sulfolobus Solfataricus P2.";

The complete genome of the crenarchaeon Sulfolobus Solfataricus P2.";

Tre CONTION: 1GPS catalyzes the conversion of PRFAR and glutamine to IGP, AICAR and glutamate. The hisH subunit provides the glutamine aniotransferase activity that produces the ammonia necessary to hisF for the synthesis of IGP and AICAR (By similarity).

C. CATALYTIC ACTIVITY: 5-[(5-phospho-1-deoxyribulos-1-charboxamide + L-glutamine = imidacol-glycerol phosphate + 5-charboxamide - imidacol-glycerol phosphate + 15-charboxamide ribonucleotide + L-glutamate + H(2)0.

C. PATHMAY: Histidine biosynthesis; fifth step.

C. SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

C. SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

C. SUBCELLULAR LOCATION: Cytoplasmic emidotransferase domain.
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Gaasterland T., Garrett R.A., Gordon P., Jeffries A.C., Kozera C., Kushwaha N., Lafleur E., Medina N., Peng X., Penny S.L., She Q., St Jean A., van der Oost J., Young F., Zivanovic Y., Doolittle W.F., Ragan M.A., Sensen C.W.,
                                                                                                                                    "Gene content and organization of a 281-kbp contig from the genome the extremely thermophilic archaeon, Sulfolobus solfataricus P2."; Genome 43:116-136 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; Prool17; GATase; 1.
PROSITE; PS00442; GATASE TYPE I; FALSE NEG.
Histidine biosynthesis; Transferase; Glutamine amidotransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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BY SIMILARITY.

BY SIMILARITY.

17DB1A86724CE095 CRC64;
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Plasma retinol-binding protein precursor (PRBP) (RBP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 19; DB 1; I
100.0%; Pred. No. 3.5e+02;
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178 BN
180 BN
22533 MW;
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HAMAP, MF 00278; -; 1.
InterPro; IPR000991; GATase_1.
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199 AA;
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ACT SITE 76
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REAL TREETER TO BE SEED FOR THE SEED FOR THE
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                              Eŭkaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Perissodactyla, Equidae, Equus.
NCBI_TaxID=9796,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasma retinol-binding protein precursor (PRBP) (RBP) (PRO2222) RBP4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, U21208; AAC48461.1;
PIR; 146257; 146257
HSSP; P27485; 1AQB.
InterPro; IRR002345; Lipocalin.
InterPro; IRR002345; Lipocalin.
PROSTE; PRO0061; Lipocalin.
PRINTS; PRO0179; LIPOCALIN.
PROSTE; PRO0179; Lipocalin.
PROFTE; PROFTE; Liver; Signal; SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
PLASNA RETINOL-BINDING PROTEIN.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 19; DB 1; Length 201; 100.0%; Pred. No. 3.5e+02;
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19 201 PL
22 178 BY
86 192 BY
138 147 BY
201 AA; 23022 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
                            Equus caballus (Horse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                          rissum=Endometrium;
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DISULFID
DISULFID
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ETB HUMAN
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TISSUE-Liver;

XX STELLiver;

XX STELLiver;

XX STELLiver;

XX STELLiver;

XX STELLiver;

XX STELLIVER;

XX STALL STANDOLD E.A., Grouse L.H., Derge J.G.,

XX STALLED A. Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

XX Strauberg R.L., Felberg B., Bustow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Marng J., Hsieh F.,

XX Stapleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheefer T.E.,

XX Stapleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheeter T.E.,

XX Brownstein M.J. Usdin T.B., Toshhyuki S., Carninci P., Prange C.,

XX Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millahy S.J.,

XX Raha S.S., Morley K.C., Halfe S., Garcia A.M., Gay L.J., Hulyk S.W.,

XX Norley K.C., Halfe S., Garcia A.M., Gay L.J., Hulyk S.W.,

XX Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

XX Nillalon D.K., Madan A., Young A.A., Rodrigues S., Sanchez A.

XX Milting M., Madan A., Young A.C., Shevohenko Y., Bouffard G.G.,

XX Blakesley R.W. Touchman J.W., Green E.D., Dickson M.C.,

XX Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

XX Generation and initial analysis of more than 15,000 full-length

XX Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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MEDLINE-55395382; PubMed=7666002;
Jaconi S., Rose K., Hughes G.J., Saurat J.-H., Siegenthaler G.;
Jaconi S., Rose K., Hughes G.J., hughes G.J., hughes G.J., hughes G.J., hughes G.J., hughes G.J., hughes best-translationally processed forms of human serum retinol-binding protein: altered ratios in chronic renal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rISSUE-Fetal liver;
Zhang C., Yu Y., Zhang S., Wei H., Zhang Y., Zhou G., Bi J., Liu M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Structural and functional studies of vitamin A-binding proteins."; Ann. N.Y. Acad. Sci. 359:79-90(1981).
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MEDLINE=86055755; PubMed=2998779;
D'Onofrio C., Colantuoni V., Cortese R.;
Structure and cell-specific expression of a cloned human retinol binding protein gene: the 5'-flanking region contains hepatoma specific transcriptional signals.";
EMBO J. 4:1981-1989(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 19-201, AND DISULFIDE BONDS.
MEDLINE-88019004; PubMed-2444024;
Rask L., Anundi H., Fohlman J., Peterson P.A.;
"The complete amino acid sequence of human serum retinol-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=80004132; PubMed=573217;
Rask L., Anundi H., Peterson P.A.;
"The primary structure of the human retinol-binding protein.";
FEBS Lett. 104:55-58(1979).
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MEDLINE-81254137; PubMed-6942701;
Rask L., Anundi H., Boehme J., Eriksson U., Ronne H., Sege K.,
retinol-binding protein.";
Nucleic Acids Res. 11:7769-7776(1983).
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MEDLINE=91017498; PubMed=2217163;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lipid Res. 36:1247-1253(1995).
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Peterson P.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RANCE-17-199.
DISEASE: Defects in RBP4 are a cause of retinol-binding protein DISEASE: Defects in RBP4 are a cause of retinol-binding protein deficiency [MIM:180250]. This condition causes night vision problems. It produces a typical "fundus xerophthalmicus," featuring a progressed atrophy of the retinal pigment epithelium. DISEASE: A deficiency of vitemin A blocks secretion of the binding protein posttranslationally and results in defective delivery and supply of vitemin to the epidermal cells (a condition associated with a dermatosis).
                                                                                                                                                                                                                                                                                                                                            VARIANTS RBP DEFICIENCY ASN-59 AND ASP-93.
MEDLINE=99103495; WubMed=9888420;
Seeliger M.W., Blessalski H.K., Wissinger B., Gollnick H., Gielen S.,
Frank J., Beck S., Zrenner E.;
"Phenotype in retinol deficiency due to a hereditary defect in retinol binding protein synthesis."
Invest. Ophthalmol. Vis. Sci. 40:3-11(1999).
                                                                                                                                                                                                                                                    "The structure of human retinol-binding protein (RBP) with its carrier protein transthyretin reveals an interaction with the carboxy terminus of RBP.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: Belongs to the lipocalin family.
DATABASE: NAME=Mutations of the RBP4 gene;
NOTE=Retina International's Scientific Newsletter;
WWW="http://www.retina-international.com/sci-news/rlbp4mut.htm".
       "Crystallographic refinement of human serum retinol binding protein at 2-A resolution.";
                                                                                           MEDLINE=92322903; PubMed=1623143;
Monaco H.L., Zanotti G.;
"Three-dimensional structure and active site of three hydrophobic
molecule-binding proteins with significant amino acid sequence
                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS) OF COMPLEX WITH TTR MEDLINE=99162254; PubMed=10052934;
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EMBL; X02775; CAA26553.1; -
EMBL; X02775; CAA26553.1; -
EMBL; AF119868; AAF69622.1; -
EMBL; AF025334; AAC02945.1; -
PIR; A93494; VAHU.
PDB; IRBF; IS-ULL-91.
Cowan S.W., Newcomer M.E., Jones T.A.;
                                                                                                                                                                                                                                                                                                              Biochemistry 38:2647-2653(1999).
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                                                                                                                                                                similarity.";
Biopolymers 32:457-465(1992)
                                                                                                                                                                                                                                                Naylor H.M., Newcomer M.E.;
                                             Proteins 8:44-61(1990).
                                                                             K-RAY CRYSTALLOGRAPHY
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X-RAY CRYSTALLOGRAPHY (1.65 ANGSTROMS), AND REVISIONS TO 134 AND 185. MEDLINE-98437649; PubMed=9757135, Zanotti G., Panzalorto M., Marcato A., Malpeli G., Folli C., Berni R.; "Structure of pig plasma retinol-binding protein at 1.65-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDURNCE FROM N.A.
MEDLINE-92131064; PubMed=1723146;
Trout W.B., McDonnell J.J., Kramer K.K., Baumbach G.A., Roberts R.M.;
Trout W.B., McDonnell J.J., Kramer E.K., Baumbach G.A., Roberts R.M.;
"The retinol-binding protein of the expanding pig blastocyst:
molecular cloning and expression in trophectoderm and embryonic
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
VCDI_TaxID=9823;
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                                                                      00; G0:0005615; C:extracellular space; TAS.
C0; G0:0005501; F:retinoid binding; TAS.
InterPro; IPR002345; Lipocalin.
InterPro; IPR000566; Lipocalin.
Pfam; PR00061; Lipocalin.
Pran; PR00061; Lipocalin.
PRNINTS; PR00013; LIPOCALIN.
PROSITE; PS000213; LIPOCALIN.
PROSITE; PS00213; LIPOCALIN.
Lipocalin; Diseas mutation, Vision; 3D-structure.
SIGNAL
                                                                                                                                                                                                                                    I -> N (in RBP deficiency).
/FIId=VAR_009276.
G -> D (in RBP deficiency).
/FIId=VAR_009277.
F -> L (IN REF. 1 AND 3).
LGSGR -> WAA (IN REF. 1 AND 3).
                                                                                                                                                                                           PLASMA RETINOL-BINDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 201;
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15-UUL-1998 (Rel. 36, Last sequence update)
15-REB-2003 (Rel. 41, Last amoctation update)
Plasma retinol-binding protein precursor (PRBP) (RBP).
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PDB; 1BRP; 31-JAN-94.
PDB; 1BRQ; 31-JAN-94.
PDB; 1QAB; 09-APR-99.
SWISS-2DPAGB; P02753; HUMAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 4; Conservative
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                                          Siena-2DPAGE; P02753; -
Genew; HGNC:9922; RBP4.
MIM; 180250; -.
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MEDILINE-88207643; PubMed=3838985;

A MEDILINE-88207643; PubMed=3838985;

A MEDILINE-88207643; PubMed=3838985;

A MEDILINE-88207643; PubMed=3838985;

A Bjoerck L., Erikson U., Aakerstroem B., Jones A., Newcomer M.,

B Joerck L., Rask L.;

Terinol-binding proceins.

I J. Biol. Chem. 260:4726-878 (1985).

- I- FUNCTION: Delivers retinol from the liver stores to the peripheral tissues. In plasma, the RBP-retinol complex interacts with transthyretin, this prevents its loss by filtration through the kidney glomeruli.

C - SUMCENIULAR LOCATION: Secreted.

- SUMCENIULAR LOCATION: Secreted.
                                                                   Oryctolagus cuniculus (Rabbit).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteléostomi,
Mammalia, Butheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=93011736; PubMed=1339354;
MEDLINE=93011736; PubMed=1339354;
MEDLINE=9101736; PubMed=1339354;
"The lacrimal gland synthesizes retinol-binding protein.";
Exp. Eye Res. 55:163-171(1992).
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Plasma retinol-binding protein precursor (PRBP) (RBP).
                                                                                                                                                                                                                                                              SEQUENCE OF 19-201.
                                                                                                                        NCBI_TaxID=9986;
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                    Acta Crystallogr. D 54:1049-1052(1998).
-!- PUNCTION: Delivers retinol from the liver stores to the peripheral tissues. In plasms. The RBP-retinol complex interacts with transthyretin, this prevents its loss by filtration through the kidney glomerall.
-!- SUBCELUTAR LOCATION: Secreted.
-!- SUBCELUTAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00179; LIPOCALIN.
PROSITE; PS00213; LIPOCALIN; 1.
Plasma; Vitamin A; Retinol-binding; Transport; Liver; Signal;
Lipocalin; 3D structure.
SIGNAL 1 18
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PLASMA RETINOL-BINDING PROTEIN.
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PDB; 1AQB; 28-JAN-98.
Interpro; IPR002345. Lipocalin.
InterPro; IPR000566; Lipocln. cytFABP.
Pfam; PF00061; lipocalin; 1.
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       resolution.";
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PRINTS; PR00179; LIPOCALIN.
PROSITE; PS00213; LIPOCALIN; 1.
Plasma; Vitamin A; Retinol-binding; Transport; Liver; Lipocalin;
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                                                                                                                                                                                                                                                                                                                                                                         PLASMA RETINOL-BINDING PROTEIN
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Pred. No. 3.5e+02;
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16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein yigZ.
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BY SIMILARITY.
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PIR, A49178; VARB.
HSSP, P1890.2; JFEN.
InterPro; IPR002345; Lipocalin.
InterPro; IPR000566; Lipocln_cytFABP.
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RETB RABIT STANDARD; P06912; 01-JAN-1988 (Rel. 06, Created)

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                                                                                                                                                                                                                                           MEDLINE-94147996; PubMed=8313894;
Koonin E.V., Bork P., Sander C.;
"Yeast chromosome III: new gene functions.";
EMBO O. 13:493-503(1994).
-!- SIMILARITY: BELONGS TO THE UPF0029 FAMILY. STRONG, TO H.INFLUENZAE HI0722.
                                           [1] SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE 2 / MG1655,
MEDLINE=92358234, PubMed=1379743;
MEDLINE=92358234, PubMedt G. III, Burland V.D., Blattner F.R.;
Daniels D.L., Plunkett G. III, Burland v.D., Blattner F.R.;
"Analysis of the Escherichia coli genome: DNA sequence of the region from 84.5 to 86.5 minutes";
Science 257:771-778(1992).
                                                                                                                                                                                Nakahigashi K., Inokuchi H.; "Nucleotide sequence between the fadB gene and the rrnA operon from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
         Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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16-0CT-2001 (Rel. 40, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Mitotic spindle assembly checkpoint protein MAD2A (MAD2-like 1)
(HSMAD2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 100.0%; Score 19; DB 1; Length 204; Local Similarity 100.0%; Pred. No. 3.6e+02; es 4; Conservative 0; Mismatches 0: Tndalm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DICELELY, PEO1205, UPF0029; 1.
TICHERMS; TIGR00257; 1.
PROSITE; PS00910; UPF0029; 1.
Hypothetical protein; Complete proteome.
CONFLICT 125 125 L -> V (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 205 AA.
                                                                                                                                                                                                                Nucleic Acids Res. 18:6439-6439(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M87049; AAA67645.1; ALT INIT.
EMBL; AE000460; AAC76851.1; ALT INIT.
EMBL; X54687; CAA38501.1; ALT_INIT.
                                                                                                                                                                     MEDLINE=91057145; PubMed=2243799;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EcoGene; EG11484; yigZ.
InterPro; IPR009022; EFG III V.
InterPro; IPR001498; UPF0029.
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                                                                                                                                                                                                      Escherichia coli.";
                                                                                                                                               SEQUENCE FROM N.A.
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                                 NCBI_TaxID=562;
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Q13257;
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Matches
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SECURATE STORM MUSCLE;

X SECURATE STORM MUSCLE;

X REDLINE 22388257; PubMed=12477932;

X RIAURE 22388257; PubMed=12477932;

X RIAURE 2. Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

A Altechul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altechul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heibh F.,

Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Aramson R.D., Mullahy S.J.,

Richards S., Morley K.C., Hale S., Garcia A.M., Gabba R.A.,

Vilalon D.K., Muzny D.M., Sodergren E.J., iu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Galbbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,

Rodriguez A.C., Grimwood J., Schwutz J., Myers R.W.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,

Rodriguez A.C., Grimwood J., Schwutz J., Myers R.W.,

Rodriguez
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Nat. Struct. Biol. 7:224-229(2000).

-! FUNCTION: REQUIRED FOR THE EXECUTION OF THE MITOTIC CHECKPOINT WHICH MONITORS THE PROCESS OF KINETOCHORE-SPINDLE ATTACHMENT AND DELAYS THE ONSET OF ANAPHASE WHEN THIS PROCESS IS NOT COMPLETE. IT INRIBITS THE ACTIVITY OF THE ANAPHASE PROMOTING COMPLETE. IT SEQUESTERING CDC20 UNTIL ALL CHROMOSOMES ARE ALIGNED AT THE METAPHASE PLATE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Klebert S., Barnikol-Watanabe S., Kratzin H.D., Hilschmann N.; Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
MEDLINE=96421709; PubMed=8824189;
Li Y., Benezra R.;
"Identification de a human mitotic checkpoint gene: hsMAD2.";
Science 274:246-248(1996).
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Luo X., Fang G., Coldiron M., Lin Y., Yu H., Kirschner M.W.,
Wagner G.;
                                                                                                                                                                                                                                                                                                                                                     Jin D.-Y., Jeang K.-T.; Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
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Submitted (FBB-2001) to the EMBL/GenBank/DDBJ databases.
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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23598 MW;
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PROSITE; PS50815; HORMA; 1.
Cell cycle; Mitosis; Nuclea
DOMAIN 14
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4; Conservative
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EMBL; AF261919; AAF6952
HSSP; Q13257; 1DUJ.
MGD; MGI:1860374; Mad21
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205 AA;
                                                                                                                                                                         SEQUENCE FROM N.A.
                                               NCBI_TaxiD=10090;
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MAD2L1 OR MAD2A
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Best Local S
Matches 4
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            -i- SUBCELLULAR LOCATION: Nuclear.
-i- SIMILARITY: BELONGS TO THE MAD2 FAMILY.
-i- SIMILARITY: Contains 1 HORMA domain.
-i- DATABASE: NAME-Atlas Genet. Cycgenet. Oncol. Haematol.;
-i- DATABASE: NAME-Atlas Genet. Cycgenet.
                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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0921B5; 09J153;
16-0CT-2001 (Rel. 40, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Mitotic spindle assembly checkpoint protein MAD2A (MAD2-like 1).
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SUBUNIT: INTERACTS WITH CDC20 AND WITH ADAM17 (TACE)
                                                                                                                                                                                                                                                                                    GO; GO:0005699; C:Xinetochore; TAS.
GO; GO:0007669; P:mitosis; TAS.
GO; GO:0007063; P:mitosis; TAS.
InterPro; IPR003511; DNAbind HORMA.
Pfam; PF02301; HORMA; 1.
PROSITE; PS50815; NORMA; 1.
CCII cycle; Mitosis; Nuclear protein; 3D-structure.
CCII cycle; Mitosis; Nuclear protein; 3D-structure.
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                                                                                                                                                                                                                               EMBL; AJ000186; CAA03943.1; --
EMBL; BAD654160; BAB63410.1; --
EMBL; BC000356; AAH00356.1; --
EMBL; BC005945; AAH05945.1; --
PIR; G01942; G01942.
PDB; LDUJ; 08-MAR-00.
Genew; HGNC:6763; MAD2L1.
                                                                                                                                                                                                       EMBL; U65410; AAC50781.1; -. EMBL; U31278; AAC52060.1; -.
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205 AA;
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              checkpoint protein Mad2.";

(call 101:635-646:2000).

-!- FUNCTION: REQUIRED FOR THE EXECUTION OF THE MITOTIC CHECKPOINT

WHICH MONITORS THE PROCESS OF KINETOCHORE-SPINDLE ATTACHMENT AND

DELAYS THE ONEST OF ANAPHASE WHEN THIS PROCESS IS NOT COMPLETE. I

INHIBITS THE ACTIVITY OF THE ANAPHASE PROMOTING COMPLETE. I

SEQUESTERING CDC20 UNTIL ALL CHROMOSOMES ARE ALIGNED AT THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20348739; PubMed=10892650;
Dobles M., Liberal V., Scott M.L., Benezra R., Sorger P.K.;
"Chromosome missegregation and apoptosis in mice lacking the mitotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=C57BL/61; IISSUE=Embryo;
Jin D.-Y., Jeang K.-T.;
"Identfication of assembly checkpoint in mammalian cells.";
submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
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C -> S (IN REF. 1).
T -> I (IN REF. 1).
A9F3F28BC4C9738E CRC64;
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HSSP; Q13257; 1DUJ.
MGD; MG1:1860374; MGd211.
GQ; GO:0000776; C:kinetochore; IDA.
GQ; GO:0000776; C:kinetochore; IDA.
GQ; GO:0000776; P:mitcotic chromesome segregation; IMP.
GQ; GO:00000799; P:mitcotic spindle checkpoint; IMP.
InterPro; IPR003511; DNAbind_HORMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           METAPHASE PLATE (BY SIMILARITY).
--- SUBCNIT: INTERACTS WITH CDC20.
--- SUBCELLULAR LOCATION: Nuclear (By similarity).
--- SIMILARITY: BELONGS TO THE MADZ FAMILY.
--- SIMILARITY: Contains 1 HORMA domain.
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(Rel. 29, Last sequence update)
(Rel. 40, Last annotation update)
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197
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YACI LEGEN
ID YACI LEGEN
AC P37033;
DT 01-UTN-1994
DT 16-OCT-2001 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Legionella pneumophla.
Bacteria, Froteobacteria; Gammaproteobacteria, Legionellaceae; Legionellaceae; Legionellaceae; NCBI_TaxID=446;
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 19; DB 1; Length 208; 100.0%; Pred. No. 3.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .l protein.
208 Aa; 23714 MW; 1E5C75E63A20C800 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P711<u>1</u>9;
15-DEC-1998 (Rel. 37, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Heme oxygenase (EC 1.14.99.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     215 AA.
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                                                                                                                                                                                                                                                                                                                                                                                        J. Bacteriol. 175:5666-5676(1993).
                                                                                                                                                                                                              STRAIN=Philadelphia 1;
MEDLINE=93374864; PubMed=8366052;
Mengaud J.M., Horwitz M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97158681; PubMed=9006041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteriol. 179:838-845(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; L22081; AAA25294.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR, A48642, A48642.
Hypothetical protein
SEQUENCE 208 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45 VAEF 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=1717;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 VAEF 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schmitt M.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HMUO CORDI
                  à
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                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
E -> K (IN REF. 1).
A -> V (IN REF. 1).
A -> GS (IN REF. 1).
N -> H (IN REF. 1).
-!- FUNCTION: Allows the bacteria to use the host heme as an iron source. Involved in the oxidation of heme and subsequent release of iron from the heme moiety.
-!- CATALYTIC ACTIVITY: Heme + 3 AH(2) + 0(2) = biliverdin + Fe(2+) + CO + 3 A + 3 H(2)0.
-!- SIMILARITY: Belongs to the heme oxygenase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae; Cucumovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 19; DB 1; Length 215; 100.0%; Pred. No. 3.8e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60D9E8E2ED7ED456 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last amnotation update)
Coat protein (Capsid protein) (CP).
Coucumber mosaic virus (strain Ixora) (CMV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                218 AA.
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InterPro; IPR008975; Viral_cap_coat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; BX248358; CAESO198.1; -.
HSSP; P09601; 1008.
InterPro; IPR002051; Heme_oxygenase.
Pfan, PF01126; Heme_oxygenase; 1.
PRINTS; PR00089; HABNOXYGNASE.
PROSITE; PS00593; HEME_OXYGENASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 IN
34 E
60 A
93 DC
192 N
24116 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U73860; AAC44832.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Heme; Oxidoreductase.
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60
92
192
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39 VAEF 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 VAEF 4
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Q66120;
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CONFLICT
CONFLICT
SEQUENCE
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             SPTTTTT BBRARRARA BETTTTT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis virus genome."; Virology 229:381-399(1997).
-!- FUNCTION; COULD BE INACTIVE AS THE ACTIVE SITE CYSTEINE IS MODIFIED TO TRYPTOPHAN.
-!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tyrosine + phosphate.
-!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
TYROSINE PHOSPHATASE FAMILY. CDC14 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                        Orgyia pseudotsugata multicapsid polyhedrosis virus (OpMNDV).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.
NCBI_TAXID=164623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 19; DB 1; Length 220; 100.0%; Pred. No. 3.9e+02; ive 0; Mismatches 0; Indels
                                                                                        100.0%; Score 19; DB 1; Length 218; 100.0%; Pred. No. 3.8e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=97271300; PubMed=9126251;
Ahrens C.H., Russell R.R., Funk C.J., Evans J., Harwood S.,
Rohrmann G.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EQUIVALENT OF ACTIVE SITE CYS. D3FC093F1953D425 CRC64;
                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Putative protein-tyrosine phosphatase 1 (EC 3.1.3.48).
                                                              218 AA; 24185 MW; 130E82D17BD75224 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000387; TYR phosphatase.
PROSITE; PS00383; TYR PHÖSPHATASE 1; FALSE NEG
PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
                                                                                                                                                                                                                                                                  220 AA.
Pfam; PF00760; Cucumo_coat; 1.
PRINTS; PR0222; CUCUMOCOAT.
ProDom, PD001284; Cucumovirus_coat; 1.
Coat protein.
SEQUENCE 218 AA; 24185 MW; 130E82D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SITE 162 162 B
SEQUENCE 220 AA; 25234 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U75930; AAC59009.1; -.
                                                                           Query Match
Query Match
Best Local Similarity 100.vv
Best Local 54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.v
                                                                                                                                                                                                                                                                  STANDARD;
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                                                                                                                                                                                      96 VAEF 99
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                                                                                                                                                          1 VAEF 4
                                                                                                                                                                                                                                                               PTP1 NPVOP
010274;
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                                                                                                                                                                                                                                   ESULT 65
TP1_NPVOP
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                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIR=98049343; PubMed=9389475;
Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
Klenk H.-P., Clayton R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Richardson D.L., Kerlavage A.R., Carham D.E., Kyrpides N.C.,
Rithmess E.F., Dougherty B.A., Moremney K., Adams N.D., Loftus B.,
Kirkness E.F., Dougherty B.A., Moremey K., Adams N.D., Loftus B.,
Peterson S., Reich C.I., Moweill L.K., Badger J.H., Glodek A., Zhou L.,
Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
Sadow P.W., D'Andrea K.P., Bowman C., Fujil C., Garland S.A.,
Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBDILT: Component of the archaeal exosome multienzyme ribonuclease complex (Potential).
-!- SUBGELULAR LOCATION: (Stoplasmic (Potential).
-!- SIMILARITY: Contains 1 KH domain.
-!- SIMILARITY: Contains 1 S1 motif domain.
                                                                                                                 Archaeoglobus fulgidus.
Archaea; Buryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Probable exosome complex RNA-binding protein 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMAXI, SECONDAL, C., T. PROSITE, PROSITE, PS50126; S1; 1. Exceede: RNA-binding; Complete proteome. DOMAIN 136 127 S1 MOTIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HAMAP; MF 0623; -; 1.
InterPro; IPR004089; KH dom.
InterPro; IPR004089; KH type_1.
InterPro; IPR008994; Nucleic_acid_OB.
InterPro; IPR003029; S1.
Pfam; PP00573; S1; 1.
SMART; SM00322; KH; 1.
SMART; SM00322; KH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE001070; AAB90745.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; D69311; D69311
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                                                                                                                                                                                            NCBI_TaxID=2234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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209 VAEF 212

RESULT 67 RAN\_TETPY

PRT; 223 AA.

STANDARD;

ESULT 66 CRI\_ARCFU D\_ECRI\_ARCFU .C\_029758;

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10-OCT-2003 (Rel. 42, Created)

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Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 100 nes 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BUNIT: Monomer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN=B1868;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 VAEF 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=5911;
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                               NCBI_TaxID=274;
                                                                                                                                                                                                                              H(+)(Out)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RAN TETTH P41915;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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16-OCT-2001 (Rel. 40, Last sequence update)
15-VAR-2004 (Rel. 43, Last annotation update)
V-type ATP synthase subunit D (EC 3.6.3.14) (V-type ATPase subunit D).
Thermus thermophilus.
                                                                                                                                                                                                                                                                                         control of cell cycle (By similarity).
      01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last sequence update)
GP-ED-2003 (Rel. 41, Last annotation update)
GTP-binding nuclear protein RAN/TC4.
Terrahymena pyriformis.
Ebkaryota, Alveolata, Ciliophora, Oligohymenophorea, Hymenostomatida;
NCBL TAXID=5908;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                     -1- SUBUNIT: Monomer.
-1- SUBCELLULAR LOCATION: Nuclear (By similarity).
-1- SIMILARITY: Belongs to the small GTPase superfamily. Ran family.
                                                                                                                                                                                                                                           "Cloning of cDNAs encoding a cell-cycle-regulatory GTP-binding low-M(r) (GBLM) protein, Ran/TC4, from micronucleated Tetrahymena thermophila and amicronucleated Tetrahymena pyriformis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                  MEDLINE=94299154; PubMed=8026746;
Nagata K.-I., Takemasa T., Alam S., Hattori T., Watanabe Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 19; DB 1; Length 223; 100.0%; Pred. No. 3.9e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
IBB (BY SIMILARITY).
W, 5474DADB5ABF0977 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGRFAMS; TIGRO0231; small GFP; 1.
PROSITE; PS01115; RAN; 1.
GTP-binding; Nuclear protein; Protein transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               223 AA.
    223 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, D21825, BAA04849.1; -.
HSSP, P17080; 1A2K.
InterPro; IPR002041, RAN.
InterPro; IPR001806; Ras trnsfrmug.
InterPro; IPR005255; Small_GTP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPRO05225; Small_GTP-
Pfam; PF00071; rag; 1.
PRINTS; PR00627; GTPRANTC4.
PRINTS; PR00449; RASTRNSFRWNG.
SMART; SM00176; RAN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           223 AA; 25422 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
    STANDARD;
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Matches 4, Conserv
                                                                                                                                                      [1]
SEQUENCE FROM N.A.
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VAID THETH
ID VAID THETH
AC 087880;
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NP_BIND
NP_BIND
DOMAIN
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-!- FUNCTION: GTP-binding protein involved in nucleocytoplasmic transport. Required for the import of protein into the nucleus and also for RNA export. Involved in chromatin condensation and control of cell cycle (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enkaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
Tetrahymenina; Tetrahymena.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                        Yoshida M.;

Yoshida M.;

Lucype H.ATPase/synthase from a thermophilic eubacterium, Thermus thermophilus. Subunit structure and operon.";

J. Biol. Chem. 275:13955-13961(2000).

-!- FUNCTION: Produces ATP from ADP in the presence of a proton
                                                                                                                                                                                                                                                                                                                                                         gradient across the membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Cloning of cDNAs encoding a cell-cycle-regulatory GTP-binding low-M(r) (GBLM) protein, Ran/TC4, from micronucleated Tetrahymena thermophila and amicronucleated Tetrahymena pyriformis.";
                                                                                                                   Yokoyama K., Ohkuma S., Taguchi H., Yasunaga T., Wakabayashi T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: Belongs to the V-ATPase D subunit family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 19; DB 1; Length 22 100.0%; Pred. No. 3.9e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pram; PF01813; ATP-synt D; 1.
ProDom; PD004122; ATP-synt Dsub; 1.
TIGRPAMs; TIGR00309; V ATFase subD; 1.
Hydrolase; ATP synthesis; Hydrogen ion transport.
SEQUENCE 223 AA; 24677 MW; B666AE00DFE0B08B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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SEQUENCE FROM N.A.
STRAIN=HB8 / ATCC 27634;
MEDLINE=20250964; PubMed=10788522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; D63799; BAA33198.2; -.
HAMAP; MF_00271; -; 1.
InterPro; IPR002699; ATPSYNt_Dsub.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDILINE-89293088; PubMed=2661722;
Gombart A.F., Blisgard G.W., Rohrmann G.F.;
G'Aracterization of the genetic organization of the HindIII M region of the multicapsid nuclear polyhedrosis virus of Orgyia pseudotsugata reveals major differences among baculoviruses.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-WAR-1992 (Rel. 21, Created)
1-WAR-1992 (Rel. 21, Last sequence update)
01-WAR-1997 (Rel. 35, Last annotation update)
Hypothetical 26.0 kDa protein in PP34-EXO intergenic region (ORF 4).
Cypyia peeudotsugata multicapsid polyhedrosis virus (OpWNPV).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear by Divhedrosis virus genome."; Virology 229:881-339(1997).
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Ahrens C.H., Russell R.R., Funk C.J., Evans J., Harwood S.,
Rohrmann G.F.;
                                                                                                                                                               100.0%; Score 19; DB 1; Length 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 3.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gen. Virol. 70:1815-1828(1989).
                                                                                                                                        EMBL; D17748; BAA04600.1; -.
HSSP; P17080; 1A2K.
                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=164623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 VAEF 12
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P24080;
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Pyridine nucleotide biosynthesis; Transferase; Nucleotidyltransferase; NAD; Complete protecome.
NAD; Complete protecome. S2091 MW; 4CF04E8F70E48941 CRC64;
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-!- CATALYTIC ACTIVITY: ATP + nicotinate ribonucleotide = diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,
Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,
Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzez A.,
Utterback T., Rizzo M., Lee K., Kosack D., Mosstl D., Wedler H.,
Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
10-0CT-2003 (Rel. 43, Last annotation u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete genome sequence and comparative analysis of the metabolically versatile Pseudomonas putida KT2440."; Environ. Mirobiol. 4:799-808(2002).
-!-FUNCTION: Catalyzes the reversible adenylation of nicotinate mononucleotide (NaMN) to nicotinic acid adenine dinucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          °
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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                                                                                                                                                                                                                                  ll protein; Late protein.
228 AA; 25962 MW; F0766AD21F60039D CRC64;
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-!- SIMILARITY: Belongs to the nadD family.
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InterPro; IPR004820; Cytidylyltransf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas putida (strain KT2440).
                              EMBL; D13796; BAA02952.1; -.
EMBL; D13929; BAA03030.1; -.
EMBL; U75930; AAC59129.1; -.
PIR; D30857; D30857.
Hypochetical protein; Late pro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Conservative
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Q88DL5;
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NADD PSEPK
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UBIE_CORGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chloroplast.
Bukaryota, Rhodophyta, Bangiophyceae, Bangiales; Bangiaceae, Forphyra.
NCBL_TaxID=2787;
                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reith M.E., Munholland J.; "Complete nucleotide sequence of the Porphyra purpurea chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Flant Moi. Biol. Rep. 13:333-335(1995).
-!- SUBDINIT: Part of the 30S ribosomal subunit.
-! SUBCELLULAR LOCATION: Chloroplast.
-!- SUBLIARITY: Belongs to the S3P family of ribosomal proteins.
-!- SIMILARITY: Contains 1 KH type-2 domain.
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R HAVAP; MF 01109; -1; ...

INTERPRO; IPR004087; KH dom.

R INTERPRO; IPR004087; KH dom.

R INTERPRO; IPR004081; KH DOM.

R INTERPRO; IPR004081; KH DOM.

R INTERPRO; IPR004081; KH TYPE 2.

INTERPRO; IPR004081; Ribosomal 33.C.

R INTERPRO; IPR00819; Ribosomal 53.N.

R Pfam; PF00417; Khbosomal 53.N.

R Ffam; PF00417; Khbosomal 33.C; 1.

R Ffam; PF00417; Khbosomal 33.C; 1.

R TGRRAMS; TGR01009; FDG. Lact; 1.

R TGRRAMS; TGR01009; TDG. Lact; 1.

R RIBOSOMAL; RSO0548; RIBOSOMĀL, S3.1.

R RIBOSOMAL; RABOSOMĀL, S3.1.

R RIBOSOMAL; RABOSOMĀL, S3.1.

R RIBOSOMAL; SABOSOMAL; S4.1.

R RIBOSOMAL; SABOSOMAL; S4.1.

R RIBOSOMAL; SABOSOMAL; S4.1.

R RIBOSOMAL; SABOSOMAL; SABOSOMAL; S4.1.

R RIBOSOMAL; SABOSOMAL; SABOSOM
  100.0%; Score 19; DB 1; Length 230; 100.0%; Pred. No. 4e+02; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                      01-0c7-1996 (Rel. 34, Created)
01-0c7-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Chloroplast 30S ribosomal protein S3.
Ouery Match
Best Local Similarity 100.0
Matches 4; Conservative
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les 4; Conservative
                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                Porphyra purpurea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                          42 VAEF 45
                                                                                      1 VAEF 4
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P51308;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome Res. 13:1572-1579(2003).
--- FUNCTION: Methyltransferase required for the conversion of dimethylmenaquinone (DKHZ2) to menaquinone (WHHZ) (By similarity).
--- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + demethylmenaquinol =
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Comparative complete genome sequence analysis of the amino acid replacements responsible for the thermostability of Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Menaquinone biosynthesis methyltransferase ubiE (EC 2.1.1.-).
                                                                                                                                                                                                                                                                                                        Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacterium.
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10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Menaquinone biosynthesis methyltransferase ubiE (EC 2.1.1.-).
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Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Corynebacteriaceae, Corynebacterium.
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InterPro; IPR001601; Methyltransf.
InterPro; IPR001601; SAM bind.
InterPro; IPR004033; UDiE/COO5_Metrf.
Pfam; PF01209; Ubie methyltran; 1.
PROSITE; PS01183; UBIE_1; PALSE_NBG.
PROSITE; PS01184; UBIE_2; PALSE_NBG.
Menaquinone biosynthesTs; Transferase; Methyltransferase;
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-1- PATHWAY: Menaquinone biosynthesis; last step.
-1- SIMILARITY: Belongs to the ubiE family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
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es 4; Conservative 0
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SEQUENCE 230 AA;
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QBNT39;
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RESULT 73 UBIE\_COREF

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                             "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Methyltransferase required for the conversion of
dimethylmenaquinone (DMKH2) to menaquinone (MKH2) (By similarity).
-!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + demethylmenaquinol =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
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MEDLINE-92223101; PubMed-1314093;
Yang T.-P., Depew R.E.;
"Nucleotide sequence of a region duplicated in Escherichia coli toc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
SPECIES=B.coli, STARIN=KI2 / MG1655;
MEDLINE=97426617; PubMed=9278503,
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Man B., Shao Y.,
"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                    EMBL; AP005275; BAB97864.1; -.
HAMAP. MF 01813; -; 1.
Interpro; IPR001601; Methyltransf.
Interpro; IPR00051; SAM bind.
Interpro; IPR00051; SAM bind.
Interpro; IPR004033; UbiE/COO5_Metrf.
Pfam; PF01209; Ubie methyltran; 1.
PROSITE; PS01183; UBIE 1; FALSE_NEG.
PROSITE; PS01184; UBIE 2; FALSE_NEG.
Menaquinone blosynthes18; Transferase; Methyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome.
SEQUENCE 230 AA; 25244 MW; A8548173B7901400 CRC64;
                                                                                                                 s-adenosyl-L-homocysteine + menaquinol.
-!- PATHWAY: Menaquinone biosynthesis; last step.
-!- SIMILARITY: Belongs to the ubiz family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Hypothetical protein 91918.
YGIB OR B3037 OR C3783 OR SF3077 OR S3282.
STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 234 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mutants.";
Biochim. Biophys. Acta 1130:227-228(1992).
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NCBI_TaxID=562, 217992, 623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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Escherichia coli 06, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shigella flexneri.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145 VAEF 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 VAEF 4
                  Nakagawa S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YGIB ECOLI
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GIB ECOLI
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                               SPECIES=E.Coli; STRAIN=06:H1 / CFF073 / ATCC 700928;
MEDLINE=2388334; PubMed=12471157;
Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.D.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic Bscherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete genome sequence and comparative genomics of Shigella flexneri serotype 2a strain 2457F."; Infect. Immun. 71:2775-2786(2003).
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EMBL, U28377; AAA62205.1; -.
EMBL, AE016766; AAN62227.1; -.
EMBL, AE016766; AAN62227.1; -.
EMBL, AE016766; AAN62257.1; -.
EMBL, AE016818; AAN64555.1; ALT_INIT.
EMBL, AE016988; AAP18368.1; -.
PIR, S22360; S22360.
EGOGGER; EQ1164; ygia.
Hypochetical protein; Complete proteome.
SEQUENCE 234 AA; 24868 MW; 08D5DE931072C966 CRC64;
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SEQUENCE FROM N.A.
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QB1368 archaeeglob
QB3168 archaeeglob
QB3267 zymomornas m
QB3240 neisseria g
QVm23 nonchierella
QB1cb9 arabidopsis
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QB6tc9 drosophila
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X MEDLINE=84039134; PubMed=7693466;
A Lutz F., Whorh M., Grimmig M., Leidolf R., Linder D.;
A Lutz F., Mohr M., Grimmig M., Leidolf R., Linder D.;
Thomsome acruginosa cytotoxin-binding protein in rabbit erythrocyte membranes. An oligomer of 28 kDa with similarity to transmembrane channel proteins ";
E Bur. J. Biochem. 217:1123-1128(1993).
R Bur. J. Biochem. 217:1123-1128(1993).
R HSSP; P47865; Juth.
R GO; GO:0005215; Firansporter activity; IEA.
GO; GO:0005215; Firansporter activity; IEA.
R GO; GO:0006810; P:transporter activity; IEA.
R GO; GO:0006810; P:transporter activity; IEA.
R InterPro; IPR000425; MIP.
R Pfam; PF000230; MIP; 1.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Cytocxin-binding protein (Fragment).
Cytocxin-binding protein (Fragment).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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Q81AA7
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Q97Z372
Q91Z372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Protein database for several tissues derived from five instar of
                                                                                                      Bacteria; Poterbacteria; Betaproteobacteria; Nitrosomonadales; Nitrosomonadaces; Nitrosomonadaces; Nitrosomonas. NCBI_TaxID=915;
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McTavish H., LaQuier F., Arciero D., Logan M., Mundfrom G.,
Fuchs J.A., Hooper A.B.;
                                                                                                                                                                                                                                                                                                                                                                          Length 22;
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Local Similarity 100.0%; Pred. No. 3.46+02;
Nes 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=XINHANG X XEMING; TISSUE=Body wall, and Fat body;
MEDLINE=21177481; PubMed=11280994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-2001 (TrEMBLrel. 18, Created)
01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin regulatory light chain 2 (MLC-2) (Fragment).
Bombyx mori (Silk moth).
OSESCO;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
Cytochrome P-460 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 19; DB 5;
Pred. No. 4.7e+02;
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Gaps

us-09-594-978a-2.rspt

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048420 PRELIMINARY, PRT; 44 AA.
048420;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment).
Klebsiella pneumoniae.
Klebsiella pneumoniae.
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriaceae, Klebsiella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Giffard J.M., Brandon R.B., Bell T.K.;
"Further identification of single nucleotide polymorphisms in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Būkaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia; Butheria; Perissodactyla; Equidae; Equus.
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                                                                                        Length 35;
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                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            equine transferrin gene.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases
EMBL; AE009770; AAL62822.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 35 AA; 3934 MW; A324B4F94F6A14BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36 AA; 3802 MW; E2DDD122186D5FA8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                        'Match 100.0%; Score 19; DB 17;
Local Similarity 100.0%; Pred. No. 5.4e+02;
Les 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0005576; C:extracellular; IEA.
GO; GO:0008199; F:ferric iron binding; IEA.
GO; GO:0006879; P:iron ion homecetasis; IEA.
GO; GO:0006826; P:iron ion transport; IEA.
                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001156; Transferrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF185722; AAF05508.1; -. AF185722; AAF05501.1; -. AF185723; AAF05502.1; -. AF185724; AAF05503.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF185725; AAF05504.1; -. AF185726; AAF05505.1; -. AF185727; AAF05506.1; -. AF185728; AAF05507.1; -.
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Equus caballus (Horse)
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                                                                                                                                                                                                                       18 VAEF 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9796;
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                                                                                                                                                                             1 VAEF 4
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O9TOR7;
01-MAY-2000 (
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SEQUENCE
                                                                                        Query Match
Best Local S:
Matches 4
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EMBL;
EMBL;
EMBL;
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STRAIN=26655 / ATCC 700392;
MEDLINE=97194467; PubMed=9252185;
MEDLINE=97194467; PubMed=9252185;
MEDLINE=97194467; PubMed=9252185;
MEDLINE=97194467; PubMed=9252185;
Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A., Neleson K., Viktkness B.F., Peterson S., Loftus B., Richardson D., Dodon R., Khalak H.G., Glodek A., McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K., McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K., Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin B., Wenter J.C., Bordovsky M., Karp P.D., Smith H.O., Fraser C.M.,
    Gaps
                                                                                                                                                                                                                                                                                                                                                    Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum aerophilum.", Proc. Natl. Acad. Sci. U.S.A. 99:984-989 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRALM=IM2 / ATCC 51768 / DSM 7523;
MEDLINE-21664397; PubMed=11792869;
Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
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    Indels
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PIR; G64625; G64625.
TIGR; HP0847; -.
Hypothetical protein; Complete proteome.
SEQUENCE 33 AA; 3704 WW; FA3F52631C0DB943 CRC64;
                                                                                                                                                                                                                            01-JAN-1998 (TrEWBLrel. 05, Created)
01-JAN-1998 (TrEWBLrel. 05, Last sequence update)
01-JUN-2003 (TrEWBLrel. 24, Last annotation update)
Hypothetical protein HP0847.
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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    0; Mismatches
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PAE0485.
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    4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pylori.";
Nature 388:539-547(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pyrobaculum aerophilum.
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                                                                                        13 VAEF 16
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                                                1 VAEF 4
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    Matches
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01-OCT-2003 (TEMBLrel. 25, Created)
01-OCT-2003 (TEMBLrel. 25, Last seq
01-OCT-2003 (TEMBLrel. 25, Last ann
Hypothetical protein.
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                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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Q7UXLS
ID Q7UXLS
                                                                             025478
                     RESULT 9
025478
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                                                                                                                                                                                    SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SCORPAIN=ATCC 25955;
SKraly F.A., Willard B.L., Cameron D.C.;
Skraly F.A., Willard B.L., Cameron D.C.;
Skraly F.A., Willard B.L., Cameron D.C.;

L. Submitted (JUL-1995) to the EMBL/Genbank/DDBJ databases.

STRICELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

STRICARITY: BELONGS TO THE MIP/AQUAPORIN FAMILY (TC 1.A.8).

REMBL; U30903; AAA74254.1;

REMBL; U30903; AAA74254.1;

RO; GO:0016021; Cintegral to membrane; IEA.

GO; GO:0016021; Cintegral to membrane; IEA.

GO; GO:0016021; P:transporter activity; IEA.

RO; GO:0006810; P:transport; IEA.

RICHEPPO: P:transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STEALN=VBS) / ATCC 700802;
MEDLINE=VBSS / ATCC 700802;
MEDLINE=22550857; PubMed=1265927;
Medline=22550857; PubMed=1265927;
Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
Tettelin H., Dodson R.J., Umayam L., Brinkac L., Beanan M.,
Daugherty S., Deboy R.T., Durkin S., Kolonay J., Madupu R., Nelson W.,
Vamathevan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H.,
Ulterback T., Radune D., Retchum K.A., Dougherty B.A., Fraser C.M.;
Entercoccus faecalis.";
                           Willard B.L.;
Investigation of the Klebsiella pneumoniae 1,3-propanediol pathway:
Characterization and expression of glycerol dehydratase and 1,3-
propanediol oxidoreductase.";
Thesis (1994), Chemical Engineering, University of Wisconsin-Madison.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enterococcus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 44;
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45 AA; 5278 MW; 89CB55F5CB4C014A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0830H9;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 19; DB 2; I 100.0%; Pred. No. 6.8e+02; iive 0; Mismatches 0;
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TIGR; EF2805; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 299:2071-2074(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100...
4; Conservative
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EF2805.
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Best Local Similarity
STRAIN=ATCC 25955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria, Firmico
NCBI_TaxID=1351;
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SEQUENCE 1
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MEDLINE=97394467; PubMed=9252185;

MEDLINE=97394467; PubMed=9252185;

Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,

Tomb J.-F., White O., Kerlavage A.R., Tenk H.-P., Gill S., Dougherty B.A.,

Pleischmann R.D., Ketchnun K.A., Klenk H.-P., Gill S., Dougherty B.A.,

Infetus B., Richardenon D., Dodson R., Knalak H.G., Glodek A.,

Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,

Cotton M.D., Weidman J.M., Pujil C., Bowman C., Watthey L., Wallin E.,

Wenter J.C.,

Venter J.C.,
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                                                                                                                                                                        Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The complete genome sequence of the gastric pathogen Helicobacter
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NCBI_TaxID=117;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pylori.";
Mature 388:39-547(1997).
Mature 388:39-547(1997).
Mature 388:39-547(1997).
Mature 388:39-54019.
MAD07618; E64618.
FYGR; HP0789; --
Hypotheical protein; Complete proteome.
SEQUENCE 48 AA; 5492 MW; ED5911D96F57BFEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303 (2003).
EMBL: BX294135; CAD71991.1; -
Hypothetical protein:
SEQUENCE 51 AA, 5951 WW, 60F62389COFDA6A7 CRC64;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein HP0789.
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Last annotation update)
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Best Local Similarity 100.
Matches 4; Conservative
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32 VAEF 35
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Q8FIF3
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STRAIN-HPD1;
Ito N., Udaka S., Yamagata H.;
Ito Sacteriol. 174:2281-2287(1982).
EMBL; D00863; EMA0736.1;
EMBL; A42375; A42375.
SEQUENCE 52 AA; 5558 MM; 5D689099F84F9AAF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus brevis (Brevibacillus brevis).
Bacteria, Firmicutes; Bacillales; Paenibacillaceae, Brevibacillus.
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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STRAIN=0157:H7 / EDD933 / ATCC 700927;
STRAIN=0157:H7 / EDD933 / ATCC 700927;
STRAIN=0187:H7 / EDD935 / EDD935;
PubMed=11206551;
Perna N.T., Plunkett G. III, Burlain V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Rose D.J., Mayhew G.F., Evans P.S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
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100.0%; Pred. No. 7.8e+02; tive 0; Mismatches 0; Indels
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EMBL, ABG05369; AAG56425.1; -.
EMBL, B85745; B85745; B85745; B85745; B85745; B85745; B85745; B85745; B85745; SEQUENCE 54 AA; 6507 WW; 8BEFRACD8BE6140CE CRC64;
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Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01,
01-UNV-1996 (TrEMBLrel. 01,
01-UTN-2003 (TrEMBLrel. 24,
Short ORF.
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Best Local Similarity 100.
Matches 4; Conservative
Best Local Similarity 100.
Matches 4, Conservative
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                                                                                                                                  31 VAEF 34
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MEDLINE-203 88244; blubed=1247157; MEDLINE-203 88244; blubed=1247157; MEDLINE-203 88244; blubed=1247157; MEDLINE-203 88244; blubed=1247157; Melch R.A., Burland V., Plunkett G. III., Redford P., Roesch P., Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D., Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T., Mobley H.L.T., Donnenberg M.S., Blattner F.R.; "Extensive mosaic structure revealed by the complete genome sequence of uropathogenic Becherichia coll."; Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
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EMBL, ARSA6526, AAL72547.1, -...
GO, GO:0046821; C:extrachromosomal DNA; IEA.
Hypothetical protein; Plasmid.
SEQUENCE 61 AA, 6858 MW; FICCI7B10B28CBFC CRC64;
                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria, Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=217992;
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Shigella.
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SEQUENCE 54 AA; 5322 MW; 6B3C3D0F21ED4376 CRC64;
                                                         01-MAR-2003 (TrEMBLrel. 23, Created)
1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
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100.0%; Pred. No. 8.2e+02;
tive 0; Mismatches 0;
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PRT;
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01-MAR-2002 (TrEMBLrel. 20, C:
01-MAR-2002 (TrEMBLrel. 20, Li
01-OCT-2003 (TrEMBLrel. 25, Li
Hypothetical protein.
CP0186.
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Query Match
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Q82XI2
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"Functional prediction of the coding sequences of 79 new genes deduced by analysis of cDNA clones from human fetal liver.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF119881; AAF69635.1;
SEQUENCE 61 AA; 7467 MW; 6433950D4657C1D4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPECIES-Helicoverpa zea single nucleocapsid nucleopolyhedrovirus;
Chen X., Zhang W.-J., Wong J., Chun G., Lu A., McCutchen B.F.,
Presnail J.K., Herrmann R., Dolan W., Tingey S., Hu Z.-H., Vlak J.M.;
"Genome sequence analysis of Helicoverpa zea single nucleocapsid
                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Zhang C., Yu Y., Zhang S., Wei H., Zhang Y., Zhou G., Bi J., Liu M.,
                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Deng F., Chen X., Vlak J.M., Arif B.M., Hu Z.;
"Sequence analyysis of the gp37 gene of Heliothis armigera single-nucleocapsid nucleoplyhedrovirus.";
Zhongguo Bingduxue 15:35-42(2000).
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100.0%; Score 19; DB 2; Length 61; 100.0%; Pred. No. 9.3e+02; ive 0; Mismatches 0; Indels
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100.0%; Score 19; DB 4; Length 61;
Best Local Similarity 100.0%; Pred. No. 9.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indel8
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01-JUN-2001 (TERMBLrel. 17, Created)
01-JUN-2001 (TERMBLrel. 17, Last sequence update)
01-OCT-2003 (TERMBLrel. 25, Last annotation update)
ORF49 (Hypothetical protein) (Unkown).
Helicoverpa aemigera nucleocapsid nucleopolyhedrovirus,
Helicoverpa armigera nucleopolyhedrovirus G4, and
Helicoverpa armigera nuclear polyhedrosis virus.
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
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Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
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SPECIES-Heliocoverpa armigera nucleopolyhedrovirus G4,
                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                           61 AA.
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Q9P166;
01-OCT-2000 (TrEMBLrel. 15, C;
01-OCT-2000 (TrEMBLrel. 15, L;
01-OCT-2000 (TrEMBLrel. 15, L;
PRO2435.
                                              4; Conservative
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Query Match
Best Local Similarity
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Q9P166
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SPECIES-Heliocoverpa armigera nucleopolyhedrovirus G4;
MEDLINE=21078302; PubMed=11210934;
Wang H., Chen X., Wang H., Arif B.M., Vlak J.M., Hu Z.;
"Nucleotide sequence and transcriptional analysis of a putative basic DNA-binding protein of Helioverpa armigera polyhedrovirus.";
Virus Genes 22:113-120(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPECIES-Helicoverpa armigera nuclear polyhedrosis virus;
Fang M., Hu Z., Chen X., Vlak J.M.;
"Genetic organization of the HindIII-L region of Helicoverpa armigera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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PubMed-12050807;
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Wang H., Hu Z., Sun X., Vlak J.M., Chen X.;
"Sequence analysis of the lap3 gene of Heliothis armigera single-
nucleocapsid nucleopolyhedrovirus.";
Zhongguo Bingduxue 15:43-49(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhang C.X., Wu J.C.; mudithe pl0 gene of the Helicoverpa armigera mucleopolyhedrovirus."; Sheng Wu Wu Li Hsueh Pao 33:179-184(2001)
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MEDLINE=21064569; Pubmed=11125177;
Chen X., IJKel W.:
Peters S., Zuidema D., Lankhorst R.K., Vlak J.M., Hu Z.;
"The sequence of the Hellocoverpa armigera single-nucleocapsid
nucleopolyhedrovirus genome.";
J. Gen. Virol. 82:241-257(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPECIES=Heliocoverpa armigera nucleopolyhedrovirus G4;
Chen X., IJkel W.F., Tarchini R., Sun X., Sandbrink H., Wang
Peters S., Zuidema D., Lankhorst R.K., Vlak J.M., Hu Z.;
submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
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Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases
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01-07N-2003 (TrEMBLrel. 24, Last sequence update)
01-07N-2003 (TrEMBLrel. 24, Last annotation update)
Helix-turn-helix protein, CopG family.
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NO X S B D M 4 4 4 4 5 5 6 8 8 8

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"Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, APPOSSE0, EMBP93300.1;
Hypothetical protein; Complete proteome.
SEQUENCE 69 AA; 7815 MM; COEZA072C2295DDZ CRC64;
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Salmo trutta (Brown trout).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii, Neopterygii; Teleostei; Buteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
                                                          Bacreria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
NCBI_TaxID=1718;
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                             Corynebacterium glutamicum (Brevibacterium flavum).
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Last annotation update)
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STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
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PRINTS; PR0422; TRANSFERRIN.
NON_TER 71 71
SEQUENCE 71 AA; 7546 MW; 89
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01-MAR-2003 (TrEMBLrel. 23,
01-OCT-2003 (TrEMBLrel. 25,
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Best Local Similarity 100..
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Matches 4; Conservative
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OBAUO2;
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Han B., Feng Q., Huang Y.C., Li Y., Zhu J.J., Zhang L.,
Liu Y.L., Mu J., Yu Z., Chen L., Fan D.L., Weng Q.J., Zhang L.,
Liu Y.Q., Yu S.L., Liu X.H., Lu T.T., Zhang Y.J., Lu Y., Li T.,
Lu Y.Q., Yu S.L., Liu Y.H., Jia P.X., Qian Y.M., Ying K., Zhou B., Chen Z.H.,
A Rang Y., Hu H., Jia P.X., Qian Y.M., Ying K., Zhou B., Chen Z.H.,
A Ran S.X., Lv G., Lin W., Qu W.Q., Zhu G.F., Tu Y.F., Jia J., Yin H.F.,
A Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y., Shao C.Y., Sun Y.,
A Hu Q.P., Zhang W.L., Zhang W., Wang L.J., Ding C.W., Sheng H.H.,
A Q.J.L., Chen S.T., Ni L., Zhu F.H., Hong G.F.,
Submitted (MAX-2002) to the EMBL/GenBank/DDBJ databases.
B EMBL, AL731801, CAB05527.11, ...
R EMBL, AL731801, CAB05527.11, ...
R EMBL, AL731801, CAB05527.11, ...
R EMBL, AL731801, CAB05527.11, ...
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                                                                                                                       SEQUENCE FROM N.A.
STRAINS-TCC 19718 / IFO 14298;
MEDLINE-22586410; PubMed=12700255;
MEDLINE-22586410; PubMed=12700255;
Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M., Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A., Arciero D.M., Hommes N.G., Whittaker M.M., Arp D.J.;
"Complete genome sequence of the ammonia-oxidizing bacterium and obligate chemolithoautocroph Nitrosomonas europaea.";
EMBL: MAS1867; CAD84200.1; -.
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
05-0CT-2003 (TrEMBLrel. 25, Last annotation update)
05-0CT-2003 (TrEMBLREL. 25, Last annotation update)
05-0CT-2003 (TrEMBLREL. 25, Last annotation)
05-0CT-2003 (TrEMBLREL. 25, Last annotation
Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
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01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein Cgl1907.
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                                Nitrosomonadaceae; Nitrosomonas
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                                                                        NCBI_TaxID=915;
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097JU4
AC 097JU4,
DT 01-0CT-2
DT 01-0CT-2
DT 01-0CT-2
DE HYDCHET OCC CLOSTING
OC CLOSTING
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AC 082XX
AC 082XX
DT 01-JU
DT 01-JU
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DT 01-JU
DT 8XV15
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CX STRAIL
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STRIN=Ssa-1, and Ssa-2;

STRIN=Ssa-1, and Ssa-2;

STRIN=S2213992; PubMed=12140239;

A MEDLINE=2213992; PubMed=12140239;

A Antines A., Templeron A.R., Guyomard R., Alexandrino P.;

T genealogy of the transferrin gene in the brown trout.";

Mol. Biol. Evol. 19:127-1287 (2002).

EMBL; AF488831; AAN17017.1;

REMBL; AF488841; AAN17027.1;

REMBL; AF488841; AAN17022.1;

CO; GO:0006879; Ficric iron binding; IEA.

GO; GO:0006879; P:iron ion transport; IEA.

GO; GO:0006879; P:iron ion transport; IEA.
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MEDLINE=97251358; PubMed=9097040;
Itoh T., Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T.,
Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y.,
Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y.,
Sivasundaram S., Tagami H., Takeda J., Takemoto K., Wada C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                     Transferrin (Fragment).
Salmo salar (Atlantic salmon).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei; Buteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
NCBI_TaxID=8030;
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Enterobacteriaceae; Escherichia.
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                                                                                                                                                                                                                                                                                                      01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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P97252;
01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-2000 (TrEMBLrel. 13, Last annot Late control gene D protein (Fragment)
                                                                                                                                                                                                                                                   PRT;
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Pfam; PF00405; transferrin; 1.
PRINTS; PR00422; TRANSFERRIN.
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Best Local Similarity luv.
4, Conservative
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                           1 VAEF 4
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NON TER
SEQUENCE
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QBAUPO;
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Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
NCBI_TaxID=1488;
Yamamoto Y., Horiuchi T.;
"A 460-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 40.1-50.0 min region on the linkage map.";
DNA Res. 3:379-392 (1996).
EMBL; D90847; BAA1549.1; -.
EMBL; D90846; BAA15938.1; -.
NON TER.
1 SEQÜENCE 72 AA; 8099 MW; 42A63B25B00EADCE CRC64;
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces.
NCBI_TaxID=33903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 19; DB 16; Length 74; 100.0%; Pred. No. 1.18+03; tive 0; Mismatches 0; Indels
                                                                                                                                                                                      100.0%; Score 19; DB 2; Length 72; 100.0%; Pred. No. 1.1e+03; Live 0; Mismatches 0; Indels
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SEQUENCE FROM N.A.
STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=21477403; PubMed=11572948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein CAC1179.
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Last annotation update)
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STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE=21359325; PubMed=11466286;
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-01-JUN-2003 (TrEMBLrel. 24, Last seq.
01-JUN-2003 (TrEMBLrel. 24, Last annowanchetical protein.
SAVIS32.
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Matches 4; Conservative
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Hanamoto A., Takahashi C.

Ikeda H., Ishikawa J

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Lactobacillus plantarum.
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Submitted (DEC-1995)
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Mol. Reprod. Dev. 65:9-18(2003).
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Wakaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos
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Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T., Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces avermitiiis: deducing the ability of producing secondary metabolites.";
                                                                                                                                                                                                                                                                                           h Similarity 100.0%; Score 19; DB 16; Length 74; Similarity 100.0%; Pred. No. 1.1e+03; 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h Similarity 100.0%; Score 19; DB 6; Length 77; Similarity 100.0%; Pred. No. 1.2e+03; 4; Conservative 0; Mismatches 0; Indels
                                                                                                                          STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=22608306; PubMed=12692562;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to MAD2 protein (Fragment).
                                                                                Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
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01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
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Interpro, IPR003511; DNAbind HORMA.
PROSITE; PS50815; HORMA; 1.
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MEDLINE=22544902; PubMed=12658628;
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                    36 VAEF 39
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NON TER
SEQUENCE
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188VS7
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962M8
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Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,
Kuipers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M.,
Fiers M.W.B.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,
Hoffer S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing B.,
B. Complete genome sequence of Lactobacillus plantarum WCFS1.";
Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995(2003).

Bypothatical protein; Complete proteome.
SEQUENCE 77 AA; 8618 MW; CO0E2EFFID401F2F CRC64;
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MEDLINE=20478054; PubMed=11021991;
Sun L., Gurnon J.R., Adams B.J., Graves M.V., Van Etten J.L.;
"Characterization of a beta-1,3-glucanase encoded by chlorella virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Kaiser A., Vollmert M., Tholl D., Graves M.V., Gurnon J.R., Xing W.,
Lisec A.D., Nickerson K.W., Van Etten J.L.;
"Chlorella virus PBCV-1 encodes a functional homospermidine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96400199; PubMed=8806566; Kutish G.F., Van Etten J.L.; Kutish G.F., Li Y., Lu Z., Furuta M., Rock D.L., Van Etten J.L.; "Analysis of 76 kb of the chlorella virus PBCV-1 330-kb genome: map positions 182 to 258.";
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Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Chlorovirus.
NCBI_TaxID=10506;
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                                                                       Bacteria, Firmicutes; Lactobacillales; Lactobacillaceae; Lactobacillus.
NCBI_TaxID=1590;
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Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
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                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=NCIMB 8826 / WCFS1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100...
4; Conservative
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                   Hypothetical protein.
LP_1960.
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Gaps
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EMBL; APO01514; BABG5901.1; -.

PIN; R83922; R83925.

Hypothetical protein, Complete protecome.

SEQUENCE 84 AA, 9669 WW; GCDE3768ED9F5D84 CRC64;
                                                                                                                   SEQUENCE FROM N.A.
STRATE-SDA 110;
MEDLINE-2248498; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashina K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
Tabata S.,
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                                                                                                                                                                                                                                                                                                                          "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";
BNA Res. 9:189-197(2002).
EMBL; APO5937; BAC45927.1; -.
Complete proteome.
SEQUENCE 81 AA; 9235 MW; D512A9FFEDODA6C7 CRC64;
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STRAIN=C-125 / JCM 9153;
MEDLINEE-20512582; PubMed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
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   Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus halodurans.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=86665;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein.
CCA01010.
Chlamydophila caviae.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein BH2182.
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                            Bradyrhizobiaceae; Bradyrhizobium
NCBI_TaxID=375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43 VAEF 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38 VAEF 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 VAEF 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fuji F., Hiran
Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0821D2
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Q821D2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Winans S.C., Zhu J., Oger P.M., Schrammeijer B., Hooykaas P.J.,
Farrand S.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmid Ti.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 19; DB 2; Length 80;
100.0%; Pred. No. 1.2e+03;
Attive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                         Van Etten J.L.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

Gurnon J.R., Graves M.V., Van Etten J.L.;

Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, V42580; AAC96899.1; -.

PIR; T18034; T18034.

SEQUENCE 79 AA, 8698 MW; B191C627F5D5C5A7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Octopine type Ti plasmid sequence.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF242881; AAF77180.1; -.
GO; GO:0046821; C:extrachromosomal DNA; IEA.
                                                                                                                                                SEQUENCE FROM N.A.
Graves M.V., Van Etten J.L.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Graves M.V., Van Etten J.L.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 AA; 8723 MW; 4E8379C1D907CA8E CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OSKI36;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0;
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01-JUN-2003 (TrEMBLrel. 24, Le
01-JUN-2003 (TrEMBLrel. 24, Le
Baro662 protein.
BSR0662.
Bradyrhizobium japonicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Agrobacterium tumefaciens.
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Best Local Similarity 100.
Matches 4; Conservative
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[6]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49 VAEF 52
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Q9KI36

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SEQUENCE

Q89WL6 RESULT 29 Q89WL6 ID Q89WL6

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Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;
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HSSP; P19134; ITFD.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:000599; F:Eerric iron binding; IEA.
GO; GO:0006879; F:iron ion homeostasis; IEA.
GO; GO:0006826; P:iron ion transport; IEA.
INEA-Pro; IPRO1156; F:ansferrin.
SMART; SM0094; IR FER; I.
PROSITE; PSO0205; TRANSFERRIN_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87 AA.
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Tron transport; Metal-binding.
Tron transport; Metal-binding.
Tron Tex
Tr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Conservative
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es 4; Conserv
                                                                                                                                                            SEQUENCE FROM N.A.
                                                               Glomerella.
NCBI_TaxID=5457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45 VAEF 48
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Q99149;
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Matches
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Matches
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                               SOTITE DESCRIPTION OF THE STATE OF THE STATE
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Geng M. M., Schuhmacher A., Muchldorfer I., Bensch K.W., Schaefer K.P.,
Schneider S., Pohl T., Essig A., Marre R., Melchers K.;
Schneider S., Pohl T., Essig A., Marre R., Melchers K.;
The genome sequence of Chlamydia pneumoniae TW183 and comparison with
other Chlamydia strains based on whole genome sequence analysis.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE017159; AAP98704.1;
Hypothetical protein.
SEQUENCE 84 AA; 9260 MW; 7786DF8BDD7B3AB8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                        STRAIN-GPIC;
Read T.D., Myers G.S.A., Brunham R.C., Nelson W.C., Paulsen I.T.,
Read T.D., Myers G.S.A., Brunham R.C., Nelson W.C., Paulsen I.T.,
Heidelberg J., Holtzapple E., Khouri H., Federova N.B., Carty H.A.,
Mindyam L.A., Haft D.H., Peterson J., Beanan M.J., White O.,
Salzberg S.L., Hsia R.-C., McClarty G., Rank R.G., Bavoil P.M.,
Fraser C.M.;
Fraser C.M.;
esquence of Chlamydophila caviae (Chlamydia psittaci GPIC):
examining the role of niche-specific genes in the evolution of the
Chlamydiacese.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Hypothetical protein.
CPB0775.
CPB0775.
Chlamydia pneumoniae (Chlamydophila pneumoniae)
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
VCBI_TaxID=83857;
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01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment).
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Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 19; DB 16; Length 84; 100.0%; Pred. No. 1.3e+03; tive 0; Mismatches 0; Indels
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SEQUENCE 84 AA; 9191 MW; 7DF6009729C7093A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic Acids Res. 31:2134-2147(2003).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100...
4; Conservative
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Best Local Similarity 100...
4, Conservative
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7VPV6
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Tu G.F., Achen M.G., Aldred A.R., Southwell B.R., Schreiber G.;
Tu G.F., Achen M.G., Aldred A.R., Southwell B.R., Schreiber G.;
The distribution of cerebral expression of the transferrin gene is species apecific.";
J. Biol. Chem. 266.6201-6208(1991).
J. Biol. Chem. 266.6201-6208(1991).
I- FUNCTION. TRANSPERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOWNS OF PERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE.
EMBL. M64691; AAA31585.1;
PIR. A38725; A38725.
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Stephenson S.-A., Maclean D.J., Manners J.M.;
"Disruption of a novel pathogenicity gene of Colletotrichum
glocosporioides results in a hypersensitive response in the host
stylosanches guianensis.";
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U94183; AAB92222.1; -.
EMBL; U94183; AAB92222.1; -.
EMBL; PR001387; HTH 3.
InterPro; IPR001387; HTH 3.
Pfam; PF01381; HTH 3; 1.
Pfam; PF01381; HTH 3; 1.
Hypothetical protein.
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                                                                                                                                                                                                                                                                                                                                                                                    85 AA; 9316 MW; BFB9A0E5F44E9CF2 CRC64;
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Last annotation update)
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PRELIMINARY;
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Best Local Similarity
                                                                                                                                                                                             SEQUENCE FROM N.A.
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RESULT 37
Q41185
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Matches
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"Construction of tryptophan requiring-mutant of Nitrosomonas europaea
by inactivation of tryc gene using homologous recombination.";
submitted (JUL.1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB030031; BAA83388.1; -
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                                                                                                                                                                                                                              Hertwig S., Klein I., Schmidt V., Beck S., Hammerl J.A., Appel B.; Sequence analysis of the genome of the temperate Yersinia enterocolitica phage PY54."
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                  01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Bacteriophage PY54.
Viruses; GabNA viruses, no RNA stage; Caudovirales; Siphoviridae.
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Nitrosomonadaceae, Nitrosomonas.
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                                                                                                                                                                                                                                                                                                       Hertwig S.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AAJ564013; CAD91786.1; -.
Exonuclease; Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88 AA; 9765 MW; A59003348F4E280C CRC64;
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1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UTN-2001 (TrEMBLrel. 17, Last annotation update)
Cytochrome P460 (Fragment).
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Best Local Similarity
Matches 4; Conserv
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Matches 4; Conserv
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                                    VAEF 16
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01-MAY-2000 (
01-MAY-2000 (
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SEQUENCE
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Shih M.C., Heinrich P., Goodman H.M.;
"Cloning and chromosomal mapping of nuclear genes encoding chloroplast and cytosolic glyceraldehyde-3-phosphate-dehydrogenase from Arabidopsis thaliana.";
Gene 119:317-319(1992).
GENBL; $45911; AAB23533.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; euroaids II; Brassicales; Brassicaceae; Arabidopsis.
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ENDL, APO74611, AAC82761.1; -.
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                                               Q41185;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Glyceraldehyde-3-phosphate-dehydrogenase subunit GapB (Fragment).
GAPB.
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Local Similarity 100.0%; Pred. No. 1.3e+03;
les 4; Conservative 0; Mismatches 0; Indels
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NON TER 88 88
SEQUENCE 88 AA; 9198 MW; FCDB6A7E37B6999D CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).
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NCBI_TaxID=632;
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Conservative
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Best Local Similarity
Loca 4; Conserv
Query Match
Best Local Similarity
Matches 4; Conserv
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Q812X3
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MEDLINE-21146866; PubMed=11248100;

May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;

I "Complete genomic sequence of Pasteurella multocida Pm70.";

Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).

EMBL; AE006066; AAX02385.1;

R MSSP; Pa00378; IAB3;

GO; GO:0005622; Cintracellular; IEA.

GO; GO:0005640; Cintbosome; IEA.

GO; GO:0006412; P:protein biosynthesis; IEA.

GO; GO:00063135; F:structural constituent of ribosome; IEA.

GO; GO:0006312; P:protein biosynthesis; IEA.

InterPro; IPR00129; Ribosomal_S15.

InterPro; IPR00129; Ribosomal_S15.

R Prod) PD157043; R815 bact; 1.

R TIGRFAMS; TIGR00952; S15 bact; 1.

PROSITE; PROSITE; PROSOWAL_S15; 1.
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STRAIN=IL1403,
STRAIN=IL1403,
MEDLINE=1203EDE PubMed=11337471;
BOIOtin A., Wincker P., Mauger S., Jaillon O., Malarme K.,
Weissenbach J., Ehrlich S.D., Sorokin A.;
"The complete genome sequence of the lactic acid bacterium Lactococcus
lactis sep. lactis IL1403.";
Genome Res. 11:731-7531(201).
BMBL, AR005885, AAK05648.1; -.
BIRE, P86818; P86818.
Hypothetical protein; Complete proteome.
SEQUENCE 89 AA; 10403 MW; D90DF3CF71D12D06 CRC64;
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
NCBI_TaxID=1360;
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Pasteurellaceae, Pasteurella.
NCBI_TaxID=747;
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01-UTN-2001 (TrEMBLrel. 17, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein ypjB.
                                                                                                                                                                                                                                        Last sequence update)
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RPS15 OR PM0301.
Pasteurella multocida.
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Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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   VAEF
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Preproinsulin (Fragment).
Ambloplites rupestris (Rock bass).
Ambloplites rupestris (Rock bass).
Actinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei, Actinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei, Centrarchidae; Ambloplites.
                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Al-Wahrouki A.A., Irwin D.M., Youson J.H.;

Al-Wahrouki A.A., Irwin D.M., Youson J.H.;

Molecular cloning of preproinaulin cDNA from the rock bass.";

Li Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.

-1- SINGELLULAR LOCATION: SECRETED (BY SINILARITY).

C -1- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.

R MEBL, AF195844, AAX28708.1; -.

R GO; GO:0005179; LDH.

R GO; GO:0005179; Fhormone activity; IEA.

R GO; GO:0005179; Fhormone activity; IEA.

R GO; GO:0005219; Piphyalological processes; IEA.

R DATE: PRO0049: Insulin; 1.

R PRIMTS; PRO00277; INSULIN.

R PRIMTS; PRO00771; INSULIN.

R PRIMTS; PRO00771; INSULIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryora; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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0
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h Similarity 100.0%; Score 19; DB 16; Length 89; Similarity 100.0%; Pred. No. 1.38+03; 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vin F., Fan D.M.;
"Identifying a new variant of MADZL1.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
BMBL; AF394735; AAN74648.1; -..
INTERPRO'S INTROUSEL1; DNAbind HORMA.
PF02301; HORMA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50815; HORMA; 1.
SEQUENCE 90 AA; 10335 MW; 8209F5A7A7D8D09B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                     QBIZX3;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 25, Last sequence update)
10-CT-2003 (TrEMBLrel. 25, Last annotation update)
MAD2 mitotic arrest deficient-like 1 variant.
MAD2L1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 19; DB 4; 1
100.0%; Pred. No. 1.4e+03;
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Query Match
Best Local Similarity 100..
From 4; Conservative
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Q89WX7
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  S T T W D D R R D R R D R R D R R D R R D R R D R R D R R D R R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cevallos M.A., Izquierdo J., Porta H., Tun C., Davila G., Brom S., "Rhizobium etli CE3 contains at least three plasmids of the RepABC family: A structural and an evolutionary analysis.";
Submitted (OCT-2000) to HE EMBL/GenBank/DDBJ databases.
EMBL; AR313446; AAM88940.1; --
GO; GO:0046821; C:extrachromosomal DNA; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              046425;
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-1998 (TrEMBLrel. 25, Last annotation update)
Aquaporin 1 (Fragment).
Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa; Chordata; Craniata, Vertebrata; Buteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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                                                                                                                   100.0%; Score 19; DB 13; Length 91; larity 100.0%; Pred. No. 1.4e+03; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 19; DB 2; Length 94; 100.0%; Pred. No. 1.4e+03; trive 0; Mismatches 0; Indels
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94 AA; 10222 MW; C09D6EA3DFF1E2BA CRC64;
                                           91 91
91 AA; 10100 MW; E86C8B256DC69D39 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Putative transcriptional regulator (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                           94 AA.
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  PS00262; INSULIN; 1.
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Best Local Similarity 100.
Matches 4; Conservative
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                                                                                                                                              Local Similarity
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                          1 VAEF 4
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PROSITE; IN NON TER NON TER SEQUENCE
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SEQUENCE
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Best Local S
Matches 4
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046425
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
NCBI_TaxID=176299;
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Best Local Similarity 100.0%; Score 19; DB 16; Length 96;
Best Local Similarity 100.0%; Pred. No. 1.48+03;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                   Length 94;
                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 19; DB 6; Length 94 100.0%; Pred. No. 1.4e+03; tive 0; Mismatches 0; Indels
                                                                                                                                                 Science 294:2317-2323(2001).

EMBL, AB009334; AAL44840.1; -.
PIR, AB3053; AB3053.

Hypothetical protein; Complete proteome.

SEQUENCE 96 AA; 11193 MW; FBD635894846A8AE CRC64;
GO; GO:0005741; C:mitochondrial outer membrane; IEA.
GO; GO:0015288; F:porin activity; IEA.
GO; GO:0005215; F:transporter activity; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR000425; MIP.
PFam; PF00230; MIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein Atu4039.
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01-UUN-2003 (TrEMBLrel. 24, Created)
01-UUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Bs10551 protein.
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Gaps

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STRAIN=EGD-e / Serovar 1/2a;

SA Glaser P., Frangeul L., Buchteser C., Rusniok C., Amend A.,

A Glaser P., Frangeul L., Buchteser C., Rusniok C., Amend A.,

B Advarotr A., Checuani F., Couve E., de Daruvar A., Dehoux P.,

Charbit A., Checuani F., Couve E., de Daruvar A., Dehoux P.,

B Entlan K.-D., Faihi H., Garcia-del Portillo F., Garrido P.,

B Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,

Johes L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,

Madueno E., Maltournam A., Mata Vicente J., Ng E., Nedjari H.,

Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

Remmel B., Rose M., Sohlueter T., Simose N., Tierrez A.,

Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;

Comparative genomics of Listeria species.";
        Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
Hepatovirus.
NCBI_TaxID=12092;
                                                                                                                                                                                                Characterization of a hepatitis A virus strain suitable for vaccine
                                                                                                                                          MEDLINE-92348853; PubMed=1668326;
Fineschi N., Cavalieri F., Garelick H., Prugnola A., Pellegrini V.,
Zuckerman A.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 97;
                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 19; DB 12; Length 97; Best Local Similarity 100.0%; Pred. No. 1.5e+03; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Listeria monocytogenes.
Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
NCBI_TaxID=1639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                          F. Heparci... 13:S146-S151(1991).

EMBL; S44109; AAB22740.2; -.

NON TER 97 97

SEQÜENCE 97 AA; 10614 MW; D207F7CB93110DDF CRC64;
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97 AA; 10979 MW; 9E758586E94218E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UIN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein lmo2579.
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100.0%; Pred. No. 1.5e+03;
tive 0; Mismatches 0;
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EMBL; AL591983; CAD00657.1; -.
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InterPro; IPR007138; ABM.
Pfam; PF03992; ABM; 1.
Hypothetical protein; Comp
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Matches 4; Conserv
                                                                                                  SEQUENCE FROM N.A. STRAIN=LSH/S;
Hepatitis A virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44 VAEF 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 VAEF 18
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                                                                                                                                                                                                                                 production.";
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Q8Y476;
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Q8Y476
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01-JUN-2002 (TrEWBLrel. 21, Last annotation update)
Hypothetical protein PF1620.
Pyrococcus furiosus.
Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaces;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                            STRAIN-USDA 110;
MEDLINE-2246498; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
                                                                                                                                                                                                                                                                "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";
DNA Ree. 9:189-197(2002).
EMBL; AP005936; BAC45816.1;
GO; GO:0016020; C:membrane; IEA.
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STRAIN=VC1 / DSM 3638 / ATCC 43587 / JCM 8422;
Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
Withe complete sequence of the Pyrococcus furiosus genome.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
BMBL, AEGO10262, AALS174-1, -
Hypothetical protein; Complete proteome.
SEQUENCE 96 AA, 10804 MW; D6DAE09D096D577A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 19; DB 16; Length 96; 100.0%; Pred. No. 1.4e+03; Attive 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels
                   Bradyrhizobium japonicum.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                       96 AA; 10976 MW; A9E11F9AA4BC7734 CRC64;
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Pfam; PF02325; YGGT; 1.
Complete proteome.
SEQUENCE 96 AA; 10976 MW.
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Best Local Similarity
Matches 4; Conserv
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SEOUENCE FROM N.A.
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                                                                                 NCBI_TaxID=375
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Best Local Similarity 100.
Matches 4; Conservative
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                                                                                                                                       62 VAÈF 65
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                                                                                    1 VAEF 4
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Q8VS54
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ID O9
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STRANN=DCO000;

We would R., Joardar V., Khouri H., Fedorova N., Tran B., Russell D.,
Berry K., Utterback T., Van Aken S., Feldblyum T., Gwinn M.,
Dodson R., DeBoy R., Durkin A., Kolonay J., Madupu R., Daugherty S.,
Brinkac L., Beanan M., Haft D., Selengut J., Nelson W., Davidsen T.,
White O., Fraser C., Collmer A.,
"Complete sequence of Pseudomonas syringae.";
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.

TIGR: PSPTO1808:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pseudomonas syringae (pv. tomato).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                Pseudomonas aeruginosa.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=287;
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99 AA; 10504 MW; 62836007E4849392 CRC64;
                                                                                                         01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein PA3202.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Conserved hypothetical protein.
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Pfam; PP03795; YCII; 1.
Hypothetical protein; Compl
SEQUENCE 99 AA; 10504 MW
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Best Local Similarity 100..
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                                                            PRELIMINARY;
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                                                         Q9HZ38
Q9HZ38;
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                                 Q9HZ38
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STRAIN=ATCC 55739;

Num S.J., Kim J.K.;

Nam S.J., Kim J.K.;

Nam S.J., Kim J.K.;

Nam S.J., Kim J.K.;

Nam S.J., Kim J.K.;

Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AF401482; AAR60142.1;

EMBL, AF401482; AAR60142.1;

EMBL, AF401482; AAR60142.1;

EMBL, AF40148; AF40148;

EMBL, AF40148;

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STRAIN=ATCC 19718 / IFO 14298;
MEDLINE=22586410; PubMed=12700255;
MEDLINE=22586410; PubMed=12700255;
MEDLINE=22586410; PubMed=12700255;
Hauser L., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M.,
Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A.,
Arciero D.M., Hommes N.G., Mihitraker M.M., Arp D.J.;
Arciero D.M., Hommes N.G., Mihitraker M.M., Arp D.J.;
Arciero D.M., Hommes N.G., Mihitraker M.M., Arp D.J.;
J. Complete genome sequence of the ammonia-oxidizing bacterium and
obligate chemolithoautotroph Nitrosomonas europaea.";
J. Bacteriol. 185:2759-2773(2003).
BMBL, BAZ21861; CAD85330.1;
InterPro). IPR005545; YCII.
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Nitrosomonadaceae, Nitrosomonas.
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100.0%; Score 19; DB 16; Length 1
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                     Indels
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Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
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SEQUENCE 100 AA, 10836 MW; 82DC1153BABFAE27 CRC64;
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Last annotation update)
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Q8VS54;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 24, Last annotation update)
Elongation factor TS (Fragment).
Pred. No. 1.5e+03;
Mismatches 0;
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Homo sapiens (Human)
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NON TER
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SEQUENCE 103
                                                                                          Fraser C.M.;
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Q7Z2N2;
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Q9F368
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SEQUENCE FROM N.A.

SEQUENCE TROM N.A.

STRAIN=ATCC 35092 / DSW 1617 / P2;

MEDINE=2132296; PubMed=11427726;

A She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,

A Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,

De Moors A., Brauso G., Fletcher C., Gordon P.M.K.,

A Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

A Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,

Charlebois R.L., Dolittle W.F., Duguet M., Gaasterland T.,

Charlebois R.L., Dolittle W.F., Duguet M., Gaasterland T.,

Charlebois S.L., Sensen C.W., Van der Oost J.,

The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";

PRED, AR006755; ARK41631;

PRED, AR006755; ARK41631;

PRED, PROMOFOST, PROCEST, PROCES
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Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T., Nelson K.E., Tettelin H., Fouts D.E., Bisen J.A., Gill S.R., Holtzapple E.K., Ostad O.A., Helgason E., Rilstone J., Wu M., Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M., DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H., Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
                                                                                                                                                                                                                                                                                                                                                                                                                              Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
Sulfolobus.
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100.0%; Score 19; DB 2; Length 101; 100.0%; Pred. No. 1.5e+03; ive 0; Mismatches 0; Indels
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
NCBI_TaxID=198094;
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Hypothetical protein; Complete proteome.
SEQUENCE 101 AA; 11936 MW; A7C338AD76202E17 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein.
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Pro; IPR003799; DUF196.
PF02647; DUF196; 1.
    Query Match 100.
Best Local Similarity 100.
Matches 4; Conservative
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                                                                                                                                        62 VAEF 65
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Pfam; PF02
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Q81R27;
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Matches
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Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S.L.,
Thomason B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,
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01-0Cr-2003 (TrEMBLrel. 25, Last annotation update)
BK150C2.6 (Putative novel protein similar to APOBEC1 (Apolipoprotein mRNA editing protein) and Phorbolin) (Fragment).
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                                                                                                                            "The genome sequence of Bacillus anthracis Ames and comparison to closely related bacteria.";
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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MEDLINE-21996410; PubMed-12000953;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
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                                                                                                                                                                                                                                                                    Hypothetical protein; Complete proteome.
SEQUENCE 102 AA; 11925 MW; 13B8E296C8A341B1 CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2003 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein SCO4420.
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100.0%; Pred. No. 1.5e+03;
iive 0; Mismatches 0;
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EMBL; AE017031; AAP26109.1; -.
TIGR; BA2232; -.
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Matches 4; Conservative
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Gaps

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Mycobacteriophage Corndog.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
NCBI_TaxID=205875;
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MEDLINB=21576510; PubMed=11719806;
Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F., Prensier G., Barbe V., Peyretaillade E., Brottier P., Wincker P., Delbac F., El Alaoui H., Peyret P., Saurin M., Gouy M., Weissenbach J., Vivares C.P.;
Weissenbach J., Vivares C.P.;
Weephalitozoon cuniculi.";
Nature 414:450-453[2001].
Nature 414:450-453[2001].
BMBL; ALS99445; CADZ6596.1; -.
Hypothetical protein.
SEQUENCE 105 AA; 11897 MW; 08059108C05D3BB9 CRC64;
SEQUENCE FROM N.A.

MEDLINE=22592660; PubMed=12705866;

MEDLINE=22592660; PubMed=12705866;

Dedulla M.L., Ford M.E., Houtz J.M., Karthikeyan T., Wadsworth C lewis J.A., Jacobs Bera D., Falbo J., Gross J., Pannunzio N.R., Brucker W., Kumar V., Kandasamy J., Keenan L., Bardarov S., Kriakov J., Lawrence J.G., Jacobs W.R. Jr., Hendrix R.W., Hatfull G.F.,

"Origins of highly mosaic mycobacteriophage genomes.";

Cell 113:171-182(2003).

EMBL, AY129339; AAN12111.1; -

SEQUENCE 104 AA; 11074 MW; BB806EAC401E9FD0 CRC64;
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Eukaryota; Fungi; Microsporidia; Unikaryonidae; Encephalitozoon.
NCBI_TaxID=6035;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein ECU05_0770.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Teuruoka H., Wada T., Yamada M.,
Tabata S.;
       Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch B., Rajandream M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Marren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
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BNA Res. 9:189-197(2002).
ENBL; ABOO5550; BAC49378.1; -.
Complete proteome.
SEQUENCE 103 AA; 11104 MW; BF27CB9F90FBB723 CRC64;
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Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
NCBI_TaxID=205880;
[1]
                                                                                                                                                                                                                                              Hopwood D.A.;

Complete genome sequence of the model actinomycete Streptomyces collicolor A3(2).;

Nature 417:141-147(2002).

EMBL, A1939120, CAC08429.1; -.

Hypothetical protein; Complete proteome.

SQUENCE 103 AA; 11387 MW; 55C2B80589EB75B5 CRC64;
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Matches 4; Conservative 0; Mismatches 0; Indels
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Bradyrhizobium japonicum.
Bradyrhizobiacee; Bradyrhizobium.
NCBL_TaxID=375;
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Q856B5;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Gp57.
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01-JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 24,
Blr4113 protein.
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Archaea; Euryarchaeota; Methanococci; Methanococcales;
Methanococcaceae; Methanococcus.
NCBL_TaxID=39152;
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Bertage 4; Conservative
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Q9BGL5
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C STRAIN=JCM 10545 / 7;

K MEDLINE=21456156; PubMed=11572479;

K RAWATEDAYEB 1 Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,

A Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fikui S.,

A Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,

Noshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Oshima T., Kikuchi H.;

A Ooki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,

A Ooki R.-I., Kikuchi H.;

Complete genome sequence of an aerobic thermoacidophilic

T Complete genome sequence of an aerobic thermoacidophilic

T Crenarchaeon, Sulfolobus tokodaii strain? ";

DNA Res 8.123-140(2001)

E EMBL; APO00988 BAB67095.1; -.

R FABL; PRO0898; PAB67095.1; -.

R Pfam; PRO0898; Transposase 29; 29.

R Pfam; PRO0898; Transposase 29; 2.

R Pfam; Protein; Complete proteome.

Q SEQUENCE 105 AA; 11997 MW; AFEGABD4DF2DECCE CRC64;
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MEDLINE-22592660, PubMed=12705866;

MEDLINE-22592600, PubMed=12705866;

Pedulla M.L., Ford M.B., Houtz J.M., Karthikeyan T., Wadsworth C.,

Lewis J.A., Jacobs-Sera D., Falbo J., Gross J., Pannunzio N.R.,

Enucker W., Kumar V., Kandasamy J., Keenan L., Bardarov S.,

Kriakov J., Lawrence J.G., Jacobs W.R. Jr., Hendrix R.W.,

Hatfull G.F.,

Coll 113:171-182(2003).

EMBL, AN129335, AAN01935.1;

EMBL, AN129355, AAN01935.1;

ENGLENCE 105 AA; 11955 MW; 7D0EC09F5F2AF2DD CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein $T2000.
$T2000.
Sulfolobus tokodain. The management of the sequence of
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Best Local Similarity 100.03
Matches 4; Conservative
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P71530;
01-FEB-1997
01-FEB-1997
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 25, Last annotation update)
Matrilysin (Fragment).
Matrilysin (Fragment).
Eukaryota: Sheep).
Busaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                              STRAINEL;
MEDLINE=97144542; PubNed=8990309;
Kessler P.S., McIarnan J., Leigh J.A.;
Kessler P.S., McIarnan J., Leigh J.A.;
Kessler P.S., McIarnan J., Leigh J.A.;
Mitrogenase phylogeny and the molybdenum dependence of nitrogen fixation in Methanococcus maripaludis.";
J. Bacteriol. 1979:541-543(1997).
EMBL, U75887; AAC45519.1;
Interpro.; IPR003731; DUF153.
PIR; T10097, ILL097.
Interpro.; IPR003731; DUF153.
PÉRM; PF02579; Nitro FeMO-CO; 1.
SEQUENCE 106 AA; 11862 MW; 4734D89CFED33F3B CRC64;
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MEDLINE=56011360; PubMed=7592322;
Blank C.E., Kessler P.S., Leigh J.A.;
"Genetics in methanogens: transposon insertion mutagenesis impendence maripaludis niff gene.";
"Bacteriol. 177:5773-5777 (1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 19; DB 1; Length 106; 100.0%; Pred. No. 1.6e+03; ive 0; Mismatches 0; Indels
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Smith G.W., Cassar C.A., Smith M.F.;
Smith G.W., Short M.A., Cassar C.A., Smith M.F.;
Submitted (WAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF67158; AAG59846.1;
RESPOR, M.D. 1008;
RESPOR, M.D. 1008;
C. G. G. 10065278; F. metalloendopeptidase activity; IEA.
G. G. 1006508; P. proteclylais and peptidolysis; IEA.
InterPro; IPR001818; Pept MIOA_MI2B.
REAM; PR001318; PAPILAISE.
REAM; PR001318; MATRIXIN.
SWART; SM00235; ZMG; 1.
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"Complete genomic sequence of Corynebacterium glutamicum ATCC 13032."; Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AP005276; BAB98308.1; -.
InterPro; IPR007138; ABM.
Pfam; PF03992; ABM; 1.
Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22255705; PubMed=12368864; Gardinan M., Hyman R.W., Gardner M.J., Hall N., Fung B., White O., Berriman M., Hyman R.W., Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K., Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S., Chan M.S., None V., Shallom S.J., Subl. B., Peterson J., Angilon S., Perrea M., Allen J., Selengut J., Haft D., Marher M.W., Vaidya A.B., Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A., McRent J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W., Fraser C.M., Barrell B.J., Hoffman S.L., Newbold C., Davis R.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria; Actinobacteria; Actinobacteridae; ActinomyCetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
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Plasmodium falciparum (isolate 3D7).
Bukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBL_TaxID=36329;
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 Length 107;
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100.0%; Pred. No. 1.6e+03;
ative 0; Mismatches 0; Indels
                                  Indels
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EMBL, AE014842; AAN36006.1; -.
Hypothetical protein.
SEQUENCE 107 AA; 12714 MW; CA351258FCF46EF5 CRC64;
                                                                                                                                                                                                                     01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Mypothetical protein.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
100.0%; Score 19; DB 3; L
100.0%; Pred. No. 1.6e+03;
ive 0; Mismatches 0;
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STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
Nakagawa S.;
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Matches 4; Conservative
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CGL0915.
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SEQUENCE FROM N.A.
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QBNRX6
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MEDLINE=21135672; PubMed=11238395;
Bean L.E., Dvorachek W.H. Jr., Braun E.L., Errett A., Saenz G.S.,
Giles M.D., Werner Washburne M., Nolson M.A., Natvig D.O.;
"Analysis of the pdx-1 (snz-1/sno-1) region of the Neurospora crassa genome. Correlation of pyridoxine-regulring phenotypes with mutations
                                                                                                                                                                                                                                                                                                                         PEGETRIAL COLUMBIA:
FEGETRIAL N.A., COLWAY A.B., COLWAY A.R., Davis K., Brendel V.,
Federspiel N.A., Corway A.B., Colway A.R., Davis K., Buehler E.,
Palm C.J., Au M., Araujo R., Chung E., Kurtz D.B., Buehler E.,
Dewar K., Feng J., Kim C., Li Y., Shinn P., Sun H., Oji O.,
Osborne B., Shen Y.K., Toriumi M., Vyotskaia V., Yu G., Theologis A.,
"Geronic sequence of Arabidopsis BAC 77123.";
"Genomic sequence of Arabidopsis BAC 77123.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
BMBL, 108959; AAC24377.1; -.
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                                                                                                                                                                                      T7123.13.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 19; DB 10; Length 106; 100.0%; Pred. No. 1.6e+03; ive 0; Mismatches 0; Indels C
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Genetics 15:1067-1075(2001).
EMBL; AF30068; AAK07845.1; -..
HSSP; P80028; 170F.
GO; GO:0005489; F:electron transporter activity; IEA.
GO; GO:000518; F:electron transport; IEA.
InterPro; IPR006662; Tiloredo.
Pfam; PF00085; Thiored.
PRINTS; PR00421; THIOREDOXIN.
Redox-active center.
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107 AA; 11676 MW; CF4E6EAF85BE3776 CRC64;
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                                                                                                                  01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Cathepsin B-like cysteine proteinase (Fragment).
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01-JUN-2001 (TrEMBirel. 17, Last sequence update)
01-JUN-2003 (TrEMBirel. 24, Last annotation update)
Putative thioredoxin G6G8.7.
                                                                                     106 AA.
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Best Local Similarity 1000.
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                                                                                     PRELIMINARY;
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SEQUENCE FROM N.A.
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01-JAN-1998 (
01-JAN-1998 (
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SEQUENCE
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023682
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Query Match
Best Local Similarity 100.
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Best Local Similarity 100.
Matches 4; Conservative
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Q7TX28;
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Q7TX28
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
Gordon S.V., Eiglmeier K., Gas S., Barry C.B. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Deviln K., Fellwell T., Gentles S., Hamlin N., Holroyd S.,
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Retinol binding protein (Fragment).
Retinol binding protein (Fragment).
Excoodylus niloticus (Nile crocodile) (African crocodile).
ENkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Crocodylidae; Crocodylinae; Crocodylus.
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MEDLINE=20022983; PubMed=10555283;
Hughes S., Zelus D., Mouchiroud D.;
"Warm-blooded isochore structure in nile crocodile and turtle.";
MO1. Biol. Evol. 16:1521-1527(1999).
EMBL; AJ011392; CABS6418.1; -.
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Similarity 100.0%; Score 19; DB 16; Length 107;
Similarity 100.0%; Pred. No. 1.6e+03;
4; Conservative 0; Mismatches 0; Indels C
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107 AA; 12373 MW; B5ACF23621078018 CRC64;
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01-0TM-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein Rv3183.
RV3183 OR MTV014.27 OR MT3275.
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GO; GO: 0005215; F: transporter activity; IEA.

GO; GO: 0006810; P: transports IEA.

InterPro; IPR002345; Libocalin.

InterPro; IPR00566; Libocalin.

Pfam; PF00061; Lipocalin; 1.

PRINTS; PR00179; LIPOCALIN; 1.

PRINTS; R00179; LIPOCALIN; 1.

NON TER 109

SEQUENCE 109 AA; 12552 MW; ODCAE93895591A2.
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3Q SEQUENCE
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STRAIN-CDC 1551 / Oshkosh,
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann K.D., Alland D., Eisen J.A., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
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Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,
Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
Parkhill J., Barrall B.G., Cole S.M., Gordon S.V., Hewinson R.G.;
The complete genome sequence of Mycobacterium bovis.";
Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882 (2003).

Complete protector.

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"Whole genome comparison of Mycobacterium tuberculosis clinical and
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
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Bacteria, Actinobacteridae; Actinomycetales;
Corymebacterineae; Mycobacteriaceae; Mycobacterium.
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AL021646; CAA16648.1; -.
EMBL; AS007140; AAK47615.1; -.
PIR; E70949; F10949.
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SWART; SM00530; HTH XRE; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 109 AA; 11802 MW; A66DBE160D79613A CRC64;
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100.0%; Pred. No. 1.6e+03;
iive 0; Mismatches 0;
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MEDLINE=22709107; PubMed=12788972;
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SEQUENCE FROM N.A.
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1 VAEF 4
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Lopez-Estebaranz J.L., Esteban M., Martin-Gallardo A.;
"A Random DNA Sequencing, Computer-Based Approach for the Generation
of a Gene Map of Molluscum Contagiosum Virus.";
Virus Genes 0:0-0(1997).
EMBL, U86919; AABS7977.1; -.
NON TER 10 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDITE=22433060; PubMed=12534463;
Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
Martins dos Santos V.A.P., Foute D.E., Gill S.R., Pop M., Holmes M.,
Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,
Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,
Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzez A.,
Utterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H.,
Lauber J., Stjepandic D., Hobelsel J., Straetz M., Heim S.,
Xiewitz C., Eisen J., Timmis K.N., Duesterhoeft A., Tuemmler B.,
                                                   01-JTL-1997 (TrEMBLrel. 04, Created)
01-JTL-1997 (TrEMBLrel. 04, Last sequence update)
01-JTL-1997 (TrEMBLrel. 04, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
XI-5 protein (Fragment).
XI-5 protein (Fragment).
XI-5 Willscum contagiosum virus subtype 1 (MCVI).
Viruses; dSDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
Molluscipoxvirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas putida (strain KT2440).
Bacteria, Proteobacteria, Gammaproteobacteria, Fseudomonadales,
Pseudomonadaceae, Pseudomonas.
NCBI_TaxID=160488;
                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 19; DB 12; Length 110; 100.0%; Pred. No. 1.6e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 19; DB 16; Length 110; Best Local Similarity 100.0%; Pred. No. 1.6e+03; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete genome sequence and comparative analysis of the metabolically versatile Pseudomonas putida KT2440."; Environ. Microbiol. 4:799-808(2002).
EMBL; AEO1679: AAN70076.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
YCII-related domain protein.
                            110 AA
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Pfam, PP03795; YCII; 1.
Complete proteome.
SEQUENCE 110 AA; 11775 M
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Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
Pyrococcus.
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Robinson-Rechavi M., Maina C.V., Gissendanner C.R., Laudet V., Sludar A.;
Sludar A.;
Explosive lineage-specific expansion of the orphan nuclear receptor HNF4 in nematodes.";
EMBL, AZ204162; AA03166.1;
GO, GO:0004872; F:receptor activity; IEA.
Interfro, IPR008946; Str_ncl_receptor.
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Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                        STRAINVCI / DSM 3638 / ATCC 43587 / JCM 8422;
Weiss R.B., Dunn D.M., Robb P.T., Brown J.R.;
"The complete sequence of the Pyrococcus furiosus genome.";
submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; ABCO1208; AALB1067.1;
InterPro; IPRO7342; HEPN
Pfam; PF05168; DUF712; I.
Pypochetical proctein; Complete proteome.
Hypochetical proctein; Complete proteome.
SEQUENCE 111 Aa; 13379 MW; C6A005A6B2B6CAAE CRC64;
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NOW TER 1
SEQUENCE 112 AA, 12826 MW, 44FC60A4E3744791 CRC64;
                                           01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein PF0943.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Nuclear receptor NHR-1 (Fragment)
Caenorhabditis elegans.
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US-09-543-611A-5816
US-08-46-517-8
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US-08-580-988A-21
US-09-540-235-3612
US-08-464-517-25
US-08-463-31A-25
US-09-463-039A-915
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3. /cgn2 6/prodata/2/iaa/RGTOMS.pep:*

5. /cgn2 6/prodata/2/iaa/PCTUS COMB.pep:*

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US-08-751-189-4 Sequence 4, Applia US-09-060-836-4 Sequence 4, Applia US-09-184-445-4 Sequence 4, Applia US-09-036-987A-6 Sequence 6, Applia US-09-370-700-6 Sequence 6, Applia US-09-603-207-6 Sequence 6, Applia US-09-614-741-32 Sequence 32, Applia	9 4 US-09-372-338-6 Sequence 6, Appli 9 4 US-10-126-75-6 Sequence 6, Appli 10 2 US-08-482-228-120 Sequence 120, App 10 3 US-08-482-528-120 Sequence 120, App	11 2 US-08-934-222-99 Sequence 99, Appl 11 2 US-08-933-402-99 Sequence 99, Appl 11 2 US-09-207-621-99 Sequence 99, Appl	11 2 US-08-532-818-99 Sequence 99, Appl 11 3 US-09-231-797-99 Sequence 99, Appl 11 3 US-08-934-224-99 Sequence 99, Appl	11 3 US-08-933-843-99 Sequence 99, Appl	11 3 US-09-413-492-99 Sequence 99, Appl 19 4 US-08-835-281-10 Sequence 10, Appl	20 1 US-08-658-130-1 Sequence 1, Appli 20 2 US-08-799-825-2 Sequence 22, Appl 20 2 150-00-00-00-6 Sequence 2, Appl	20 4 US-09-1982-000-5 Sequence 5, Appl. 20 4 US-09-280-068-22 Sequence 22, Appl. 20 4 US-08-119 Sequence 12 Appl.	20 4 US-08-527-621-12 Sequence 12, Appl 20 4 US-09-537-18 Sequence 18, Appl	7 22 2 US-08-08723-1 Sequence 1, Appli 7 22 2 US-08-097-673-1 Sequence 1, Appli 23 3 TG-08-808-307-6 Sequence 1, Appli	2. 3 02-03-03-33-6 Sequence 0, Appli 7 22 4 US-09-15502-6 Sequence 6, Appli 22 5 PCT-0395-12502-6 Sequence 6, Appli	7 27 4 US-09-039-780A-82 Sequence 82, Appl 7 28 4 US-09-039-780A-81 Sequence 81, Appl	30 4 US-09-039-780A-104 Sequence 104, App 7 38 4 US-09-039-780A-83 Sequence 83, Appl 8 4 US-09-039-780A-84 Sequence 84, Appl	39 2 US-08-889-291-15 Sequence 15, Appl 39 3 US-09-098-244-15 Sequence 15, Appl	7 39 4 US-09-375-314-15 Sequence 15, Appl 7 39 4 US-09-777-395-15 Sequence 15, Appl 83 4 US-09-039-780A-89 Sequence 89, Appl	7 44 4 US-09-039-780A-88 Sequence 88, Appl 7 44 4 US-09-039-780A-99 Sequence 99, Appl	54 4 US-09-039-780A-90 Sequence 90, Appl 7 56 4 US-09-780A-93 Sequence 93, Appl 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	7 61 4 US-09-134-000C-4256 Sequence 4250, Ap 7 61 4 US-09-107-532A-4993 Sequence 4993, Ap 66 4 US-09-541-6812-5898 Seminore 5898 Ap	7 69 4 US-09-328-352-5719 Sequence 5719, Ap	08 4 US-09-/32-210-1423 Sequence 1423, Ap. 90 4 US-09-33-634-645 Sequence 76, Appl 101 101 101 101 101 101 101 101 101 10	7 105 4 US-09-489-039A-10362 Sequence 1862, A 1013 4 US-09-614-912-186 Sequence 186, App	7 116 4 US-09-489-039A-12512 Sequence 12512, A	7 122 4 US-09-340-236-3231 Sequence 3231, Ap 7 121 4 US-09-340-236-3230 Sequence 3230, Ap 7 131 4 US-09-350-350-4806 Semionne 4806 Ap	132 4 US-09-326-322-3642 Sequence 3642 Ap	136 4 US-09-73Z-210-211 Sequence 211, App. 7 142 1 US-07-951-715A-24 Sequence 24, App.	142 2 US-08-459-448A-24 Sequence 24, Appl	7 142 3 US-08-459-504B-24 Sequence 24, Appl 7 142 3 US-08-459-444-24 Sequence 24, Appl	142 4 US-09-547-422-24 Sequence 24, Appl 143 3 US-08-946-329A-52 Sequence 52, Appl	143 4 US-09-328-352-7008 Sequence 7008, Ap

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VAEF 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Anderson, John F.
APPLICANT: Doane, Minh Tam
APPLICANT: Doane, Minh Tam
APPLICANT: Doane, Minh Tam
APPLICANT: Doane, Minh Tam
APPLICANT: Frigon, No. 6627739mand
APPLICANT: Frigon, No. 6627739mand
APPLICANT: Tatsuno, Gwen
APPLICANT: Tatsuno, Gwen
APPLICANT: Wang, Shuan
APPLICANT: Wang, Shuan
APPLICANT: Mang, Shuan
APPLICANT: APPLICANTON NUMBER: G0/119, 571
PRIOR FILING DATE: 1999-02-10
PRIOR FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 104
SEQ ID NO 78
LENGTH: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 19; DB 4; Length 7; 100.0%; Pred. No. 38+05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: MOD_RES
; LOCATION: 3
; OTHER INFORMATION: Xaa is hydroxyethylene or statine
US-09-724-566A-78
                                                            US-09-252-991A-23529
US-09-053-702-2
US-09-053-702-2
US-09-372-428-4
US-09-312-448A-4
US-09-314-701-30
US-09-372-422A-16
US-09-372-422A-16
US-09-372-422A-16
US-09-372-422A-16
US-09-372-422A-16
US-09-372-422A-17
US-09-372-422A-14
US-09-372-422A-14
US-09-372-422A-14
US-09-372-422A-14
US-09-372-422A-14
US-09-372-422A-14
US-09-372-422A-14
                             9-039A-9313
9-039A-12815
82-991A-23529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Peptide inhibitor P3-P4' XD-V
                                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Anderson, John P.
APPLICANT: Anderson, John P.
APPLICANT: Doane, Minh Tam
APPLICANT: Frigon, No. 6627739mand
APPLICANT: Fower, Michael
APPLICANT: Sinha, Sukanto
APPLICANT: Sinha, Sukanto
APPLICANT: Tatsuno, Gwen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 78, Application US/09724566A
Patent No. 6627739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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Best Local Similarity
Matches 4; Conserv
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RESULT 2

RESULT 2

RESULT 3

RESULT 3

RESULT 3

RESULT 3

RESULT 3

RESULT 3

RESULT 4

RESULT 3

RESULT 4

RESULT 5

RESULT 6

RESULT 1000 P. 1000
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Patentin Release #1.0, Version #1.25
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APPLICANT: Basi, Guriqbal
APPLICANT: Boane, Minh Tam
APPLICANT: Frigon, No. 6627739mand
APPLICANT: John, Varghese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
                                   CURRENT APPLICATION DATA APPLICATION NUMBER: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: unknown
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Sinha, Sukanto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: peptide US-08-197-484-145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tatsuno, Gwen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: unknown
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Patent No. 6419931
GENERAL INFORMATION:
APPLICANT: VITIELLO, Maria A.
APPLICANT: CHESTNUT, Robert W.
APPLICANT: SETTE, Alessandro D.
APPLICANT: GELIS, Esteban
APPLICANT: GRAY, Howard
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
TITLE OF INVENTION: CALL IMMUNITY
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS: 
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                                                   COMPUTRY: US

ZIP: 94105-1493

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TEMPY disk
COMPUTER: TEMPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 07/935,811
APPLICATION NUMBER: US 07/935,811
APPLICATION NUMBER: US 07/935,811
APPLICATION NUMBER: US 07/874,491
FILING DATE: 26-AUG-1992
PRIOR APPLICATION NUMBER: US 07/874,491
FILING DATE: 26-AUG-1992
PRIOR APPLICATION NUMBER: US 07/827,682
FILING DATE: 29-ANN-1992
PRIOR APPLICATION NUMBER: US 07/749,568
FILING DATE: S6-AUG-1991
APPLICATION NUMBER: US 07/749,568
FILING DATE: S6-AUG-1991
APPLICATION NUMBER: US 07/749,568
FILING DATE: S6-AUG-1991
ATTORNEY/AGBNT INFORMATION:
NAME: PARMEINER: 18-900
TELEFONMINICATION INFORMATION:
TELEFONMINICATION DATA
TELEFONMINICATION SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TELEGOTH OF SEQ ID NO: 86:
SEGUENTE: SEGUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 4; Conservative
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           California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: un
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S-08-197-484-145
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Tung, Jay
APPLICANT: Wang, Shuwen
APPLICANT: McConloque, Lisa
APPLICANT: McConloque, Lisa
APPLICANTION: Methods
TITLE OF INVENTION: Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
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CURRENT APPLICATION NUMBER: US/09/724,566A
CURRENT PILING DATE: 2000-11-28
PRIOR PRIOR PLING DATE: 2000-02-10
PRIOR FILING DATE: 2000-02-10
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 60/119,571
PRIOR PILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 104
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 73
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
CURRENT APPLICATION DATA:

APPLICATION DATA:

CLASSIFICATION WIMBER: US/8(197,484

FILING DATE: 16-FEB-1994

CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/935,811

FILING DATE: 26-AUG-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/874,491

FILING DATE: 27-APR-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,682

FILING DATE: 29-JAN-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,568

FILING DATE: 26-AUG-1991
ATTORNAY JAGENT INFORMATION:
NAME: PARMELE, SLEVEN W.
REFERENCE, DOCKET NUMBER: 14137-26-4
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (206) 467-9600
TELEFAX: (206) 623-6793
INFORMATION FOR SEQ ID NO: 145:
SEQUENCE CHRARACTERISTICS:
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unknown
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                                                                           PCT-US95-02121-145
                                                        RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPOSITIONS AND METHODS FOR ELICITING CTL INMUNITY 153
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                                                                                                                                                                                              100.0%; Score 19; DB 4; Length 9; 100.0%; Pred. No. 3e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 86, Application PC/TUS9502121
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELITILE OF INVENTION: CTL IMMUNITY
NUMBER OF SEQUENCES: 153
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02121
FITING NUMBER: PCT/US95/02121
                                               OTHER INFORMATION: P4-P4'staD-V peptide inhibitor FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NOUSEER.
FILING DATE: 16-FEB-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/197,484
APPLICATION NUMBER: US 07/935,811
FILING DATE: 26-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/935,811
FILING DATE: 26-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/874,491
FILING DATE: 29-AAN-1992
PRIOR APPLICATION NUMBER: US 07/827,682
FILING DATE: 29-JAN-1992
PRIOR APPLICATION NUMBER: US 07/827,682
FILING DATE: 29-JAN-1992
PRIOR APPLICATION NUMBER: US 07/749,568
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: PATRIEDIES, SEEVEN W.
RESTERENCE/DOCKET NUMBER: 11,990
RELEPAN: (206) 467-9600
TELEPAN: (415) 543-5043
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                            NAME/KEY: MOD_RES
LOCATION: 5
COTHER INFORMATION: Xaa is statine moiety
32-09-724-566A-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           имвек: PCT/US95/02121
16-FEB-1995
М.
TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100. 
Matches 4; Conservative
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Best Local Similarity 100.
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STRANDEDNESS: un
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9CT-US95-02121-86
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FRESULE OF INVESTIGATION POLYUSS50121

ORDERLI INFORMATION: CONCOSITIONS AND METHODS FOR ELICITING
ITILE OF INVESTIGAT: CONCOSITIONS AND METHODS FOR ELICITING
ITILE OF INVESTIGAT: LIST OF CONCOSITIONS AND METHODS FOR ELICITING
ITILE OF INVESTIGAT: LIST OF CONCOSITIONS AND METHODS FOR ELICITING
ITILE OF INVESTIGATION: CTL INVESTIGATION AND METHODS FOR ELICITING
CONCENTES READED FORM.
MEDITAL THESE FORM. BASE AND METHODS FOR ELICITING
CONCENTES READED FORM.
MEDITAL FOR SERVER FORM.
MEDITAL FOR SERVER FORM.
MEDITAL FOR MARKER: PERSONAL FORM.
MEDITAL FOR MARKER: LIST OF MARKER: LIST OF MARKER FORMATION: FEELS SERVER FORMATION: MARKER: MEDITAL FORMATION: MEDITAL FEELS SERVER FORMATION: MEDITAL FEELS FEELS FORMATION: MEDITAL FEEL FEELS FEELS FORMATION: MEDITAL FEELS FEELS FORMATION: MEDITAL FEELS FEELS FORMATION: MEDITAL FEELS FEE
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LENGTH: 28 amino acids
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                Query Match 100.
Best Local Similarity 100.
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: not
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US-08-487-890A-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-733-825-3
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APPLICANT: Tatsuno, Gwen
APPLICANT: Tatsuno, Gwen
APPLICANT: Tatsuno, Gwen
APPLICANT: Tutsuno, Gwen
APPLICANT: Tutsuno, Gwen
APPLICANT: Tutsuno, Gwen
APPLICANT: Wang, Shuwen
TITLE OF INVENTION: Methods
FILE REFERENCE: 228-US-NEMC2
CURRENT APPLICATION NUMBER: US/09/724,566A
CURRENT FILING DATE: 2000-12-10
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 60/119,571
PRIOR FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 104
SOFTWARE: FASIEEQ for Windows Version 4.0
SEQ ID NO 97
LENGTH: 14
APPLICANT: 1 unsy, cor, APPLICANT: 1 unsy, cor, APPLICANT: Wang, Shuwen APPLICANT: Wang, Shuwen APPLICANT: McConlogue, Lisa TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and TITLE OF INVENTION: Methods FILE REFERENCE: 228-US-NEWC2 CURRENT PELLOR DATE: 2000-11-28 PRIOR APPLICATION NUMBER: US 09/501,708 PRIOR PLLING DATE: 2000-11-20 PRIOR PLLING DATE: 1999-02-10 PRIOR APPLICATION NUMBER: 60/119,571 PRIOR APPLICATION NUMBER: 60/119,571 PRIOR PLLING DATE: 1999-06-15 NUMBER OF SEQ ID NOS: 104 SOUTHARE: RastSEQ for Windows Version 4.0 SEQ ID NO 72 LENGTH: 14 TYPE: PRI TYPE: PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 19; DB 4; Length 14; 100.0%; Pred. No. 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
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OTHER INFORMATION: APP-derived fragment P10-P4'(D-V)
IS-09-724-566A-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
OTHER INFORMATION: P10-P4'staD-V peptide inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 10
OTHER INFORMATION: Xaa is statine moiety
3-09-724-566A-72
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APPLICANT: Basi, Guridpal
APPLICANT: Doane, Minh Tam
APPLICANT: Frigon, No. 6627739mand
APPLICANT: Prigon, No. 4627739mand
APPLICANT: Pohn, Varighesel
APPLICANT: Sonn, Varighesel
APPLICANT: Sinha, Sukanto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 97, Application US/09724566A Patent No. 6627739 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 4; Conservative
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Guerrative 100.04; Score 19 DB 4; Length 14;

Marches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1942 4

Db 11 Wap 14

Maches 1, Conservative 0; Mismatches 0; Indels 0; Gaps 0;

We 08-733-85-3

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Was 08-733-85-3

FRESUTI 10

Was 08-733-85-3

FRESUTI 10

WAPPLICANT: Navylex, Lealis R.

APPLICANT: Navylex, Lealis R.

FILING OF INNERTION: Conformation of CITY: East Manore CITY: Ea
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US-08-39-996-A

DETERMINENTIAL INFORMATION:

GENERAL INFORMATION:

FAPLICANT: Agre, Peter C.

TITLE OF INVENTION: Isolation, Cloning and Expression of TITLE OF INVENTION: Transmembrane Water Channel Proteins NUMBER OF SEQUENCE: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Banner & Allegretti
STREET: 1001 G Street, N.W.

CITY: Washington, D.C.

COUNTRY: US

COUNTRY: US

COUNTRY: US

COUNTRE READABLE FORM:

WEDIUM TYPE: Floppy disk

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/393,996A

FILING DATE: 24-FEB-1995

CLASSIFICIATION 1435

ATTORNEY ARBIT NUMBER: US/08/333

REFERENCEDOMUNICATION NUMBER: 1107.48633

TELEPHONE: 202 508-9299

INFORMATION FOR SEG ID NO: 1:

CELEPHONE: 202 508-9299

INFORMATION FOR SEG ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 19; DB 1; Length 35; 100.0%; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
          Query Match
Best Local Similarity 100.
Matches 4; Conservative
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LENGTH: 35 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-468-763-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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STRANDEDNESS: si
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STRANDEDNESS: si
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Sequence 1. Sequence 2. TITLE OF INVENTION: Isolation, Cloning and Expression of TITLE OF INVENTION: Transmembrane Water Channel Proteins 1. Sequence 2. Sequence 2. Sequence 2. Sequence 3. Addresse: Sequence 2. Sequence 2. Sequence 2. Sequence 2. Sequence 3. Sequence 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 19; DB 1; Length 35; 100.0%; Pred. No. 1.3e+02;
   APPLICANT: Gray-owen, scott
APPLICANT: Yang Yan-Ping
APPLICANT: Width Middel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
CORRESPONDENCE S: 147
CORRESPONDENCE S: 147
CORRESPONDENCE S: 140
CORPUTES: Esh Floor, 330 Unviersity Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER: READABLE FORM:
MEDIUM TYPE: Rloppy disk
COMPUTER: READABLE FORM:
MEDIUM TYPE: Rloppy disk
COMPUTER: PatentIn Release #1.0, Version #1.25
CONFRANC: APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
FILING DATE: 29-DEC-1993
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REFERENCE/DOCKET NUMBER: 1038-466 MIS:jb
TELEPHONE: (416) 595-1163
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 anino acids
TYPE: amino ATARIA
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Gray-Owen, Scott
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Best Local Similarity 100.
Matches 4; Conservative
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US-08-487-890A-69
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US-08-337-483-69
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STATE: Or
COUNTRY:
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US-08-478-373-69
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Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
Length 35;
                                                            0: Indels
                                                                                                                                                                                                                                                                                                                                                                                                   CHERRAL INCORPARTION:
CHERRAL INCORPARTION:
APPLICANT: LOOSENCE, Robin
APPLICANT: Schryvers, Anthony
APPLICANT: Schryvers, Anthony
APPLICANT: Schryvers, Anthony
APPLICANT: Gray-Owen, Scott
APPLICANT: Gray-Owen, Scott
APPLICANT: Murdin, Andrew
APPLICANT: Murdin, Andrew
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
CORRESSEE: Sim & MCBUINEY
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Onlario
CONTRY: Canada
ZIP: MGG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: PORDS/MS-DOS
SOFTWARE: Datentin Release #1.0, Version #1.25
CURRING DATE: 07-UN-1995
CLASSITCATION DATA:
APPLICATION NUMBER: US/08/478,435
FILING DATE: 08-NOV-1994
CLASSITCATION NUMBER: US/08/175,116
FILING DATE: 08-NOV-1993
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
REDEL CATION NUMBER: US 08/175,116
FILING DATE: 08-NOV-1993
ATTORNEY, AGENTY INFORMATION
APPLICATION NUMBER: US 08/175,116
FILING DATE: 08-NOV-1993
ATTORNEY, AGENTY INFORMATION:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 08-NOV-1993
ATTORNEY, AGENTY INFORMATION:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 08-NOV-1993
ATTORNEY, AGENTY INFORMATION:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 08-NOV-1993
ATTORNEY, AGENTY INFORMATION:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 08-NOV-1993
ATTORNEY, AGENTY MICHABE! US 08/175,116
                                  1.3e+02;
100.0%; Score 19; DB 2; 100.0%; Pred. No. 1.3e+02
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S-08-478-435-69
Sequence 69, Application US/08478435
Patent No. 5922323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1163
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
Query Match 100.
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                              14 VAEF 17
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S-08-478-435-69
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14 VAEF 17

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linear
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US-08-474-671-69
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Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                          COMPUTER READABLE FURM:

MEDIIM TYPE Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,373
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: US 08/337,483
FILING DATE: 08-NOV-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/337,483
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 18-NOV-1993
FIL
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APPLICANT: Harkness, Robin
APPLICANT: Harkness, Robin
APPLICANT: Ghong, Pers, Anchony
APPLICANT: Gray-Owen, Scott
APPLICANT: Yang, Yan-Ping
APPLICANT: Murdin, Andrew
APPLICANT: Murdin, Andrew
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: Suite 701, 330 University Avenue CITY: Toronto STATE: Ontario COUNTRY: Canada
       Suite 701, 330 University Avenue
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
STREET: Suite 701, 33C
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIF: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear
US-08-478-373-69
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STRANDEDNESS: si
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SOFFWARE APPLICATION DATA:

APPLICATION NUMBER: US 004744,671

PRILOR APPLICATION NUMBER: US 008/37,483

PRILOR APPLICATION NUMBER: US 004/148,568

PRILOR APPLICATION NUMBER: US 004/148,508

PRILOR HERRICANT: UCOMORTOR SHEEN

PRILOR HERRICANT: MAGE IN APPLICANT: MAGE IN AP
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TYPE: amino acid
STRANDEDNESS: sir
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US-08-897-438-69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 19; DB 3; Length 35; 100.0%; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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ZIPEET: 6th Floor, 330 University Avenue
STREET: 6th Floor
STREET: 6th 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ESULT 19
S-08-897-438-69
Sequence 69, Application US/08897438
Patent No. 6262016
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Harkness, Robin
APPLICANT: Schrevers, Anthony
APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Wang, Yan-Ping
APPLICANT: Wang, Yan-Ping
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 160
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/175,116

FILING DATE: 29-DEC-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/148,968

FILING DATE: 08-NOV-1993

ATORNEY/AGENT INFORMATION:

NAME: Stewart, Michael I

REGISTRATION NUMBER: 24,973

REFERNICE/DOCKET NUMBER: 1038-511

TELEPHONE: (416) 595-1155

TELEPHONE: (416) 595-1153

INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:

LENGTH: 35 amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNMERE: US 08/483,577
FILING DATE: 07-7UN-1995
PRIOR APPLICATION NUMBER: US 08/337,483
FILING DATE: 08-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 100.
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: sir
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PETITION DATE: 06-NOV-1993

ATOMNY/AGENT INCOMATION:
NAME: Scenart, Winches I
REGISTRATION NUMBER: 24,473

FREEDSTRATION NUMBER: 24,573

FREEDSTRATION NUMBER: 24,574

FREEDSTRATION NUMBE
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ORGANISM: Homo sapiens FEATURE:
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Best Local Similarity
Matches 4; Conserv
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100.0%; Score 19; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
  Length 35;
Query Match 100.0%; Score 19; DB 4; Length 35 Best Local Similarity 100.0%; Pred. No. 1.38+02; Matches 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 6th Floor, 330 Unviersity Avenue CITY: Toronto STATE: Otherio COUNTRY: Canada ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Clopy disk COMPUTER: IBM PC COMPATIBLE OF STATE: OTHER PROPERSITE OF STATE: PC-DOS/MS-DOS SOFTWARE: PATENTIN PC-DOS/MS-DOS SOFTWARE: PATENTIN PAPLICATION NUMBER: US/08/649,518
FILING APPLICATION NUMBER: US/08/649,518
FILING APPLICATION NUMBER: US/08/49,518
FILING APPLICATION NUMBER: US/08/48,577
FILING APPLICATION NUMBER: US/08/148,968
FILING STEWART (MICHAE) IN REPERENCE/DOCKET NUMBER: US/08/148,968
TELEPRAX: (416) 595-1163
INFORMATION FOR EQUID NO: 69:
SEQUENCE CHARACTERISTICS: INFORMATION: TELEPRAX: (416) 595-1163
INFORMATION FOR EQUID NO: 69:
SEQUENCE CHARACTERISTICS: INFORMATION FOR EQUID NO: 69:
                                                                                                                                                                                                                                                                                                                                                              APPLICANT: LOOSMOTE, Sheena
APPLICANT: LOOSMOTE, Sheena
APPLICANT: Barkness, Robin
APPLICANT: Schryvers, Anthony
APPLICANT: Chong, Pele
APPLICANT: Yang, Yan-Ping
APPLICANT: Yang, Yan-Ping
APPLICANT: Windin, Andrew
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 160
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Gth Floor, 330 Unviersity Avenue
                                                                                                                                                                                                                                                                                     Sequence 69, Application US/08649518
Patent No. 6361779
GENERAL INFORMATION:
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1 VAEF 4

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Sequence 1412, Application US/09732210
; Sequence 1412, Application US/09732210
; Patent No. 6573361
; GENERAL INFORMATION:
APPLICANT: Univers, Greg J.
APPLICANT: Mittanck, Cindy A.
APPLICANT: Mittanck, Cindy A.
APPLICANT: Seale, Jeffrey W.
APPLICANT: Mu, Yonnie S.
TITLE OF INVENTION: Atti-fungal Proteins and Methods for Their Use
FILE REFERENCE: 38-21(15036)B
; CURRENT APPLICATION NUMBER: US/09/732,210
; CURRENT FILING DATE: 2000-12-07
; PRIOR FILING DATE: 1999-12-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 19; DB 4; Length 74; 100.0%; Pred. No. 2.8e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                Sequence 10, Application US/08894139

Sequence 10, Application US/08894139

Patent No. 648376

GENERAL INFORMATION:

APPLICANT: LA THANGUR, NICHOLAS B.

APPLICANT: BERNARDS, RENE

APPLICANT: HIJMANS, ELEANORE M.

TITLE OF INVENTION: TRANSCRIPTION FACTOR E2F-5

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHYE F.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STREET: VARGINAA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBW PC Compatible

OFFRATIOS STERM: COORDETIBLE

OFFRATIOS STERM: COORDETIBLE

OFFRATIOS NOWBER: US/08/894,139

FLING DATE: 13-AUG-1997

CLASSIFICATION NUMBER: 32,955

REGISTRATION NUMBER: 32,955

REGISTRATION NUMBER: 32,955

REGISTRATION NUMBER: 32,955

REGISTRATION NUMBER: 620-22

TELEFRONE: (703) 816-4100

TELEFRAN: (703) 816-4100

INFORMATION POR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LYPE: Amino acids

LYPE: THE ADDRESSEE INFORMATION:

LYPE: Amino acids

LYPE: Amino acids

LYPE: Amino acids

LYPE: Amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-732-210-1412
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                                                                                                                                                               RESULT 26
US-08-894-139-10
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Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUWANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPRENCE: GT999-03PR
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT APPLICATION NUMBER: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEGO ID NO 7111
LENGTH: 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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Sequence 10, Application US/08321071A
Sequence 10, Application US/08321071A
GENERAL INFORMATION:
APPLICANT: CHITTENDEN, Thomas D.
TITLE OF INVENTION: APOPTOSIS RELATED PROTEIN Bc1-Y, AND METHODS
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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100.0%; Score 19; DB 1; Length 73;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       Length 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/321,071A
FILING DATE: 11-OCT-1994
CLASSITCATION: 514
PRIOR APPLICATION NUMBER: PCT/US95/10103
FILING DATE: 09-AUG-1995
RICH APPLICATION NUMBER: 08/287,427
FILING DATE: 09-AUG-1995
RICH APPLICATION NUMBER: 08/287,427
FILING DATE: 09-AUG-1995
RICH APPLICATION NUMBER: 32,073
REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 104322.121CIP
TELECOMMONICATION INFORMATION:
TELECOMMONICATION INFORMATION:
TELECOMMONICATION NUMBER: 202-942-8484
                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 19; DB 4; L
100.0%; Pred. No. 2.6e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Acinetobacter baumannii IS-09-328-352-7111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 10 SEQUENCE CHRACKTERISTICS: LENGTH: 73 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.
Best Local Similarity 100.
Matches 4; Conservative
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MOLECULE TYPE: peptide
IS-08-321-071A-10
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21 VABF 24
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                                                                                                                                                                                                                                                                                   Query Match
100.0%; Score 19; DB 4; Length 88;
Best Local Similarity 100.0%; Pred. No. 3.38+02;
Matches 4; Conservative 0; Mismatches 0. Thanh
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100.0%; Score 19; DB 1; Length 93;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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ADDRESSE:
ADDRESSE:
CUSHWAN, DARBY & CUSHWAN
SITEET: 1100 NEW YORK AVENUE, N.W.
CITY:
MASHINGTON
SITEET: 0100 NEW YORK AVENUE, N.W.
CITY: 02005
COUNTRY: 05.
COUNTRY: 05.
COUNTRY: 05.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1EM PC COMPALIALE
OPPRATING SYSTEM: PC COMPALIALE
COMPUTER: 1EM PC COMPALIALE
COMPUTER: 1EM PC COMPALIALE
COMPUTER: 1EM PC COMPALIALE
COMPUTER: 1EM PC COMPALIALE
COMPATION NUMBER: VS/07/612,674
FILING DATE: 19901114
CLASSIFICATION NUMBER: 5683/82332
ATTOREY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 5683/82332
TELEFRANCE/OCKET NUMBER: 5683/82332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: NUELL, MARK J. APPLICANT: MCLUNG, J. KEITH
APPLICANT: STEWART, DAVID A.
APPLICANT: DANNER, DAVID B.
TITLE OF INVENTION: AN ANTIPROLIFERATIVE PROTEIN
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHWAN, DANNEY & CUSHWAN
PRIOR APPLICATION NUMBER: US 60/169,340 PRIOR FILING DATE: 1999-12-07 UNDER OF SEQ ID NOS: 1753 SEQ ID NO 1412 LENGTH: 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 12, Application US/07612674
Patent No. 5658792
                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-09-732-210-1412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: AMINO ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
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Gaps ö

1 VAEF 4

ઠે д RESULT 29 US-09-543-681A-5816

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Patent No. 6605705
GENERAL INPORMATION:
PAPLICANT: GARY ERROR AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABI
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709,1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR FILING DATE: 1999-04-09
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NOS: 8344
SEQ ID NOS: 8346
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100.0%; Score 19; DB 4; 1
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0;
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PILING DATE:
CLASSIFICATION: 435

PRICR APPLICATION DATA:
PRICR APPLICATION UNMER: US 07/963,308
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
PRILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
PRICISTRATION NUMBER: 36,709
REFERENCE/POCKET NUMBER: 36,709
REPERENCE/POCKET NUMBER: 36,709
REPERENCE/FOCKET NUMBER: MII-004C
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-5941
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acide

"THE TO AMINO ACIDED AND ACIDED 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: AGII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,517
Sequence 5816, Application US/09543681A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT;
CRGANISM: Proteus mirabilis
US-09-543-681A-5816
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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13 VAEF 16
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                                                                                    Gaps
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Sequence B, Application US/08246361A
Sequence B, Application US/08246361A
Patent No. 599582
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD
STREET; 60 State Street
CITY: Boston
STATE: MA.
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                                    100.0%; Score 19; DB 2; Length 100; 100.0%; Pred. No. 3.8e+02; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-CDS/MS-DOS
SOSTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,361A
FILING DATE: 19-MAY-1994
CLASSIFICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
PRIOR APPLICATION NUMBER: US 07/888,178
FILING DATE: 16-MAY-1991
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: MATCHEN EN VINCENT
REFERENCE/DOCKET NUMBER: 36,709
REFERENCE/DOCKET NUMBER: 36,709
REFERENCE/DOCKET NUMBER: 36,709
REFERENCE/DOCKET NUMBER: 36,709
TELLEPONE: (617) 227-5941
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
TYPE: amino acid
STAPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 4; Conservative
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                                                                                    4; Conservative
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MOLECULE TYPE: peptide
                                      Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                    13 VAEF 16
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S-08-464-517-8
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Sequence 8, Application US/08463772 Patent No. 6066501

ESULT 32 IS-08-463-772-8

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ADTICANT: BEACH.

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COMMITT. INS.

ADDICATION NUMBER: US 01/663,702

FILMS OF ADDIESS. INS.

ADDICATION NUMBER: US 01/663,703

FILMS OF ADDIESS. INS.

ADDICATION NUMBER: US 01/663,703

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PRIOR APPLICATION DATA
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US-09-540-236-3612
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Patent No. 5856161
GENERAL INFORMATION:
TITLE OF INVENTION: Receptor-I-Associated Protein Kinase And Methods
ITLE OF INVENTION: Receptor-I-Associated Protein Kinase And Methods
TITLE OF INVENTION: Receptor-I-Associated Protein Kinase And Methods
ITLE OF INVENTION: Receptor-I-Associated Protein Kinase An
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benjamin Aaron Adler, Ph.D., J.D.
REGISTRATION NUMBER: 35,423
TELECHONE: 713-777-2321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 77071
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 Mb floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/580,988A
FILING DATE: January 3, 1996
                                                                                               PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/888,178
FILING DATE: 25 FMAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL91-02A
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION SEQ 10 NO: 8: SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
TYPE: AMINO ACID
TOPOLOGY: unknown
APPLICATION NUMBER: PCT/US93/05000
FILING DATE: 19930525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 713-777-6908
INFORMATION FOR SEQ ID NO: 21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 101 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / MOLECULE TYPE: protein
PCT-US93-05000-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                         FILING DATE: 1
CLASSIFICATION:
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TOPOLOGY: 112
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US-08-580-988A-21
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Sequence 3612, Application US/09540236

Patent No. 6673910
GENERAL INFORMATION:
APPLICANT: GATY
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATA
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 2709, 2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT PILLING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 3612
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US-08-464-517-25

Sequence 25. Application US/08464517
; Sequence 25. Application US/08464517
; Patent No. 5869640
; GENERAL INFORMATION:
; APPLICANT: BEACH, David H.
; TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
; VORRESPONDENCE ADDRESS:
; ADDRESSE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
                                                                                                                                                                Length 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 19; DB 4; Length 10
100.0%; Pred. No. 3.9e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                           Query Match
100.0%; Score 19; DB 2; 1
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISH PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-007-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 4; Conservative
                                                                       internal
DESCRIPTION: protein POTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: M.catarrhalis
US-09-540-236-3612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 435
                   HYPOTHETICAL: no

MATI-SENSE; no

FRAGMENT TVRE: in

ORIGINAL SOURCE:

US-08-580-988A-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 VAEF 68
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: BEACH, David H.
APPLICANT: BEACH, David H.
TILE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STREET: MA
COUNTRY: USA
ZIP: 02109
                                                                       100.0%; Score 19; DB 2; Length 106; 100.0%; Pred. No. 4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 19; DB 3; Length 106; 100.0%; Pred. No. 4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46+02;
0; Indels
                                                                                                                   0, Indels
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                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION.
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: 36,709
REGISTRATION NUMBER: 36,709
REGISTRATION NUMBER: 36,709
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 227-594
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
SEGUENCE CHARACTERISTICS:
SEMENT: 106 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8721, Application US/09489039A Patent No. 6610836
                                                                                                                                                                                                                                                                                                               US-08-463-772-25
; Sequence 25, Application US/08463772
; Patent No. 6066501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Conservative
                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear

MOLECULE TYPE: peptide
US-08-463-772-25
     peptide
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Best Local Similarity
Matches 4; Conservat
                                                                          Query Match
Best Local Similarity
Matches 4; Conserva
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                                                                                                                                                                         1 VAEF 4
     , MOLECULE TYPE:
US-08-246-361A-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 39
US-09-489-039A-8721
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Patent No. 5998582
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
100.0%; Score 19; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIE: 02109
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,361A
FILING DATE: 19-MAY-1994
CLASSIFICATION: 435
PRIGA APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
PRIGA PAPLICATION DATA:
APPLICATION NUMBER: US 07/963,108
FILING DATE: 16-MAY-1991
ATTONNEY, ADENT INFORMATION:
NAME: MATCHAW DATA: 36,709
REFERENCY/DOCKET NUMBER: 36,709
REPRENCY/DOCKET NUMBER: 36,709
REPROMENCY/DOCKET NUMBER: 36,709
REPRENCY/DOCKET NUMBER: 36,709
TELECHONE: (617) 227-7400
TELECHONESS: single
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-004C
TELECOMMUNICATION INPORMATION:
TELEPAX: (617) 227-7400
TELEPAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
STRANDEDNESS: single
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 VAEF 69
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GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: APRUGAINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US 60/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR PLILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 21614
                                                                                                                                               APPLICANT: GATY Breton et. al
APPLICANT: GATY Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT PILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 9915
LENGTH: 115
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APPLICATIVE: GATY PRECON Et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
THER REPERBENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT PILING DATE: 2000-01-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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Similarity 100.0%; Pred. No. 4.4e+02;
4; Conservative 0; Mismatches 0:
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; Sequence 21614, Application US/09252991A
; Patent No. 6551795
                                                                                                    Sequence 9915, Application US/09489039A Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7200, Application US/09489039A Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21614
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Conservative
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
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US-09-489-039A-7200
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GENERAL INFORMATION:

APPLICANT: Gary Breton et. al

TITLE OF INVENTION: MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT PPLIORION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 8721
LENGTH: 106
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GENERAL INFORMATION:
APPLICANT: MITOTIX
TITLE OF INVENTION: D-Type Cyclin and Uses Related Thereto NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSES: Hamilton, Brook, Smith & Reynolds, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 19; DB 4; Length 106; 100.0%; Pred. No. 4e+02; o; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
100.0%; Score 19; DB 5; Length 106;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 02173
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PC-DOS/MS-DOS
GURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05000
FILING DATE: 19930525
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER:
US/07/888,178
FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Granaban, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL91-02A
TELECHANTICATION INFORMATION:
TELECHAN: 617-861-6240
TELEFAX: 616-861-9540
                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 25: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 106 amino acide
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Lexington
STATE: Massachusetts
COUNTRY: US
ZIP: 02173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43 VAEF 46
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Gaps

66 VAEF 69

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                                                                                                                                                                                                                                       Length 123;
                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Briles, David E.
APPLICANT: McDaniel, Larry S.
APPLICANT: Swiatlo, Edwin
APPLICANT: Swiatlo, Edwin
APPLICANT: Swiatlo, Edwin
APPLICANT: Brooks-Walter, Alexis
TITLE OF INVENTION: Pherwococcal Genes, Portions
TITLE OF INVENTION: Therefrom, and Uses of Such Genes,
NUMBER OF SEQUENCES: 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCUNTRY: USA

ZIF: 10036
COMPUTER READABLE FORM:
MEDILUM TYPE: Floppy disk
COMPUTER: Tal PC Compatible
COMPUTER: Tal PC Compatible
COMPUTER: Tal PC COMPACIBLE
COMPUTER: Tal PC COMPACIBLE
COMPUTER: Tal PC COMPACIBLE
COMPUTER: Datentin Release #1.0, Version #1.30
CURSENING SYSTEM: PC-DOS/MS-DOS
CURSENING SYSTEM: 15-SEP-195
CLASSIFICATION NUMBER: US/08/529,055
FILING DATE: 15-SEP-195
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 45-4312-2400
REFERENCE/DOCKET NUMBER: 45-4312-2400
REFERENCE/DOCKET NUMBER: 45-4312-2400
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION S3:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 anhino acids

WYDE: Amino acids
                                                                                                                                                                                                                                 Query Match
100.0%; Score 19; DB 4; I
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Curtis, Morris & Safford, P.C. STREET: 530 Fifth Avenue CITY: New York
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 7200
LENGTH: 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-529-055-53; Application US/08529055; Patent No. 6592876; GENERAL INFORMATION:
APPLICANT: Briles, David E.
                                                                                                                                                     GRGANISM: Klebsiella pneumoniae US-09-489-039A-7200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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                                                                                                                                  TYPE: PRT
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US-09-198-452A-167

1 Sequence 167, Application US/09198452A
1 Patent No. 6559294
1 Patent No. 6559294
1 Patent No. 6559294
1 PAPLICANT: Griffals, R.
1 TILE OF INVENTION: Thereof and uses thereof, in particular for the diagnosis, prev. TILE OF INVENTION: and treatment of infection
1 TILE OF INVENTION: And treatment of infection
2 TILE REFERENCE: 9710-003-599
3 CURRENT APPLICATION NUMBER: US/09/198,452A
3 CURRENT FILING DATE: 1998-11-24
3 UNDER OF SEQ ID NOS: 6849
  Parent No. 6610836, Application US/09489039A

Parent No. 6610836
GENERAL INFORMATION:
APPLICANT: GATY BRECON et. al
APPLICANT: GATY BRECON ET. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUMBER FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 12835
LENGTH: 143
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Requence 4222, Application US/09134000C

Requence 4222, Application US/09134000C

Retreat Information:

APPLICANT: Lynn Doucette-Stamm et al

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: NUCLEC ACID AND AMINO ACID SEQUENCES AND THERAPEUTICS

FILE REPERENCE: 032796-032

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/055,778

PRIOR APPLICATION NUMBER: US 60/055,778

PRIOR APPLICATION NUMBER: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 143;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 19; DB 4; I
100.0%; Pred. No. 5.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GORGANISM: Chlamydia pneumoniae US-09-198-452A-167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     138 VAEF 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31 VAEF 34
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JS-09-489-039A-12835
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LENGTH: 145
TYPE: PRT
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0; Indels

0; Mismatches

1 VAEF 4

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COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
LENGTH: 150 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
                   STREET: 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 VAEF 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 VAEF 4
                                                                                   COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-460-744-3
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                                                                                                                     100.0%; Score 19; DB 4; Length 145; 100.0%; Pred. No. 5.6e+02; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                         GENERAL NO. SECULOR:
GENERAL INFORMATION:
APPLICANT: Arnold, Andrew
TITLE OF INVENTION: PRADI Cyclin and its CDNA
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Waehington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MBDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPANING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin RC-Bos/MS-DOS
SOFTWARE: Patentin RC-Bos/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,694
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
ATTONEY AGENT INFORMATION:
NAME: MCCONCATN NUMBER: 35,279
REFERENCE/DOCKET NUMBER: 35,279
REFERENCE/DOCKET NUMBER: 0609.4070002
TELEFAK: 202-371-2600
ITELEFAK: 202-371-260
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 150 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 19; DB 2; Similarity 100.0%; Pred. No. 5.8e+02; 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/08460744
Patent No. 6107541.
GANEAL INFORMATION.
APPLICANT: Arnold, Andrew
TITLE OF INVENTION: PRADI Cyclin and its CDNA
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                        US-08-460-694-3; Sequence 3, Application US/08460694; Patent No. 5858655
; SEQ ID NO 4292
; LENGTH: 145
; TYPE: PRT
; OKGANISM: Enterococcus faecalis
US-09-134-000C-4292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: not relevant
                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                     Query Match
Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                           113 VAEF 116
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STATE:
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Gaps
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Sequence 3, Application US/07667711B

Sequence 3, Application US/07667711B

Patent No. 6110700

GENERAL INFORMATION:
APPLICANT: ARNOLD, ANDREW
TITLE OF INVENTION: Pradi Cyclin and Its CDNA
NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:
ADDRESSER: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600

CITY: WASHINGTON

STRIE: DC
                                                                                                          CALF: 2000.

CARPUTER: READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TAN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/460,744
FILING DATE: 02-UN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MCCONATHY, EVELYN H.
REGISTRATION NUMBER: 35,279
REGISTRATION NUMBER: 0609.4070055
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/667,711B
FILING DATE: 11-MAR-1991
CLASSIFFCATION: 435
ATTORNEY/AGENT INFORMATION:
RAGISTRATION NUMBER: 35,811
REFERENCE/DOCKET NUMBER: 0609.4070000
TELECOMMUNICATION:
1100 New York Avenue, N.W., Suite 600
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4; Conservative
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CORGANISM: Homo sapien
US-09-370-838-203
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Matches 4, Conserv
                         101 VAEF 104
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                                                                                                                    RESULT 53
US-09-252-991A-20805
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US-09-370-838-203
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LENGTH: 164
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Patent No. 6617156

SENERAL INFORMATION:

SENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION:

FILE REPERENCE: 032796-032

CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT PILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/055,778

PRIOR APPLICATION NUMBER: US 60/055,778
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Sequence 208, Application US/08679493A
Patent No. 6302295
GENERAL INPORMATION: Ethan W.
TITLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS
FILE REFRERENCE: 55-95
CURRENT APPLICATION NUMBER: US/08/679,493A
CURRENT FILING DATE: 1996-07-12
PRIOR PELICATION NUMBER: 60/001203
PRIOR FILING DATE: 1995-07-14
PRIOR PILING DATE: 1995-07-10
PRIOR FILING DATE: 1995-07-10
PRIOR FILING DATE: 1995-07-10
PRIOR FILING DATE: 1995-07-10
PRIOR FILING DATE: 1995-09-01
NUMBER OF SEQ ID NOS: 216
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 153;
                                                                                                                                                                                                           Length 150;
                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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100.0%; Score 19; DB 4; L
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Enterococcus faecalis-09-134-000C-4087
LENGTH: 150 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Sest Local Similarity 100.
Matches 4; Conservative
                                                                                 TOPOLOGY: not relevan
MOLECULE TYPE: peptide
-07-667-7118-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 152
TYPE: PRT
ORGANISM: blueshark
                                                                                                                                                                                                                                                                                                                                                                                     66 VAEF 69
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-08-679-493A-208
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RESULT. 53

US-9-22-291A-20805

US-9-23-291A-20805

US-9-23-291A-2
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us-09-594-978a-2.rai

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COMPUTER: IEM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/690,095
FILLING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTATION NUMBER: 36,749
REGISTATION NUMBER: PF-0110 US
TELEPHONE: 415-65-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF-0110 US
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INPORMATION POR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 172 amino acids
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: ISM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
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MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIBRARY: GenBank
CLONE: 293274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 VARF 125
                                                       1 VAEF 4
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APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
SEQ ID NO 2222
LENGTH: 166
LENGTH: 166
TYPE: PRT
ORGANISM: M.catarrhalis
US-09-540-236-2222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 16, Application US/08471058

Sequence 16, Application US/08471058

Sequence 16, Application US/08471058

GENERAL INFORMATION:
APPLICANT: Kafet.
APPLICANT: Barr, Philip J.
TITLE OF INVENTION: NOVEL APOPTOSIS MODULATING
TITLE OF INVENTION: PREPROF
TITLE OF INVENTION: PREPROF
TITLE OF INVENTION: PREPROF
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 19; DB 4; Length 166; Best Local Similarity 100.0%; Pred. No. 6.46+02; Matches 4; Conservative 0; Mismatches 0; Indels
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100.0%; Score 19; DB 1; Length 172;
Best Local Similarity 100.0%; Pred, No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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COMPUTER: CAS
COMPUTER: READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASLSEQ for Windows Version 2.0
SOFTWARE: FASLSEQ for Windows Version 2.0
SOFTWARE: FASLSEQ for Windows Version 2.0
SOFTWARE: FALICATION NUMBER: US/08/471,058
FILING DATE: 06-UN 1995
CLASSIFICATION NUMBER: 08/320,157
FILING DATE: 07-CCT-1994
APPLICATION NUMBER: 08/160,067
FILING DATE: 30-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Lebnhard, Susan K
REFERENCE/DOCKET NUMBER: 33-43
REBERROWNICATION NUMBER: 33-43
REBERROWNICATION NUMBER: 33-43
REFERENCE/DOCKET NUMBER: 33-47-20007.12
TELEFONE: 415-413-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 706141
INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS: LENGTH: 172 amino acids TYPE: amino acid STRANDENNESS: single 1090LOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97 VAEF 100
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US-08-471-057-16
US-08-471-057-16
US-08-471-057-16
Patent No. 6015687
GENERAL INFORMATION:
APPLICANT: BARR, PHILIP J.
TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
TITLE OF INVENTION: ROCAL APOPTOSIS-MODULATING PROTEINS, DNA
TITLE OF INVENTION: ROCAL APOPTOSIS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: MORRISON & FORESTER
STREET: 755 Page Mill Road
CITY: Palo Alco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 19; DB 1; Length 172; 100.0%; Pred. No. 6.7e+02; tive 0; Mismatches 0; Indels
US-08-69-095-3
US-08-690-095-3
US-08-690-095-3
Patent No. 5792648
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Al-Young, Janice
CORRESPONDENCES: Joyce Human Macrophage ANTIGEN
NUMBER OF SEQUENCES:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
CITY: Palo Alto
STATE: Al-APPLICANT: U.S.
CONTRY: U.S.
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TYPE: amino acid
STRANDEDNESS: sir
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US-08-470-865-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 6034219
GENERAL INFORMATION:
PAPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COMPUTER: CA
COMPUTER: EASTEM: DOS
SOFTWARE: EASTEM: DOS
SOFTWARE: FREESEQ Version 1.5
CURRENT APPLICATION NUMBER: US/09/113,789
                             COMPUTER SEADABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/NS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/471,057

FILING DATE: US/08/471,057

FILING APPLICATION ATA:

APPLICATION NUMBER: 08/320,157

FILING DATE: 07-OCT-1994

ATONEY/AGENT INPORMATION:

NAME: LEHHHARDY SUSAN K.

REGISTRATION NUMBER: 33,943

REGISTRATION NUMBER: 33,943

REFERENCE/DOCKET NUMBER: 23647-20007.20

TELEPHONE: (415) 813-5600

TELEPHONE: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF-0110 US
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/690,095
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 9F-0110
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/09113789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 706141
INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS: LENGTH: 172 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 4; Conservative
California
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                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ESULT 59
IS-09-113-789-3
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Sequence 6739, Application US/09328352

Sequence 6739, Application US/09328352

Sequence 6739 and Color of Colo
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                                                                                                  Length 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08737980
; Sequence 2, Application US/08737980
; Patent No. 5843773
; GENERAL INFORMATION:
APPLICANTON: Apoptosis Regulating Gene
; VIWERR OF SEQUENCES: 2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; SOFTWARE: PLEATION NUMBER: US/08/737,980
                                                                                                                                                                0; Indels
                                                                                              100.0%; Score 19; DB 4; I
100.0%; Pred. No. 6.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: KR 1995-6266
FILING DATE: 24-MAR-1995
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , ORGANISM: Acinetobacter baumannii
US-09-328-352-6739
ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                           Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                   77 VABF 80
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              US-09-489-039A-9869
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US-09-328-352-6739
                                                                                                  Query Match
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                                                                                                                                                                                                                                            ઠે
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Patent No. 6610836
GENERAL INFORMATION

GENERAL INFORMATION

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEESIELLA

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEESIELLA

TITLE OF INVENTION: NUMBER: US/09/489,039A

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT APPLICATION NUMBER: US/09/127

PRIOR APPLICATION NUMBER: US/09/117,747
                                                                                                                                                                                                                                                                                                          KEVIN R.
KEVIN G.
PSPTIDE INHIBITORS OF THE P33CDK2 AND P34CDC2 CELL CYCLE REGULATORY KINASES AND HUMAN PAPILLOMAVIRUS E7 ONCOPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 19; DB 1; Length 173; 100.0%; Pred. No. 6.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/193,977
FILING DATE: 08-FEB-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTOREST/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGIGSTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5998-0016
TELEPHONE: (415) 617-8999
TELEPAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 173 amino acids
                                                                                                                                                                                                                       GENERAL INFORMATION:

APPLICANT: MESSTER, KEVIN R.
APPLICANT: COLEMAN, KEVIN R.
TITLE OF INVENTION: PEPTIDE INHIBITOI
TITLE OF INVENTION: PARTICO CELL CYCI
TITLE OF INVENTION: PARTICO CELL CYCI
TITLE OF INVENTION: PARTICO CELL CYCI
TITLE OF INVENTION: PAPILLOMAVIRUS ET
NUMBER OF SEQUENCES: 34
CORRESPONDENCE 3
ADDRESSEE: REED & ROBINS
STREET: 635 BRYANT STREET
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
COMMITTY: UNITED STATES OF AMERICA
COMMITTY: UNITED STATES OF AMERICA
                                                                                                                                                                                                        Sequence 4, Application US/08193977
Patent No. 5625031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 173 amino acida
TYPE: amino acid
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Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
SEQ ID NO 9869
LENGTH: 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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122 VAEF 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-193-977-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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; Batent No. 6087108
; Batent No. 6087108
; GENERAL INFORMATION:
; APPLICANT: Bandam, Olga
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL RNA EDITING ENZYME
; COMBER POR ESQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTR.:
ZIP. 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM COMPATIBLE
COMPUTER: PastSEQ for Windows Version 2.0
THEWARE: PastSEQ for Windows Version 2.0
                                                                                          MEDIUM TYPE: Diskette
COMPUTER: IERM Compatible
COMPUTER: IERM Compatible
COMPUTER: IERM Compatible
COMPUTER: IERM Compatible
COMPUTER: THEM COMPATIBLE
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION NUMBER:
FILING DATE: Filed Herewith
RIOR APPLICATION 1435
RIOR PAPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 415-65-655
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 190 amino acids
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Best Local Similarity 100.
Matches 4; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
                                                              COMPUTER READABLE FORM MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LIBRARY: PROSTUT09
; CLONE: 1646823
US-08-816-241-1
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USA
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          Sequence 24341, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ASRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR PAPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 24341
LENGTH: 185
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Sequence 7113, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION WUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 7313
LENGTH: 189
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Patent No. 5804185
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
TITLE OF INVANTION:
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
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Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity
Matches 4; Conserv
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      09-252-991A-24341
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EARLIER FILING DATE: 1998-07-20
EARLIER APPLICATION NUMBER: 60/110,941
EARLIER FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FESTSEQ for Windows Version 3.0
SEQ ID NO 85
LENGTH: 199
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EARLIER APPLICATION NUMBER: 60/071,374
EARLIER FILING DATE: 1998-01-15
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US-09-212-201-85
; Sequence 85, Application US/09232201A
; Patent No. 6348321
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Sequence 85, Application US/09232197A
Patent No. 6300096
GENERAL INFORMATION:
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                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Aspergillus nidulans
US-09-232-200-85
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
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Sequence 3800, Application US/09134000C
Sequence 3800, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICATION: BUTERCCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR PEDLICATION NUMBER: US 60/055,778
PRIOR PEDLICATION NUMBER: US 60/055,778
PRIOR PILING DATE: 1997-08-15
SOFTWARE: Patentin version 3.1
SEQ ID NO 3800
LENGTH: 194
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Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 7.4e+02;
tive 0; Mismatches 0; Indels
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Sequence 85, Application US/09232200A
Sequence No. 6288213
GENERAL INPORMATION:
APPLICANT: Stahl, Andreas
APPLICANT: Hisch, David J.
APPLICANT: Hisch, David J.
APPLICANT: Gimeno, Ruth E.
APPLICANT: Gimeno, Ruth E.
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: FAITY ACID TRANSPORT PROTEINS
FILE REFERENCE: WHI97-21p3MB
CURRENT FILING DATE: 1999-01-14
EARLIER APPLICATION NUMBER: 60/071,374
EARLIER APPLICATION NUMBER: 60/071,374
EARLIER APPLICATION NUMBER: 60/093,491
                                                                                                        PF-0239 US
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-02
TELECOMMUICATION INFORMATION:
TELEPHONE: 415-85-0555
TELEPAX: 415-85-0555
INFORMATION FOR ESO ID NO: 1:
SEQUENCE GHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDENKES: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBBARY: PROSTUT09
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Best Local Similarity 100.
Matches 4; Conservative
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IS-09-134-000C-3800
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100.0%; Score 19; DB 3; Length 199; 100.0%; Pred. No. 7.8e+02;
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GENERAL INFOCATION:
APPLICANT: Stahl, Andreas
APPLICANT: Hisch, David J.
APPLICANT: Hodish, Harvey F.
APPLICANT: Gimeno, Ruth E.
APPLICANT: Tarteglia, Louis A.
ITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
FILE REFERENCE: WHI97-21p3MA
CURRENT FILING DATE: 1999-01-14
EARLIER APPLICATION NUMBER: 60/071,374
EARLIER APPLICATION NUMBER: 60/071,374
EARLIER APPLICATION NUMBER: 60/093,491
EARLIER FILING DATE: 1998-01-15
HEARLIER FILING DATE: 1998-11-04
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FRSIESEQ for Windows Version 3.0
SEQ ID NO 85
LEARLIER FILING
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APPLICANT: Stahl, Andreas
APPLICANT: Hisch, David J.
APPLICANT: Lodish, Harvey F.
APPLICANT: Gimeno, Ruth E.
APPLICANT: Tartealia, Louis A.
TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
FILE REFERENCE: WHIS7-21p3MC
                                                         0; Mismatches
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FILING DATE: 19-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1747/46621-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 203 amino acids TYPE: amino acid
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MOLECULE TYPE: protein
HYPOTHETICAL: YES
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Sequence 4622, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
FITTLE OF INVENTION: ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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APPLICANT: Stahl, Andreas.
APPLICANT: Stahl, Andreas.
APPLICANT: Hissch, David J.
APPLICANT: Hissch, David J.
APPLICANT: Gimeno, Ruth E.
APPLICANT: Gimeno, Ruth E.
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
FILE REFERENCE: WH197-21p3MD
CURRENT APPLICATION NUMBER: 08/09/232,195A
CURRENT FILLING DATE: 1999-01-04
EARLIER APPLICATION NUMBER: 60/071,374
EARLIER FILLING DATE: 1998-07-05
EARLIER PILLING DATE: 1998-07-06
EARLIER APPLICATION NUMBER: 60/110,941
EARLIER FILLING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FABECRO for Windows Version 3.0
SEQ ID NO SES
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ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
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100.0%; Pred. No. 7.8e+02;
Live 0; Mismatches 0;
EARLIER APPLICATION NUMBER: 60/093,491
EARLIER FILING DATE: 1998-07-20
EARLIER APPLICATION NUMBER: 60/110,941
EARLIER RILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 85
LENGTH: 199
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STATE: Massachusetts
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                                                                                                                                                                                          TYPE: PRT
ORGANISM: Aspergillus nidulans
:-09-232-201-85
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Best Local Similarity luv.
4, Conservative
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Best Local Similarity 100.
Matches 4; Conservative
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Sequence 1, Application US/08684024
Secuent No. 5834298
GENERAL INFORMATION:
APPLICANT: BENEZIA, ROBERT
TITLE OF INVENTION: GENE ENCODING THE HUMAN HOMOLOG OF MAD2
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
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100.0%; Score 19; DB 4; Length 203;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READELE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/684,024
TITING DATE: 19-UUL-1996
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
CORPUTER: PC
CORPUTER: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: JUNy 2, 1997
ATTORNEY AGENT INFORMATION:
FILING DATE: AND 2, 1997
ATTORNEY AGENT INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
TELECOMMUNICAT
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEPAX: (212) 391-0526
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 205 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: Innear
MOLECULE TYPE: protein
IS-08-684-024-1
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Query Match 100.0%; Score 19; DB 2; Length 205; Best Local Similarity 100.0%; Pred. No. 8e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 VAEF 4 |||| 20 VAEF 23

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earch completed: May 24, 2004, 17:43:22 ob time : 14 secs

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Sequence 343, App
Sequence 206, App
Sequence 206, App
Sequence 86, Appl
Sequence 145, App
Sequence 197, App
Sequence 34, Appl
Sequence 7, Appl
Sequence 67, Seppl
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Sequence 67, Seppl
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35.179 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-791-399-206
US-10-128-711-145
US-09-908-93A-197
US-10-032-818-34
US-10-239-313A-379
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Maximum Match 100%
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    protein search, using sw model

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44932, 57728, 92406, 89066, 06883,	84, 82, 44,	Appl 18, 85,	App 22,	Appl 79,	11, Ap	App A	7 - 12 12 - 13 13 - 13	8, A App	, Ap	App	Appl App	o, a Appl	24.00	72, App	App	20, App	App , Ap	App 199,	73, App	5, A	App1 29,	Appl	App	App	App , Ap	44, 8, A	, Ap ppl	pli ppli	Appl Appl	4, 7 4 , 7
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10-424-599-144 10-424-599-257 10-424-599-192 10-424-599-189 10-424-599-228 10-424-599-206	-599-	10000	15997 19991	- 636- - 636- - 696-	-599- 626-5	-552- 761-3 -599-	242-1 599-1	-114-	-761-	-260A -415-	-379-	-122A -794-	966	-157A -157A -599-	-075-	-599- 973-2	133-2 -408A	-649A -599-	-599-	-599-	-482- -599-	-977-	-761-	761-3 301-9	297-5 -049-	-599-	-977- 156-1	633-9 -459-	-761- -519-	-122A -122A -122A
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US-09-769-864-1 US-09-769-864-2 US-09-769-864-6 US-09-769-864-6 US-09-769-864-8 US-09-769-864-8	US-09-854-346-4 US-09-854-346-4 US-09-854-346-12	US-09-804-540-15 US-09-902-188A-1 US-09-902-188A-2	US-09-902-188A-7 US-09-918-543-2 US-09-918-543-2	US-09-918-543-12 US-09-918-543-12 US-09-795-211-1	US-09-793-ZII-Z US-09-795-ZII-Z O IIS-09-925-5767-2	0 US-09-925-576C-4	0 US-09-925-576C-12 0 US-09-925-576C-13	2 US-10-665-667-1 2 US-10-665-667-2	2 US-10-665-667-6 2 US-10-665-667-7	2 US-10-665-667-8	2 US-10-025-648-2	2 US-10-025-548-7 2 US-10-327-837-1	2 US-10-327-837-2 2 US-10-327-837-6	2 US-10-327-837-7 2 US-10-327-837-8	2 US-10-327-837-24	4 US-10-209-20	4 US-10-184-771-12 5 US-10-369-493-4906	2 US-10-403-161-44 5 US-10-369-493-18040	2 US-10-425-114-45580 0 US-09-863-776-34	2 US-10-424-599-149190	2 US-110-282-122A-58846	2 US-10-424-599-284218	S US-10-614-076-70	2 US-10-4425-114-56882 5 US-10-369-493-5803	5 US-10-369-493-11919 US-09-815-242-11025	2 US-10-282-122A-58172 2 US-10-424-599-149746	5 US-10-369-493-8665	2 US-10-282-122A-63359 2 US-10-425-114-56039	US-09-738-626-7001	2 US-10-627-476-500	2 US-10-425-114-64036 5 US-10-369-493-8682	US-09-943-671-9	5 US-10-405-877-95	US-09-925-300-1285 2 US-10-424-599-146129	2 US-10-425-114-68917	US-09-986-676A-Z US-09-971-611-2
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Sequence 343, Application US/09791378

Sequence 343, Application US/09791378

Parent No. US20020142303A1

Parent No. US20020142303A1

APPLICANT: Parekh, Rajesh

TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF TITLE OF INVENTION: SCHIZOPHRENIA
FILE REFERENCE: 9195-061-999

CURRENT APPLICATION NUMBER: US/09/791,378

CURRENT PILING DATE: 2001-02-23

PRIOR PILING DATE: 2001-12-28

NUMBER OF SEQ ID NOS: 677

SOFTWARE: Patentin version 3.0

SEQ ID NO 343
Sequence 75373, A Sequence 65931, A Sequence 61529, A Sequence 1169, Apple Sequence 142, Apple Sequence 61750, A Sequence 617, Apple Sequence 617, Apple Sequence 617, Apple Sequence 611, Apple Sequence 6118, Apple Sequence 11818, Apple Sequence 11818, Apple Sequence 7018, Apple Sequence 588, Apple Sequence 38857, A Sequence 588, Apple Sequence 332, Apple Sequence 58855, Apple Sequence 5885568, Apple Sequence 58855, Apple Sequence 58855, Apple Sequence 58855, Apple Sequence 555568, Apple 55568, Apple 555568, Apple 55568, Apple 555568, Apple 555568, Apple 55568, Apple 555568, Apple 555568, Apple 555568, Ap
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Sequence 2, Appli
Sequence 6, Appli
Sequence 198664,
Sequence 198664,
Sequence 10, Appli
Sequence 10, Appli
Sequence 65911, A
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2 US-10-282-122A-75373

2 US-10-282-122A-75352

2 US-10-282-122A-75352

2 US-10-369-493-21529

6 US-10-380-566-1969

2 US-10-380-566-1969

4 US-10-100-957A-142

4 US-10-100-957A-142

4 US-10-100-957A-142

2 US-10-282-122A-65302

US-10-282-122A-65302

US-10-282-122A-65302

US-10-282-122A-65302

US-10-282-122A-65302

2 US-10-282-14-42248

2 US-10-425-114-42248

2 US-10-425-114-42248

2 US-10-312-359-186118

2 US-10-312-359-186118

2 US-10-312-362-8

US-10-312-362-8

US-10-282-11305-8

US-10-282-122A-58657

US-10-282-122A-58657
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US-10-289-762-332
US-10-444-599-255268
US-10-431-449-2
US-10-431-449-4
US-10-431-449-4
US-10-431-449-4
US-10-431-449-4
US-10-431-449-4
US-10-444-599-198064
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Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
S-09-791-378-343
      1 VAEF 4
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S-09-791-378-343
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ESULT 2 S-09-791-393-206

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GENERAL INFURANTION:

APPLICANT: Herath, Rajesh Bhikhu
APPLICANT: Parekh, Rajesh Bhikhu
APPLICANT: Transtan Alexander
APPLICANTION: Proteins, Genes and Their Use for
TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
TITLE OF INVENTION: and Unipolar Depression
FILE REFERENCE: 2543-1-001 N2
CURRENT APPLICATION NUMBER: US 0004412.3
PRIOR PILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-12-08
PRIOR FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 308
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 206
LENGTH: B
                                                                                                        APPLICANT: Herath, Mudiyanselage Athula Chandrasiri,
APPLICANT: Herath, Herath Mudiyanselage Athula Chandrasiri,
APPLICANT: Parekh, Rajesh Bhikhu
APPLICANT: Rohliff, Christian
TITLE OF INVENTION: Proteins, Genes and Their Use for
TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
TITLE OF INVENTION: and Unipolar Depression
TITLE OF INVENTION: and Unipolar Depression
TITLE OF INVENTION: and Unipolar Depression
FILE REFERENCE: 2543-4-001 NI
CURRENT FILING DATE: 2000-02-24
EARLIER APPLICATION NUMBER: GB 0004412.3
EARLIER FILING DATE: 2000-12-08
EARLIER PAPEL AND EARLIER PAPEL EARLIER FABRES F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 19; DB 10; Length 8; 100.0%; Pred. No. 1e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
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ilarity 100.0%; Pred. No. 1e+06;
Conservative 0; Mismatches 0;
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Application US/09791393
5. US20030032200A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 4; Conservative
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US-09-791-389-206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: homo sapien
US-09-791-393-206
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Best Local Similarity
Matches 4; Conserv
         Sequence 206, Applic Publication No. US20 GENERAL INFORMATION:
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US-09-791-389-206
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                                                                                                                                SETTE, Alessandro D.
CELIS, Esteban
GRAY, Howard
TITLE OF INVENTION: CTL IMMUNITY
CTL IMMUNITY
                                                                                                                                                                                                                                                                                                                                                                                    COMPUTE: US

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/128,711

FILING DATE: 22-Apr-2002

CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 19; DB 14; Length 9; 100.0%; Pred. No. 1e+06; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSE:
ADDRESSEE: Townsend and Townsend Khourie and Ci
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US/08/197,484

FILING DATE: 16-FEB-1994

APPLICATION NUMBER: US 07/935,811

FILING DATE: 26-AUG-1992

APPLICATION NUMBER: US 07/874,491

FILING DATE: 27-APR-1992

APPLICATION NUMBER: US 07/827,682

FILING DATE: 29-JAN-1992

APPLICATION NUMBER: US 07/49,568

FILING DATE: 26-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-26-4
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: unknown MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO: 86: $1-10-128-711-86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (206) 467-9600
TELEFAX: (206) 623-6793
INFORMATION FOR SEQ ID NO: 86:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3-10-128-711-145
Sequence 145, Application US/10128711
Publication No. US20030099634A1
GENERAL INFORMATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Parmelee, Steven W.
              Sequence 86, Application US/10128711
Publication No. US20030099634A1
GENERAL INFORMATION:
APPLICANT: VITIELLO, Maria A.
CHESTNUT, RODERT W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: VITIELLO, Maria A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
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Best Local Similarity
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-10-128-711-86
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APPLICANT: Yan, Kiqiang
APPLICANT: Tomasselli, Alfredo G.
APPLICANT: Tomasselli, Mark E.
APPLICANT: Emmons, Thomas L.
APPLICANT: Emmons, Thomas L.
APPLICANT: Heinrikson, Robert L.
APPLICANT: Heinrikson, Robert L.
APPLICANT: PINVENTION: SUBSTRATES AND ASSAYS FOR BETA-SECRETASE ACTIVITY FILE REFERENCE: 29915/00281A.US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING CILL INMUNITY
NUMBER OF SEQUENCES: 153
                                                                                                                                                                                                                                                                                                                                            COUNTIER READABLE FORM:

MEDIUM TYPER: RIOPPY disk

MEDIUM TYPER: RIOPPY disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/128,711

FILING DATE: 22-Apr-2002

CLASSIFICATION NUMBER: US/8197,484

FILING DATE: 16-FEB-1994

APPLICATION NUMBER: US/935,811

FILING DATE: 16-FEB-1994

APPLICATION NUMBER: US 07/935,811

FILING DATE: 27-APR-1992

APPLICATION NUMBER: US 07/874,491

FILING DATE: 29-JAN-1992

APPLICATION NUMBER: US 07/874,491

FILING DATE: 29-JAN-1992

APPLICATION NUMBER: US 07/874,682

FILING DATE: 29-JAN-1992

APPLICATION NUMBER: US 07/874,682

FILING DATE: 29-JAN-1992

APPLICATION NUMBER: US 07/874,682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 19; DB 14; Length 9; 100.0%; Pred. No. 1e+06; ative 0; Mismatches 0; Indel8
                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 14137-26-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: Unknown

NOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 145:
US-10-128-711-145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Parmelee, Steven W. REGISTRATION NUMBER: 31,990
CHESTNUT, Robert W.
SETTE, Alessandro D.
CELIS, Esteban
GRAY, Howard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT.6
US-09-908-943A-197
IS-09-908-943A-197
Publication US/09908943A
Publication No. US20030017991A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (206) 623-6793 INFORMATION FOR SEQ ID NO: 145: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                         CITY: San Francisco
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 4; Conserv
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APPLICANT: KLINGTER - HAMOUR, Christine
APPLICANT: ECK, Aladia
APPLICANT: CORVAIA, Nathalie
APPLICANT: CORVAIA, Nathalie
APPLICANT: CORVAIA, Nathalie
APPLICANT: CORFICH, Liliane
TITLE OF INVENTION: WOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS
TITLE OF INVENTION: WOLECULE OF PHARMACEUTICAL OR A GLUTAMINE IN THE FORM
TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
FILE REFERENCE: 343 727 - US
CURRENT APPLICATION NUMBER: US 1002-03-19
FRIOR PILING DATE: 2002-03-19
FRIOR PILING DATE: 2000-03-23
FRIOR PILING DATE: 2001-03-22
NUMBER OF SEQ ID NOS: 697
SOFTWARE: PETENTING UNDER: 2001-03-22
NUMBER OF SEQ ID NOS: 697
SEQ ID NO 379
LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/10119528; Publication No. US20030175722A1; Publication No. US20030175722A1; GENERAL INFORMATION: APPLICANT: Mann, M. APPLICANT: Mann, M. APPLICANT: MOYENBER, P. TITLE OF INVENTION: METHODS AND SYSTEMS FOR SEARCHING GENOMIC DATABBASES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
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                                            APPLICANT: GASA, ALUM K.

TITLE GO INVENTION: Inhibitors of Memapsin 2 and Use Thereof
FILE REPERENTE: 2932.1006-007
CURRENT APPLICATION NUMBER: US/10/032,818
CURRENT FILING DATE: 2001-12-28
PRIOR PILING DATE: 2001-03-14
PRIOR PILING DATE: 2000-12-28
PRIOR FILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 83
SOPTHARE: FastSEQ for Windows Version 4.0
SEQ ID NO 34
LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 19; DB 14; Length 12; Best Local Similarity 100.0%; Pred. No. 1.6e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 19; DB 14; Length 13; 100.0%; Pred. No. 1.7e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Synthetic peptide US-10-032-818-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 379, Application US/10239313A Publication No. US20030175285A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Mycobacterium leprae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
                APPLICANT: Koelsch, Gerald APPLICANT: Ghosh, Arun K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100. Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-239-313A-379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
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LOCATION: (4)...(4)

COTHER INFORMATION: amino acid at position 4 has been derivatized with a statine of 05-908-943A-196
                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: SITE
LOCATION: (4)..(4)
OTHER INFORMATION: amino acid at position 4 has been derivatized with a statine
NAME/KEY: SITE
LOCATION: (10)..(10)
OTHER INFORMATION: amino acid at position 10 has been derivatized with Bodipy FL
IS-09-908-943A-197
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Publication No. US20030017991A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Tomasselli, Alfredo G.
APPLICANT: Generaly, Mark E.
APPLICANT: Bennons, Thomas L.
APPLICANT: Bennons, Thomas L.
APPLICANT: Bennons, Thomas L.
APPLICANT: Bennons, Robert L.
APPLICANT: Bienkowski, Mike J.
APPLICANT: Bie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
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Best Local Similarity 100.0%; Pred. No. 1.38+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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CURRENT APPLICATION NUMBER: US/09/908,943A
CURRENT FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: 60/219,795
PRIOR FILING DATE: 2000-07-19
NUMBER OF SEQ ID NOS: 197
SOFFWARE: Patentin Ver. 2.0
SEQ ID NO 197
LENGTH: 10
                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: synthetic peptide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 34, Application US/10032818; Publication No. US20330092629A1; GENERAL INFORMATION: APPLICANT: Tang, Jordan J.N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 VAEF 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 VAEF 8
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JS-09-908-943A-196
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LENGTH: 12
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Length 20;

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Query Match
Best Local Similarity 100.
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
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STRANDEDNESS: si:
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                                                                                                                    13 VAÈF 16
                                                                             1 VAEF 4
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US-09-171-432A-63
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Publication No. US20030187184A1
GENERAL INFORMATION:
APPLICANT: Fields, Howard A.
APPLICANT: Khudyakov, Yury E.
TITLE OF INVENTION: Antigenically Reactive Regions of the TITLE OF INVENTION: Hepatitis A Virus Polyprotein NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: ALPATION CORRESPONDENCE ADDRESSE:
ADDRESSEE: 3424 Peachtree Road, N.E.
                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Atlanta
STATE: Georgia
COMPRY: USA
ZIP: 30326
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPTATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/09/171,432A
FILING DATE: 23-NOV-1998
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CLASSITCATION:
ATTORNEY/AGENT INFORMATION:
NAME: Greene, Jamite L.
REGISTRATION NUMBER: 32,467
REFRENCE/DOCKET NUMBER: 03063-0231US
TELEPHONE: (404) 949-2400
TELEPHONE: (404) 949-2409
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acid
STRANDEDNESS: single
FILE REFERENCE: MDSP-P01-004
CURRENT APPLICATION NUMBER: US/10/119,528
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/282,51
PRIOR FILING DATE: 2001-04-09
PRIOR FILING DATE: 2001-04-09
RIOR FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 112
SOUTWARR: PATENTIN VERSION 3.1
ENGTH: 15
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LOCATION: 1..20
OTHER INFORMATION: /label= XK-1368
3-09-171-432A-62
                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Arabidopsis thaliana
-10-119-528-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
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FRAGMENT TYPE:
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; Sequence 63, Application No. US20030187184A1
; Publication No. US20030187184A1
; GENERAL INFORMATION:
    APPLICANT: Fields, Howard A.
    APPLICANT: Khudyakov, Yury B.
    APPLICANT: Khudyakov, Yury B.
    TITLE OF INVENTION: Hepatitis A Virus Polyprotein
    TITLE OF INVENTION: Hepatitis A Virus Polyprotein
    NUMBER OF SEQUENCES:
    ADDRESSEE: Kilpatrick Stockton LLP
    STRET: 3424 Peachtree Road, N.E.
    CITY: Atlanta
    STATE: Georgia
    COUNTRY: USA
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                                                                                                     Indels
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ZIP: 30326

COMPUTER READABLE FORM:
MEDITUM TYPE: Rloppy disk
COMPUTER: READABLE FORM:
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: DATE: DC-DOS/MS-DOS
SOUTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/171,432A
FILING DATE: 23-NOV-1998
CLASSIFICATION NUMBER: 32,467
REGISTRATION NUMBER: 32,467
REGISTRATION NUMBER: 03063-0231US
TELEPHONE: (404) 949-2400
TELEPHONE: USAGAID NO: 63: SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TUTE OF THE OF T
Query Match
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , OTHER INFORMATION: /label= YK-1369
US-09-171-432A-63
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; Sequence 65, Application US/09171432A
; Publication No. US20030187184A1
; GENERAL IRFORMATION:
APPLICANT: Fields, Howard A.
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and Other Molecules Associated With
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; Sequence 216297, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
    APPLICANT: La Rosa Thomas J
    APPLICANT: A Rosa Yonger
    TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Ass
    TITLE OF INVENTION: Plants and Uses Thereof for Flant Improvement
    TITLE OF INVENTION: Plants and Uses Thereof for Flant Improvement
    CURRENT APPLICATION NUMBER: US/10/424,599
    CURRENT FILING DATE: 2003-04-28
    SEQ ID NOS: 285684
    SEQ ID NOS: 285684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-
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ORGANISM: Glycine max
PREATURE: OTHER INFORMATION: Clone ID: PAT_MRT3847_37345C.1.pep
US-10-424-599-216297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 19; DB 9; I
100.0%; Pred. No. 3.7e+02;
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Sequence 47201, Application US/09864761

Patent No. US20020048763A1

GENERAL INFORMATION:

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David R.

APPLICANT: Hanzel, David R.

APPLICANT: Chem, Wensheng

TITLE OF INVENTION: HUMAN GENE EXPRESSION ANALYSIS BY MICROARRAY

FILE REFERENCE: Acemica-X-1

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT PILING DATE: 2000-02-04

PRIOR FILING DATE: 2000-02-04

PRIOR PLILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR PLILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR PLILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 69/632,366

PRIOR FILING DATE: 2000-06-36

PRIOR FILING DATE: 2000-06-36

PRIOR FILING DATE: 2000-06-36

PRIOR FILING DATE: 2000-08-36

PRIOR PLILING DATE: 2000-08-36

PRIOR PLILING DATE: 2000-08-36
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                                               TITLE OF INVENTION: Antigenically Reactive Regions of the TITLE OF INVENTION: Hepatitis A Virus Polyprotein NUMBER OF SEQUENCES:

NUMBER OF SEQUENCES:

ADDRESSES: ADDRESS:

ADDRESSES: Kilpatrick Stockton LLP
STREET: A144 Peachtree Road, N.E.
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 19; DB 10; Length 25; 100.0%; Pred. No. 3.3e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                             ZUNNURY: UDDAY
ZIT: 30326
COMPUTER SEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/171,432A
FILING DATE: 23-NOV-1998
CLASSIFICATION:
NAME: Greene, Jamie L.
REGISTRATION NUMBER: 32,467
REJERPATION NUMBER: 32,467
REJERPATION NUMBER: 32,467
TELEPHONE: (404) 949-2499
INPORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TWEENER = 25 amino acids
TWEENER = 25 amino acids
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OTHER INFORMATION: /label= YK-1832
                             APPLICANT: Khudyakov, Yury E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Conservative
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FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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IS-09-864-761-47201
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100.0%; Score 19; DB 15; 100.0%; Pred. No. 4.9e+02;
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CURRENT APPLICATION NUMBER: US/10/430,752A
CURRENT AILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: 09/485,286
PRIOR FILING DATE: 2000-02-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-430-752A-49
. Sequence 49, Application US/10430752A
; Publication No. US20040005669A1
; GENERAL INFORMATION:
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Best Local Similarity 100...
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                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-242-355-570
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Publication No. US2003023531A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENITION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PCO03C1
CURRENT APPLICATION NUMBER: US/10/242,355
CURRENT FILING DATE: 2002-09-13
PRIOR APPLICATION NUMBER: 09/764,897
PRIOR APPLICATION NUMBER: 06/179,065
PRIOR PILING DATE: 2000-01-31
PRIOR PILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR PILING DATE: 2000-02-04
PRIOR PILING DATE: 2000-02-04
PRIOR PILING DATE: 2000-06-28
PRIOR PELING DATE: 2000-06-18
PRIOR PLING DATE: 2000-06-19
PRIOR PILING DATE: 2000-06-19
PRIOR PILING DATE: 2000-07-11
PRIOR PELING DATE: 2000-07-11
PRIOR PELING DATE: 2000-07-12
PRIOR PELING DATE: 2000-07-12
PRIOR PELING DATE: 2000-07-12
PRIOR PELING DATE: 2000-07-12
PRIOR PILING DATE: 2000-07-14
PRIOR PILING DATE: 2000-07-14
PRIOR PILING DATE: 2000-08-14
Query Match
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                              GENERAL INCRMATION:
APPLICANT: LOCEMOTE, Sheena M.
APPLICANT: LOCEMOTE, Sheena M.
APPLICANT: GATY-VEFS, RObin E.
APPLICANT: Schryvers, Anthony B.
APPLICANT: Gray-Owen, Scott
APPLICANT: Gray-Owen, Scott
APPLICANT: Mucdin, Andrew D.
APPLICANT: Mucdin, Andrew D.
APPLICANT: Mucdin, Michel H.
TILLE OF INVENTION: TRANSFERRIN RECEPTOR GENES
FILE REFERENCE: 1038-1221 MIS
CURRENT APPLICATION NUMBER: US/10/043,344
CURRENT FILING DATE: 2002-07-01
PRIOR FILING DATE: 1996-05-17
NUMBER OF SEQ ID NOS: 160
SCOFTWARE: PARCHIN Ver. 2.1
SEQ ID NO 63
LENGTH: 35
                                                                                                                                                                                                                              SULT 16
-10-043-344-69
-10-043-344-69
Sequence 69, Application US/10043344
Publication No. US20030088086A1
GENERAL INFORMATION:
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ORGANISM: Haemophilus influenzae
-10-043-344-69
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Best Local Similarity
Matches 4; Conserv
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Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1267
SOFTWARE: Patentin Ver. 2.0
LENTH: 37
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APPLICANT: Jonasson, Per
APPLICANT: Jonasson, Per
APPLICANT: Nydran, Per-Ake
APPLICANT: Nydran, Per-Ake
APPLICANT: Nydran, Per-Ake
APPLICANT: Nydran, Per-Ake
APPLICANT: Nydranon Recomminant
TITLE OF INVENTION: C-PEPTIDE
FILE REFERENCE: 11541-003001
CURRENT APPLICATION NUMBER: US/10/430,752A
CURRENT APPLICATION NUMBER: 09/485,286
PRIOR FILING DATE: 2000-02-07
PRIOR FILING DATE: 1990-08-07
PRIOR FILING DATE: 1990-08-07
PRIOR FILING DATE: 1997-08-07
NUMBER: PER PRIOR PRIOR NUMBER: GB 9716790.2
NUMBER: PER PRIOR PRIOR DATE: 1997-08-07
NUMBER: PER PRIOR FILING DATE: 1997-08-07
NUMBER: PER PRIOR FILING DATE: 1997-08-07
SOFTWARE: FRACESOF FOR WINDOWS VERBION 4.0
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Sequence 45, Application US/10430752A
Sequence 45, Application US/10430752A
Publication No. US20040005669A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Stain
APPLICANT: Unjern, Per-Ake
APPLICANT: Unjern, Mathias
TITLE OF INVENTION: RECOMBINANT EXPRESSION OF INSULIN
TITLE OF INVENTION: C-PEPTIDE
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US-10-424-599-183032
US-10-424
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OTHER INFORMATION: MAP TO AL035530.11
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.86
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.95
OTHER INFORMATION: SKIRESSED IN BT474, SIGNAL = 0.95
OTHER INFORMATION: SKIRESPROT HIT: P33485, BVALUE 3.60e+00
US-09-864-761-37202
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PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR PILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2000-06-30
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Best Local Similarity 100..
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 22
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Sequence 37202 Application US/09864761
Sequence 37202 Application US/000048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Savid R.
APPLICANT: Hanzel, David R.
APPLICANT: Chen, Wensheno TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REPERENCE: APPLICANT: HUMAN GENIE EXPRESSION ANALYSIS BY MICROARRAY
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT APPLICATION NUMBER: US 60/180,312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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Publication No. US20030215846A1
GENERAL INFORMATION:
APPLICANT: Matt, Paul
APPLICANT: Thomas, Wayne
APPLICANT: Thomas, Wayne
APPLICANT: Hopkins, Richard
TITLE OF INVENTION: Methods of constructing and screening
TITLE OF INVENTION: Methods of constructing and screening
TITLE OF INVENTION: Miverse expression libraries
FILE REFERENCE: FBRIC40.001CP1
CURRENT APPLICATION NUMBER: US/10/372,003A
CURRENT FILING DATE: 2000-05-05
PRIOR PELING DATE: 1999-05-05
NUMBER OF SEQ ID NOS: 81
SCHWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 71
LENGTH: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 19; DB 15; Length 41; 100.0%; Pred. No. 5.5e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 19; DB 15; Length 38; 100.0%; Pred. No. 5.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                 PRIOR APPLICATION NUMBER: PCT/GB98/02382
PRIOR FILING DATE: 1998-08-07
PRIOR FILING DATE: 1997-08-07
NUMBER OF SEQ ID NOS: 63
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 45
LENGTH: 38
                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Lophius piscatorius 5-10-430-752A-45
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity 100.
Matches 4; Conservative
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IS-09-864-761-37202
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S-10-372-003A-71
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Sequence 205632, Application US/10424599
Sequence 205632, Application US/10424599
Sublication No. U520040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rose Thomas J
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILER REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 205632
LENGTH: 52
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N: EXPRESSED IN FETAL LIVER, SIGNAL = 0.96
N: EXPRESSED IN BONE MARROW, SIGNAL = 1
N: EXPRESSED IN HEBLIOO, SIGNAL = 1.1
N: EXPRESSED IN HEBLY, SIGNAL = 1.2
N: EXPRESSED IN HELA: SIGNAL = 1.2
N: EXPRESSED IN HELA: SIGNAL = 1.2
N: EXPRESSED IN PLACENTA, SIGNAL = 2.1
N: EXPRESSED IN PLACENTA, SIGNAL = 2.1
N: EXPRESSED IN TIT: P11299, EVALUE 7.90e+00
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Similarity 100.0%; Pred. No. 6.4e+02;
4; Conservative 0; Mismatches n: TnAple
          PRIOR APPLICATION UNDBER: US 60/236,359
PRIOR APPLICATION UNDBER: US 60/236,359
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-29
PRIOR PILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SEQTIMARE: Annomax Sequence Listing Engine vers: 1.1
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OTHER INFORMATION: EXPRESSED IN ADULT
OTHER INFORMATION: EXPRESSED IN PETAL
OTHER INFORMATION: EXPRESSED IN HELL
OTHER INFORMATION: EXPRESSED IN HELL
OTHER INFORMATION: EXPRESSED IN HELLA,
OTHER INFORMATION: EXPRESSED IN HELLA,
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Best Local Similarity
Matches 4; Conserv
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US-10-424-599-205632
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Sequence 38166, Application US/09864761
Sevent No. US20020048763A1
SENERAL INFORMATION:
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUPAN GENOME-DERIVED SINGLE EXON NUCLEIC ACTITLE OF INVENTION: HUPAN GENOME-DERIVED SINGLE EXON NUCLEIC ACTITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY FILLE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PRILING DATE: 2000-05-26
PRIOR PRILING DATE: 2000-08-03
PRIOR PRILING DATE: 2000-08-03
PRIOR PRILING DATE: 2000-08-03
PRIOR PRILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
                                                                                                                                                                                                                                                                                  h Similarity 100.0%; Score 19; DB 12; Length 43; Similarity 100.0%; Pred. No. 5.7e+02; 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 19; DB 12; Length 45; 100.0%; Pred. No. 6e+02;
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                                                                                                                                                                                                          OTHER INFORMATION: Clone ID: PAT_MRT3847_136291C.1.pep-10-424-599-183032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Clone ID: PAT_MRT3847_125715C.1.pep 10-424-599-171318
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CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
UNDRER OF SEQ ID NOS: 285684
IRO ID NO 183032
LENGTH: 43
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                                                                                                                                TYPE: PRT
ORGANISM: Glycine max
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ORGANISM: Glycine max
FEATURE:
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sest Local Similarity
fatches 4; Consern
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Synthetic clone BGF05 with first open reading ; OTHER INFORMATION: frame US-10-372-003A-63
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US-10-372-03A-67

Sequence 67, Application US/10372003A

Publication No. US2003015846A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TROUGHS, Watt, Paul
APPLICANT: Thomas, Wayne
TITLE OF INVENTION: Mathods of constructing and screening
TITLE OF INVENTION: Mathods of constructing and screening
TITLE OF INVENTION: Mathods of constructing and screening
FILE REFRENCE: FRIC40.001CP1
CURRENT APPLICATION NUMBER: US/10/372,003A
CURRENT FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: US 09/568,229
PRIOR APPLICATION NUMBER: US 09/568,229
PRIOR APPLICATION NUMBER: US 60/132,711
PRIOR APPLICATION NUMBER: US 60/132,711
PRIOR FILING DATE: 2000-05-05

NUMBER OF SEQ ID NOS: 81

SEQ ID NOS: 81

SEQ ID NOS: 81

SEQ ID NOS: 81
                                                                                                                                                                                                                                                                                                                                                General Inventorial
General Inventorial
General Inventorial
APPLICANT: Watt, Paul
APPLICANT: Thomas, Wayne
APPLICANT: Thomas, Wayne
APPLICANT: Thomas, Wayne
TITLE OF INVENTION: Methods of constructing and screening
FILE REFRENCE: FBRICAO.001CP1
CURRENT APPLICATION NUMBER: US/10/372,003A
CURRENT FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: US 69/568,229
PRIOR APPLICATION NUMBER: US 60/132,711
PRIOR PILING DATE: 1999-05-05
NUMBER OF SEQ ID NOS: 81
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 63
LENGTH: SS
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100.0%; Score 19; DB 15; Length 5
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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Pred. No. 7.3e+02;
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US-10-372-003A-63
i. Sequence 63, Application US/10372003A
i. Publication No. US20030215846A1
i. GENERAL INFORMATION:
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100.0%;
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ORGANISM: Artificial Sequence
PEATURE:
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ORGANISM: Artificial Sequence
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Best Local Similarity
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                                VAEF 4
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Sequence 233502
Sexpence 23500
Sexpence 2350
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Sequence 192247, Application US/10424599
Sequence 192247, Application US/20040031072A1
GENERAL INFORMATION:
APPLICANT: LA ROSA Thomas J
APPLICANT: Kovalic David K
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILER REFERENCE: 38 = 221(5322) B
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 192247
LENGTH: 55
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                                                                                                                                                                                                    Length 52;
                                                                                                                                                                                                                                                              0; Indels
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                                                                                                OTHER INFORMATION: Clone ID: PAT_MRT3847_27713C.1.pep S-10-424-599-205632
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OTHER INFORMATION: Clone ID: PAT_MRT3847_52879C.1.pep
S-10-424-599-233502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_1561C.1.pep
S-10-424-1929-192247
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Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                             100.0%; Score 19; DB 12;
100.0%; Pred. No. 6.9e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                          Ouery Match
Best Local Similarity 100.
Matches 4: Conservative
TYPE: PRT ORGANISM: Glycine max FEATURE:
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ORGANISM: Glycine max
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Matches

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Sequence 260762, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION:
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Sequence 4, Application US/10219561
Publication No. US20030166567Al
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  , ORGANISM: Homo sapiens
US-10-219-561-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Glycine max
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Best Local Similarity
Matches 4; Conserv
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US-10-424-599-260762
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                                                                                                                                                                       Sequence 4, Application US/10219329
Sequence 4, Application US/10219329
Sublication No. US20030096757A1
SEMERAL INFORMATION:
APPLICANT: Quirk, Stephen
APPLICANT: Weart, Inona f.
TITIE OF INVENTION: AALT-Cancer and Wound Healing Compounds
FILE REFERENCE: 1443.035W01
CURRENT APPLICATION NUMBER: US/10/219,329
CURRENT PILING DATE: 2002-08-15
PRIOR PILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: US 60/312,726
PRIOR FILING DATE: 2001-08-16
PRIOR FILING DATE: 2001-08-16
PRIOR FILING DATE: 2001-08-16
PRIOR SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/10153185
Sequence 4, Application No. US20030148959A1
GENERAL INFORMATION:
APPLICANT: Onlik, Schall
TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds
TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds
FILE REPERENCE: 143.034081
CURRENT APPLICATION NUMBER: US/10/153,185
CURRENT FILING DATE: 2002-08-13
PRIOR FILING DATE: 2001-12-21
PRIOR FILING DATE: 2001-12-21
RAIOR APPLICATION NUMBER: US 60/312,726
PRIOR FILING DATE: 2001-08-16
NUMBER OF SEQ ID NOS: 20
SOFTWARR: FastSEQ for Windows Version 4.0
SEQ ID NO SEQ ID NOS: 26
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100.0%; Score 19; DB 14;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 4; Conservative 0; Mismatches 0;
         0; Mismatches
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Best Local Similarity 100.
Matches 4; Conservative
           4; Conservative
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ORGANISM: Homo sapiens
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10-153-185-4

-10-219-329-4

-10-153-185-4

SULT 32 -10-219-561-4

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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Shou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(55223) B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 215734
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GENERAL INFOGRATIONS:
APPLICANT: Quirk, Schehen
APPLICANT: Quirk, Schehen
APPLICANT: Malik, Schail
APPLICANT: Wilanueva, Julie M.
APPLICANT: VIIOR. Arti-Aqing and Wound Healing Compounds
FILE REFERENCE: 1443.088US2
CURRENT APPLICATION NUMBER: US/10/219,561
CURRENT FILING DATE: 2002-08-15
PRIOR PILING DATE: 2001-12-21
PRIOR FILING DATE: 2001-08-16
PRIOR FILING DATE: 2001-08-16
PRIOR FILING DATE: 2001-08-16
PRIOR FILING DATE: 2001-08-16
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 56
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Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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OTHER INFORMATION: Clone ID: PAT_MRT3847_36836C.1.pep
US-10-424-599-215734
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APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
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Gaps

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Indels

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; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_36107C.1.pep
US-10-424-599-214930
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100.0%; Score 19; DB 12;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 4; Conservative 0; Mismatches 0;
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 214930
LENGTH: 58
                                                                                                                                    TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                               13 VAEF 16
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'S-10-424-599-214930
Sequence 214930, Application US/10424599
Fublication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILLE REFERENCE: 38-21 (53223) B
       APPLICANT: Cao Yongwei TITILE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITILE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILIE OF INVENTION: 18-21 (515223) B CURRENT APPLICATION NUMBER: US/10/424,599 CURRENT APPLICATION NUMBER: 2003-04-28 NUMBER OF SEQ ID NOS: 285684 SEQ ID NO 260762 LENGTH: 57
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S-10-372-003A-75
Sequence 75, Application US/10372003A
Publication No. USCO032015846A1
GENERAL INFORMATION:
APPLICANT: Watt, Paul
APPLICANT: Thomas, Wayne
APPLICANT: Hopkins, Richard
TITLE OF INVENTION: Methods of constructing and screening
TITLE OF INVENTION NUMBER: US/10/372,003A
CURRENT APPLICATION NUMBER: US 60/132,711
PRIOR FILING DATE: 1999-05-05
NUMBER OF SEQ ID NOS: 81
SEQ ID NO 75
LENGTH: 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                TYPE: PRT
ORGANIEM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_77490C.1.pep
S-10-424-599-260762
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100.0%; Pred. No. 7.6e+02;
tive 0; Mismatches 0;
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity 100.
Matches 4; Conservative
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US-0-864-761-45291, Application US/09864761, Sequence 45291, Application US/09864761, Sequence 45291, Application US/009864761, Sequence 45291, Application US/00088783A1 Sequence 45291, Application US/0008878A1 Sequence 45291, Application US/0008878A1 Sequence 45291, Application O. APPLICANT: Ranza, David R. APPLICANT: Chem. Westbern David R. APPLICANT: David R
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Gaps

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APPLICANT: Zuker, Charles S.
APPLICANT: Adder, Uon Elliot
APPLICANT: Adder, Uon Elliot
APPLICANT: Hoon, Mark
APPLICANT: Hoon, Mark
APPLICANT: The Government of the University of California
APPLICANT: The Government of the United States of America
APPLICANT: The Government of the United States of America
APPLICANT: The Government of Health and Human Services
ITIES OF INVENTION: T2R, a No. US20040038312Alel Family of Taste Receptors
FILE REFERENCE: 02307E-0980200US
CURRENT APPLICATION NUMBER: US/10/364,861
CURRENT FILING DATE: 1999-09-10
PRIOR FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 95
COFFWARE: Patentin Ver. 2.1
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APPLICANT: Adler, Jon Elliot
APPLICANT: Adler, Jon Elliot
APPLICANT: Ryba, Nick
APPLICANT: Hoon, Mark
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
APPLICANT: The Government of the United States of America
APPLICANT: The Applicant of the United States of America
APPLICANT: The Applicant of Health and Human Services
APPLICANT: Department of Health and Human Services
TILE REFERENCE: 02307E-098000US
FILE REFERENCE: 02307E-09800US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 19; DB 12; Length 68; Best Local Similarity 100.0%; Pred. No. 9.18+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                               Length 68;
                                                                                                                                                                                                                                                                                   Indels
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100.0%; Score 19; DB 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 4; Conservative 0; Mismatches 0;
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US-10-364-861-80
NUMBER OF SEQ ID NOS: 9068
SOFFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 40
LENGTH: 68
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Publication No. US20030157568A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 80, Application US/10364861 Publication No. US20040038312A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                              TYPE: PRT
CAGANISM: Homo sapiens
US-09-864-408A-40
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LENGTH: 68
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APPLICANT: Leach, Martin D.
APPLICANT: Shimkets, Richard A.
TITLE OF INVANTON: No. U220040009474Alel Human Polynucleotides and Polypeptides Enco TITLE OF INVANTON: No. U520040009474Alel Human Polynucleotides and Polypeptides Enco CURRENT APPLICATION NUMBER: U5/09/864,408A
CURRENT FILING DATE: 2001-05-24
PRIOR PELLOR DATE: 2000-05-24
PRIOR PILING DATE: 2000-05-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zuker, Charles S.

Adler, Jon Elliot
APPLICANT: Adler, Jon Elliot
APPLICANT: Mueller, Ken
APPLICANT: Mueller, Ken
APPLICANT: Hoon, Mark
APPLICANT: The Regents of the United States of America
APPLICANT: The Regents of the United States of America
APPLICANT: The Regents of the Secretary of the
APPLICANT: The Regented by the Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: SF a No. US20020051997Alel Family of Taste Receptors
FILE REFERENCE: 02307E-098000US
CURRENT PAPLICATION NUMBER: US/09/393,634
CURRENT PLING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 92
SEQ ID NO 80
LENGTH: 68
LENGTH: 68
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                                                                                     FEATURE:
OTHER INFORMATION: MAP TO AC009079.4
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.54
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.77
OTHER INFORMATION: EXPRESSED IN BARROW, SIGNAL = 0.65
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.74
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.48
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.48
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.48
OTHER INFORMATION: SMISSPROT HIT: P56315, EVALUE 2.00e+00
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100.0%; Score 19; DB 9; Length 68;
Best Local Similarity 100.0%; Fred. No. 9.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: human GR24-09-393-634-80
      LENGTH: 60
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
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                                                                                                                               FEATURE:
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.81
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.91
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.91
OTHER INFORMATION: EXPRESSED IN BALL SIGNAL = 0.72
OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 0.72
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.71
OTHER INFORMATION: STRUCTURE SIGNAL = 0.71
US-09-864-761-45716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 19; DB 9; Length 69; 100.0%; Pred. No. 9.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                      Length 69;
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1 SEQ ID NO 45716 LENGTH: 69
                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 19; DB 9; I
100.0%; Pred. No. 9.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: IXEDA, MAGATO
APPLICANT: OZAKI, AKTO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPERRNCE: 249-125
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR APPLICATION NUMBER: UP 00/159162
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SEQ ID NO 5596
LENGTH: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5596, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , ORGANISM: Corynebacterium glutamicum
US-09-738-626-5596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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ANDO, SEIKO
HAYASHI, MIKIRO
OCHIAI, KEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
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                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 100.
Matches 4; Conservative
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                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 VAEF 4
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ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
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Sequence 4516-Application U8/09864761

PREMENT INCOMENDATION: Application U8/09864761

PREMENT INCOMENDATION: Application U8/09864761

APPLICANT: Rank Sharron G.
APPLICANT: Rank Sharron G.
APPLICANT: Rank Sharron G.
APPLICANT: Rank Sharron G.
APPLICANT: General David K.
APPLICANT: ADDITION GENERAL US GO 180, 1312

PRIOR APPLICANT: ON NUMBER: US GO 120, 456

PRIOR APPLICANT: ON NUMBER: PT (1001, 0066)

PRIOR APPLICANT: ON NUMBER: PT (1001, 0066)

PRIOR APPLICANT: ON NUMBER: PT (1001, 0066)

PRIOR APPLICANT: ON UMBER: PT (1001, 0066)

PRIOR APPLICANT: NUMBER: PT (1001, 0066)

PRIOR A
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                                                                                                                                                                                                                                                                                                                                                   Length 68;
                                                                                                                                                                                                                                                                                                                                                100.0%; Score 19; DB 14; 100.0%; Pred. No. 9.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
  CURRENT FILING DATE: 2003-03-07
PRIOR APPLICATION NUMBER: US/09/393,634
PRIOR FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 92
SEGTWARE: Patentin Ver. 2.1
SEQ ID NO 80
LENGTH: 68
                                                                                                                                                                                                                                                           OTHER INFORMATION: human GR24
3-10-383-982-80
                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 100.
                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VAEF 4
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-09-864-761-45716
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Sequence 30348, Application US/10029386
| Publication No. US20030194704A1
| GENERAL INFORMATION:
| APPLICANT: Penn, Sharron G. | APPLICANT: Penn, Sharron G. | APPLICANT: Hanzel, David K. | APPLICANT: Hanzel, David K. | TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GE TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GE TITLE OF INVENTION: EXPRESSION ANALYSIS TWO | FILE REFERENCE: AEOMICA-X-2
Sequence 274981, Application US/10424599

Sequence 274981, Application US/10424599

Fublication No. US2004003172A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: La Rose Thomas J

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

LENGTH: 71
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Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
100.0%; Score 19; DB 12; Length 71;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_24978C.1.pep
US-10-424-599-202605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Clone ID: PAT_MRT3847_90329C.1.pep
US-10-424-599-274981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (1)..(71)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Glycine max
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US-10-424-599-274981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: unsure
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 48
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Publication No. US20030194704A1
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: HAnzel, David R.
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT APPLICATION DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTMARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 28645
LENGTH: 70
                                                                                                                      APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE APPLICANTON NUMBER: US/10/424,599
CURRENT APPLICANTON NUMBER: 2003-04-28
SEQ ID NOS: 285684
SEQ ID NOS: 285684
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100.0%; Score 19; DB 14; Length 70;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 8.8

OTHER INFORMATION: EXPRESSED IN BONE WARROW, SIGNAL = 9.3

OTHER INFORMATION: EXPRESSED IN FLACENTA, SIGNAL = 5.8

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5.7

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 5.7

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 5.7

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 8.7

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 8.7

OTHER INFORMATION: SWISSPROT HIT: P78716, EVALUE 3.00e-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Clone ID: PAT_MRT3847_138417C.1.pep-10-424-599-185385
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Publication No. US20040031072A1
GENERAL INFORMATION:
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Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: La Rosa Thomas J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 VAEF 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VAEF 4
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3-10-424-599-202605
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-10-029-386-28645
                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
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CITY: ARLINGTON

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: US.A.

ZIP: 2201-474

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IEM PC Compatible

COMPUTER: IEM PC Compatible

COMPUTER: IEM PC Compatible

OMPUTER: IEM PC Compatible

CURRENT APPLICATION NUMBER: US/10/214,188

FILING DATE: 13-AUG-1997

ATTORNEY/AGENT INFORMATION:

NAME: WILSON, MARY J.

REGISTRATION NUMBER: 32,955

REFERENCE/ACTON INFORMATION:

TELECOMMUNICATION INVERREY: 620-22

TELEPHONE: (703) 816-4000

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 19; DB 14; Length 74; Best Local Similarity 100.0%; Pred. No. 9.9e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                              HIJMANS, ELEANORE M.
TITLE OF INVENTION: TRANSCRIPTION FACTOR E2F-5
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gequence 9071, Application US/10156761

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIRAMA, UJUN
APPLICANT: ISHIRAMA, HINOSHI
APPLICANT: ASHIRAMA, HINOSHI
APPLICANT: APHRAZAMA, UNCENTION
APPLICANT: APARVOSHI
APPLICANT: ARAZAMIRA
ITILE OF INVENTION: NOVEL POLYNUCLEOTIDES
ITILE OF INVENTION: NOVEL POLYNUCLEOTIDES
ITILE OF INVENTION: NOVEL POLYNUCLEOTIDES
CURRENT FILING DATE: 2002-05-29
CURRENT FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 9071
LENGTH: 74
TYPE: PRI
                                                                                                                                                           ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: Linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-214-188-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGIH: 74 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 VAEF 4
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US-10-156-761-9071
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SEQUENCE 29320, Application US/10029386

SEQUENCE 29320, Application US/10029386

PUBLICARIN NO. US2030194704A1

GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Hankel, David K.
TILLS OF INVENTION: HUMAN GENONS-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR CFILE REFERENCE: ADDITION: HUMAN GENONS-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR CFILE REFERENCE: ADDITION NUMBER: US.10/029,386

CURRENT FILING DATE: 2001-12-20

NUMBER OF SEQ ID NOS: 34288

SOFTWARE: Annowax Sequence Listing Engine vers. 1.1

SEQ ID NO 29320

LENGTH: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 19; DB 14; Length 71; Best Local Similarity 100.0%; Pred. No. 9.5e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 19; DB 14; Length 72; Best Local Similarity 100.0%; Pred. No. 9.6e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                        OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.82 OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.1 OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.73 OTHER INFORMATION: EXPRESSED IN LING, SIGNAL = 6.2 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 6.2 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1 OTHER INFORMATION: SWISSPROT HIT: P21333, EVALUE 5.00e-22 S-10-029-386-30348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHER INFORMATION: MAP TO CHR2.1

CTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.98

CTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.99

CTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.6

CTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.4

OTHER INFORMATION: EXPRESSED IN BETAL LIVER, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.56

CTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.81

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.81

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.81
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILMS DATE: 2001.12-20
UNDABER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vere, 1.1
ENGTH: 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10, Application US/10214188
Publication No. US20030022260A1
GENERAL INFORMATION:
APPLICANT: LA THANGUE, NICHOLAS B.
                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 VAEF 63
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JS-10-214-188-10
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DOJACTAL DOS 253204, Application US/10424599

Sequence 253304, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: Encoa Thomas J

APPLICANT: About Yihua

APPLICANT: Covalic David K

APPLICANT: Covalic David K

APPLICANT: Covalic David K

APPLICANT: Covalic David K

APPLICANT: APPLICANT: About Yihua

APPLICANT: APPLICANT: Covalic David K

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(5323)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 253204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 211908, Application US/10424599
Sequence 211908, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
CENTRAL INFORMATION:
CENTRAL INFORMATION:
CONTRACT CAO YOUNG
APPLICANT:
CAO YOUNG
APPLICANT
CON NUMBER
TITLE OF INVENTION:
Plants and Uses Thereof for Plant Improvement
FILLING
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILLING
DATE:
CORRENT FILLING
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                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Clone ID: PAT_MRT3847_70669C.1.pep
US-10-424-599-253204
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US-10-424-599-211908
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NAME/FEX: unsure
NAME/FEX: unsure
OTHER INFORMATION: unsure at all Xaa locations
                     0; Mismatches
               4, Conservative
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ORGANISM: Glycine max
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ORGANISM: Glycine max
                                                                                                                                                                                                        12 VAEF 15
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                                                                                                              1 VAEF 4
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                                                                                                                                                                                                                                                                                                                                                       RESULT 54
US-10-424-599-253204
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LENGTH: 77
                     Matches
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Publication No. US20040031072A1
SENERAL INFORMATION:
SENERAL INFORMATION:
APPLICANT:
La Rosa Thomas J
APPLICANT:
APPLICANT:
Cao Yongwei
TITLE OF INVENTION:
Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION:
Files Reference:
Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION:
FILE REFERENCE:
Soy Nucleic Acid Molecules and Other Molecules
TITLE OF INVENTION:
FILE REFERENCE:
CURRENT APPLICATION NUMBER:
US/10/424,599
NUMBER OF SEQ ID NOS:
285684
IENGTH:
TENGTH:

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Publication No. US20040031072A1
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Each Vinus
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38 = 21(5322)B
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38 = 21(5322)B
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
ENGIN: 75
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                                                                                                                                              Query Match 100.0%; Score 19; DB 14; Length 74; Sest Local Similarity 100.0%; Pred. No. 9.9e+02; Matches 4; Conservative 0; Mismatches 0; Indels
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Pred. No. 1e+03;
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CTHER INFORMATION: Clone ID: PAT_MRT3847_78089C.1.pep
3-10-424-599-261424
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LOCATION: (1)..(75)
OOTHER INFORMATION: unsure at all Xaa locations
PEAFIURE:
ORGANISM: Streptomyces avermitilis -10-156-761-9071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
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ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                      36 VAEF 39
                                                                                                                                                                                                                                                                                                                                                 1 VAEF 4
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US-10-424-599-162039
US-10-424-599-162039
Sequence 162039, Application US/10424599
Sequence 162039, Application US/10424599
Sequence 162039, Application No. US20040031072A1
SEQUENCE TO US ROSA Thomas J
APPLICANT: APPLICANT: Cao Yongwal
APPLICANT: Cao Yongwal
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 18-21(5323)
FILE REFERENCE: 38-21(5323)
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 162039
LENGITH: 78

LENGITH
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Avalic David K
APPLICANT: Should Rules
APPLICANT: Should Rules
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE 3023-04-28
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
ERD UN 262701
LENGTH: 78
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100.0%; Score 19; DB 14; Length 77;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0: Indels
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                                                                                                                                                                                 ORGANISM: Homo sapiens
PEATURE:
CTHEN INFORMATION: MAP TO ACCO04186.1
OTHEN INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.76
OTHEN INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.5
OTHEN INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.5
OTHEN INFORMATION: SWISSFROT HIT: P14373, EVALUE 7.50e+00
US-10-029-386-32709
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CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 32709
LENGTH: 77
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Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 262701, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Glycine max
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US-10-424-599-262701
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18-10-029-386-32709
Sequence 22709, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: HANZEL, DAVID R.
APPLICANT: TUVENTION: EXPRESSION ANALYSIS TWO
FILE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
                                                                                                                                     Sequence 7493, Application US/10335977
Publication No. US20040052799A1
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: BOSCON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 19; DB 12; Length 77; 100.0%; Pred. No. 1e+03;
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PRICKENT APPLICATION DATA:

PRICK APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

ATOMNEY AGENT INFORMATION:

NAME: Mandragouras, Amy E.

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: 36,207

REFERENCE/DOCKET NUMBER: 36,207

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 72-7-400

TELEPHONE: (617) 72-7-414

INFORMATION FOR SEQ ID NO: 7493:

SEQUENCE CHARACTERISTICS:

LENGTH: 77 amino acids

TYPE: amino acids

TYPE: amino acid

TYPE: amino acid

TYPE: TYPE: TYPE: TPCCEIN

HYPOTHETICAL: YES

ORIGINAL YES

ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Massachusetts
COUNTRY: USA
ZII: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:
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LOCATION: (B) LOCATION 1...77
SEQUENCE DESCRIPTION: SEQ ID NO: 7493:
S-10-335-977-7493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 4; Conservative
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Query Match
Best Local Similarity 100.v
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Matches 4; Conservative
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US-10-367-980A-14
                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52 VARF 55
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US-10-078-090-125
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LENGTH: 84
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-10-424-599-216097
Sequence 216097, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Arou Yihua
APPLICANT: Cao Yongwin Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement TITLE OF INVENTION: 153223 B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 216097
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                                                                                                         100.0%; Score 19; DB 12; Length 78; 100.0%; Pred. No. 1e+03; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                            Sequence 368, Application US/10363616
Publication No. US20040044181A1
GENERAL INFORMATION:
APPLICANT: Hyeeq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFRENCE: 21272-113 (793)
CURRENT FILING DATE: US/10/363,616
CURRENT FILING DATE: 2003-03-03
PRIOR FILING DATE: 2000-09-01
NUMBER OF EQ ID NOS: 490
SEQ ID NO 368
LENGTH: 79
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TYPE: PRT
ORGANISM: Glycine max
PEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_79240C.1.pep
10-424-599-262701
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Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                         Query Match
Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity 100.
Matches 4; Conservative
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ORGANISM: Homo sapiens
-10-363-616-368
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ORGANISM: Glycine max
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5 VAEF 8
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                                                                                                                                                                                    1 VAEF 4
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-10-363-616-368
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35 VAEF 38

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APPLICANT: Leach, Martin D.
APPLICANT: Leach, Martin D.
APPLICANT: Elankete, Xichard A.
TITLE OF INVENTION: No. US20040009474Alel Human Polynucleotides and Polypeptides Encoc'
FILE REFERENCE: 21402-012
CURRENT APPLICATION UNMER: US/09/864,408A
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 60/206,690
PRIOR APPLICATION NUMBER: 60/206,690
NUMBER OF SEQ ID NOS: 9068
SOFTWARE: FREESEQ for Windows Version 4.0
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US-10-367-980A-14
| Sequence 14, Application US/10367980A
| Sequence 14, Application US/10367980A
| Publication No. US20030228592A1
| GENERAL INFORMATION:
| APPLICANT: St Vincent's Institute of Medical Research
| APPLICANT: Rogers, Suzanne D
| APPLICANT: Best, James D
| TITLE OF INVENTION: Human Facilitative Glucose Transport Protein GLUT8
| PILE REFERENCE: VS.AJH-IPP17928
| CURRENT FILING DATE: 2003-02-19
| PRIOR FILING DATE: 2003-02-19
| NUMBER OF SEQ ID NOS: 42
| SOFTWARE: Patentin version 3.2
| SEQ ID NO 14
| LENGTH: 82
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100.0%; Pred. No. 1.1e+03;
tive 0; Mismatches 0;
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US-09-864-408A-5282
Sequence 5282, Application US/09864408A
Publication No. US20040009474A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Salceda, Susana
APPLICANT: Macina, Roberto
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Gaps
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APPLICANT: Zyskind, Judith W.
APPLICANT: Zyskind, Judith W.
APPLICANT: Carr, Grant J.
APPLICANT: Carr, Grant J.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Rub Gantification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILER REFERENCE: ELITRA.011A
CURRENT FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/207, 727
PRIOR APPLICATION NUMBER: 60/207, 727
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/255, 625
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PELING DATE: 2000-12-22
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFITMED BASES 2001-02-16
SOFITMED BAS
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Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           ; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_24299C.1.pep
US-10-424-599-201853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.0%; Score 19; DB 12;
Matches 4; Conservative 0; Mismarrhr.
                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: unsure
NAME/KEY: unsure
OTHER INFORMATION: unsure at all Xaa locations
                                                           CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 201853
LENGTH: 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11224, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.
                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 VAEF 61
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APPLICANT: Karra, Kalpana APPLICANT: Cafferkey, Robert APPLICANT: Cafferkey, Robert APPLICANT: Cafferkey, Robert APPLICANT: Sun, Yongming APPLICANT: Liu, Chenghua TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and PRILE REPERENCE: DEX.0312
CURRENT APPLICATION NUMBER: 0502-02-14
PRIOR FILING DATE: 2002-02-14
PRIOR FILING DATE: 2001-02-15
NUMBER OF SEQ ID NOS: 210
SOFTWARE: Patentin version 3.1
SEQ ID NO 125
LENGTH: 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 155636, Application US/10424599
Sequence 155636, Application US/10424599
Eublication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: LA ROSA Thomas J
APPLICANT: Application David K
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILLE REPERENCE: 38 221(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 155636
LENGTH: 85
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Sequence 20183, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: LA Rosa Thomas J
APPLICANT: Rovalic David K
APPLICANT: Anou Yihua
APPLICANT: Cao Yongwei
TITIE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223) B
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S-10-424-599-155636
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100.0%; Pred. No. 1.1e+03;
ive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapien
S-10-078-090-125
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1 VAEF 4
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US-10-282-122A-58530
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APPLICANT: Zamudo, Carlos
APPLICANT: Zamudo, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Cheryl
APPLICANT: Obleson, Kari
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Forsyth, R.
APPLICANT: Forsyth, R.
APPLICANT: Forsyth, R.
APPLICANT: Forsyth, R.
APPLICANT: M. H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA, 2003-02-20
FILE REFERENCE: ELITRA, 2003-02-20
FURRENT FILING DATE: 2003-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
                                                                                                                                                                                                                                                              APPLICANT: Trawlex, John D.
APPLICANT: Grant J.
APPLICANT: Tawanco, Robert T.
APPLICANT: Xu, H. Howard
APPLICANT: Xu, H. Howard
APPLICANT: Xu, H. Howard
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
TITLE OF INVENTION: Prokaryotes
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR PELICATION NUMBER: 60/191,078
PRIOR PELICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PELICATION NUMBER: 60/207,727
PRIOR PELICATION NUMBER: 60/253,625
PRIOR PELICATION NUMBER: 60/253,625
PRIOR PELICATION NUMBER: 60/253,625
PRIOR PELICATION NUMBER: 60/253,931
PRIOR PELING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-12-22
PRIOR PELING DATE: 2001-12-32
PRIOR PELING DATE: 2001-13-34
PRIOR PELING DATE: 2001-13-34
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Sequence 11245, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Zyskind, Judith W.
APPLICANT: Taykind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Yammanoto, Robert T.
APPLICANT: Yammanoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 58489, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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ORGANISM: Haemophilus influenzae
-09-815-242-11245
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Matches 4; Conservative
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Gaps ô

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Mismatches
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GENERAL INFORMATION: APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
      ö
                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyakind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
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; ORGANISM: Proteus mirabilis
US-10-282-122A-68774
   4; Conservative
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US-10-424-599-180307
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US-10-282-122A-68774
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PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 76614
SOFTWARE: Patentin version 3.1
LENGTH: 89
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Publication No. US20040029129A1
GENERAL INFORMATION
APPLICANT: Mang, Liangsu
APPLICANT: Malone, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Cheryl
APPLICANT: Wall, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Grant
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ORGANISM: Haemophilus influenzae
'S-10-282-122A-58530
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ORGANISM: Pasteurella multocida
S-10-282-122A-66960
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Best Local Similarity 100.
Matches 4; Conservative
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S-10-282-122A-66960
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APPLICANT: Carr, Garnic
APPLICANT: Yammoto, Robert
APPLICANT: Yammoto, Robert
APPLICANT: Yammoto, Robert
APPLICANT: Yammoto, Robert
APPLICANT: Yau, H.
ITLE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PLING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/200,335
PRIOR APPLICATION NUMBER: 60/200,347
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 20
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Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0;
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NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 245830
LENGTH: 90
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APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVERTION: SOY Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVERTION: SOY Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21 (51223) B
CURRENT FILING DATE: 2003-44-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 180307
LENGTH: 89
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APPLICANT: La Rosa Thomas J
APPLICANT: Low Vinta
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION (53223)8
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
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Suguence 360, Application US/10097111
Sublication No. US20030138771A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
THE OF INVENTION: DELLETIER, JERRY
APPLICANT: GROS, PHILLIPPE
APPLICANT: DUBOW, MICHAEL
APPLICANT: DUBOW, MICHAEL
APPLICANT: DUBOW, MICHAEL
APPLICANT: DUBOW, MICHAEL
APPLICANT: DUBOR, MICHAEL
APPLICANTION: UNMERR: US/10/097,111
CURRENT FILING DATE: 2002-07-24
PRIOR FILING DATE: 2002-09-29
PRIOR PILING DATE: 1999-09-30
PRIOR PILING DATE: 1999-09-30
NUMBER OF SEQ ID NOS: 552
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 360
TANDEL DATE
BENEVIE SECONDER DATE
SEQ ID NO 360
TANDEL DATE
SEQ ID NO 360
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SEQ ID NO 360
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Publication No. US20040031072A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 4; Conservative
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Matches 4; Conservative
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ORGANISM: Glycine max
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TYPE: PRT
ORGANISM: Glycine max
PREATURE:
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US-10-424-599-245830
                                                                                                             100.0%; Score 19; DB 12;
100.0%; Pred. No. 1.2e+03;
tive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 4; Conservative
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                                                                                               May 24, 2004, 17:31:37 ; Search time 51.7857 Seconds (without alignments) 27.280 Million cell updates/sec
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4: geneseqp2001s:*
5: geneseqp2001s:*
6: geneseqp2003s:*
7: geneseqp2003bs:*
8: geneseqp2003bs:*
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Maximum Match 100%
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Aag39960
Abu40766
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Abb27964
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Abb61471
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Aag46908
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ABU29329
AAM39361
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AAUS6508
                                               AAG91382
AAE30494
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## ALIGNMENTS

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S chrysomallus actinomycin biosynthase protein acmC fragment #9.
AAM47151 standard; peptide; 6 AA.
                                                                                                                (first entry)
                                                                                                                12-FEB-2002
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Modular enzyme system; cyclic gene synthesis; repetitive coding sequence; antibiotic; non-ribosomal peptide synthetase; NRPS; PKS; polyketide synthase; actinomycin biosynthase.

Streptomyces chrysomallus Synthetic.

WO200181564-A2

01-NOV-2001.

25~APR-2001; 2001WO-DE001578.

26-APR-2000; 2000DE-01021267.

(ACTI-) ACTINODRUG PHARM GMBH

Schauwecker F;

2002-049276/06. N-PSDB; ABA03345

Preparing DNA encoding modular protein for e.g. producing new enzymes for synthesis of polyketide antibiotics, comprises cyclic integration of fragments into a vector.

Example 3; Page 54; 83pp; German.

The present invention relates to the preparation of DNA, in a circular vector, that encodes one or more segments of a modular polypeptide. DNA or DNA libraries produced this way are used to produce modular polypeptides, particularly enzymes, which can be used to act on

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substrates to produce compounds for therapeutic testing. Enzymes of particular interest are those involved in non-ribosomal peptide synthesis or polyketide synthesis, and compounds for testing are particularly macrolide antibiotics, including penicillins, vancomycins or erythromycins, but may also be modular receptors. The present sequence is a fragment of a protein encoded by a Streptomyces chrysomallus actinomycin blosynthesis gene which was used in a plasmid in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The specification describes a beta-secretase enzyme. The enzyme cleaves beta-amyloid precursor protein to produce beta-amyloid peptide. This enzyme is therefore implicated in the production of amyloid plague components which accumulate in the brains of individuals afflicted with Alzheimer's disease. Inhibitors of beta-secretase are administered to a mammalian subject e.g. with Alzheimer's disease or Alzheimer's disease. like pathology to test if they maintain or improve cognitive ability or reduce the plaque burden. The compounds are used for the treatment of amyloidogenic diseases e.g. Alzheimer's disease. The present sequence represents an inhibitor of beta-secretase enzyme
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Beta-secretass, beta-amyloid precursor protein, beta-amyloid peptide, amyloid plaque component, Alzheimer's disease; amyloidogenic disease;
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Tung J, Wang S, Mcconlogue L;
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/note= "hydroxyethylene"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A beta-secretase inhibitor peptide.
                                                                                                                                                                                                                                                                                                                                                                            AAB07871 standard; peptide; 7 AA.
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99US-0139172P.
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                                                                                                                                                          Sequence 6 AA;
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Modified-site
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15-JUN-1999;
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The invention relates to screening, diagnosis or prognosis of Vascular Dementia (VD) in a subject comprising analysing body fluid from the subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of features containing at least one chosen feature whose relative abundance or predicts the onset or course of VD, especially detecting in a sample of carebrospinal fluid (CSF) from the subject one of 223 VD-associated protein isoforms (VPIS) (ABB5S801-ABB56295) as fully defined in the specification. Detecting VD-associated features and VPI is useful for the screening, diagnosis or prognosis of VD, for determining the stage or severity of VD, for identifying a subject at risk of VD or for monitoring the effect of therapy administered to a subject having VD. Nucleic acids creatment of VD and for gene therapy
                                                                                                                                                                                                                               VD; VD-associated protein isoform; VPI; screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Screening, diagnosis or prognosis of vascular dementia (VD), useful determining stage of VD and monitoring the effect of VD therapy, comprises analyzing body fluid by 2-dimensional electrophoresis for features correlated with VD.
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                                                                                                                                                                                                Vascular dementia-associated protein isoform (VPI) 441.
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                                                                                                                                                                                                                                                          diagnosis; prognosis; gene therapy
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                                                                               ABB56241 standard; peptide; 8 AA.
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24-NOV-2000; 2000GB-00028734.
28-NOV-2000; 2000US-00724391.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Purified beta-secretase protein used in assays to discover inhibitors which can be used for the treatment of amyloidogenic diseases e.g. Alzheimer's disease.
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                                       DB 3; Length 7;
1.4e+06;
hes 0; Indels
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Pung J, Wang S, Mcconlogue L;
                                     95.0%; Score 19; DB 100.0%; Pred. No. 1.4 ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                             A beta-secretase inhibitor peptide.
                                                                                                                                                                                                                                                        AAB07872 standard; peptide; 8 AA.
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99US-0139172P.
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Sequence 7 AA;
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15-JUN-1999;
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WO200162785-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schizophrenia-associated protein isoform; SPI; SPI-206; SPI-218; SPI-240; neuroleptic; gene therapy; cerebrospinal fluid; serum; plasma.
                                                                                                                                                                                                                                                                                                           Novel nucleic acid encoding a protein associated with bipolar affective disorder, which is used for diagnosis, prophylaxis and therapy of neuropsychiatric disorders, such as bipolar affective disorder.
                                 Human; depression associated protein isoform; tryptic digest peptide; DPI; cerebrospinal fluid; CSF; BAD; bipolar affective disorder; neuropsychiatric disorder; bipolar mood disorder; neuroleptic; maniac-depressive illness; schizoaffective disorder.
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100.0%; Pred. No. 1.4e+06;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                             Disclosure, Page 37; 153pp; English
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            DPI tryptic digest peptide #317.
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08-DEC-2000; 2000GB-00030050.
12-DEC-2000; 2000US-0254830P.
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New schizophrenia associated protein isoforms and encoding nucleic acid molecules, useful for treatment, diagnosis and prognosis of schizophrenia and screening for potential drugs for treatment and new drug targets.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence represents a schizophrenia-associated protein isoform (SPI). These protein isoforms, e.g. SPI-206, SPI-238 and SPI-240 are detectable in cerebrospinal fluid, serum or plasma and are useful markers of schizophrenia. The sequences can be used for treatment and diagnosis of schizophrenia, screening, prognosis, monitoring the results of therapy, identifying patients most likely to respond to a particular therapy and identification of new targets for drug treatment. SPI DNA is useful as a nucleic acid probe to detect the presence of nucleic acids or SPIs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, Bipolar Affective Disorder, BAD, Depression-Associated feature, DF, Depression-Associated protein isoform; DF, Cerebor-epinal fluid, CSF, antidepressant, antimanic, nootropic, tranquiliser, neuroleptic, attention deficient disorder, schizoaffective disorder;
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                                                                                                                                                                                                                                                                   Tyson
                                                                                                                                                                                                                                                                   Terrett JA,
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                                                                                                                                                                                                                                                                   Parekh RB, Rohlff C,
                                                                                                                                                                                                          (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
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                                                                                                                24-FEB-2000; 2000GB-0000415.
28-DEC-2000; 2000US-00750395.
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08-DEC-2000; 2000GB-00030050.
12-DEC-2000; 2000US-0254830P.
                                                         23-FEB-2001; 2001WO-GB000792.
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                                                                                                                                                                                                                                                                   Herath HMAC,
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30-AUG-2001
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WPI; 2001-582081/65.

Diagnosing and monitoring Schizophrenia by detecting the presence of Schizophrenia Associated Features and Schizophrenia Associated Protein Isoforms in samples of cerebrospinal fluid. 6; Page 36; 160pp; English WPI; 2001-502868/55. Local Similarity 2 VAEF 5 2 VAEF 5 Schizophrenia; WO200163293-A2. Sequence 8 AA; Homo sapiens 24-OCT-2001 30-AUG-2001. AAU15458; Query Match Claim Best Loc Matches ESULT 8 AU15458

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The invention relates to methods and compositions for screening, diagnosis and prognosis of Schizophrenia. The method involves detecting the presence of Schizophrenia (SCH) Associated Features (SFS) and SCH. Associated Protein losforms (SFIS) in samples, e.g. by electrophoresis, immunoassay or hybridisation assay, for diagnosing and monitoring SCH, studying the effectiveness of treatments and for identifying potential therapeutic agents. The method is used for (1) screening or diagnosis of SCH and the relative abundance of at least 1 chosen feature correlates with the presence or absence of SCH and the relative abundance of at least 1 chosen feature which correlates with the severity of SCH. The expression and activity of the SFS, SFIS and related molecules (e.g. expression and activity of the SFs, SFIS and related molecules (e.g. escondary messengers) are studied to diagnose SCH, monitor the progress of the disorder and the effectiveness of treatment and as targets to identify and produce potential therapeutic agents for the treatment of SCH. The paucity of detectable neuralgic defects distinguishes neuropsychatric disorders such as SCH from neurological disorders, where manifestations of anatomical and biochemical changes have been identified in many cases. Consequently the identification and characterisation of cellular and/or molecular causative defects and neuropsychatic or improved treatment of neuropsychiatric disorders and neuropsychiatric disorder and neuropsychi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAGE 3 105-113; cytotoxic T; CTL; epitope; helper T; HTL; cell; lymphocyte; antigens; treatment; disease prevention; tumours; cancer;
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100.0%; Pred. No. 1.4e+06;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MAGE 3 105-113 cytotoxic T lymphocyte epitope.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR78909 standard; peptide; 9 AA.
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(first entry)
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27-MAR-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a preparation comprising an isolated Bipolar Affected Disorder (BAD)-Associated Protein Isoform (DPIs). The DPI's are used to screen, dispance or prognose of BAD or unipolar depression, identify a determine the stage or severity of BAD or unipolar depression, identify a subject at risk of developing BAD or unipolar depression, or monitor the effect of therapy in a subject. They are also used to screen for or identify agents that interact with a DPI. These agents, antibodies against the DPIs, and mucleic acids encoding the DPIs are used to treat or prevent BAD or unipolar depression. Diseases that can be treated are attention deficient disorder, a schizoaffective disorder, a bipolar or a unipolar affective disorder. The DPIs are used in proteomics. The DPIs are used in proteomics. The BAD or unipolar depression overcomes the problems of using gene expression analysis, such as not being able to obtain central nervous grygen present sequence is a DIP increased in the CSF (cerebro-spinal fluid) of subjects having BAD
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                                                             Preparation for diagnosing or treating bipolar affected disorder (BAD) or unipolar depression, or for screening for modulators, comprises a BAD-associated protein isoform.
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                                                                                                                                                                                   Claim 8; Page 37; 163pp; English.
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28-DEC-2000; 2000US-00750395.
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Compsn. inducing cytotoxic T lymphocyte response to pref. viral, bacterial, parasitic or tumour antigens - useful in the treatment and prevention of diseases associated with the antigen e.g. hepatitis B.

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A compsn. which induces a cytotoxic T lymphocyte (CTL) response to

Example 13; Page 71; 109pp; English

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The present sequence represents a beta-amyloid precursor protein (APP) inhibitor peptide. This peptide inhibits binding between APP and BACE (beta site APP cleaving enzyme). The specification describes a crystallized complex of BACE and the present APP inhibitor. Protein coordinate data for BACE is given in the specification. The APP inhibitor peptide is based on the P10 to P4' APP751 Swedish family mutation. The crystallized complex is used for identifying an agent that interacts with an active site of BACE or an active site of an APP binding protein or peptide. The agents are useful in the treatment and/or prevention of Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Crystallized complex of beta-site amyloid precursor protein (APP) cleaving enzyme (BACB) and APP inhibitor peptide useful for identifying agents that interact with active site of BACB or active site of APP binding protein or peptide.
human MAGE antigen (Ag) in a mammal comprises, a MAGE CTL Ag response inducing peptide (i.e. AAR78904 to AAR78917) and a lipid conjugated helper T cell inducing peptide. The compsn. is useful in the treatment and prevention of MAGE tumour Ag associated diseases, e.g. melanoma cancers. (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Beta-amyloid precursor protein, APP, APP inhibitor peptide, BACE, beta site APP cleaving enzyme; protein coordinate data, APP751; Swedish family mutation, Alzheimer's disease.
                                                                                                                                      95.0%; Score 19; DB 2; Length 9; larity 100.0%; Pred. No. 1.4e+06; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   A beta-amyloid precursor protein (APP) inhibitor peptide.
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/note= "statine"
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Misc-difference
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                                                                                                        Sequence 9 AA;
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Homo sapiens.
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Somers WS;
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ABB77871
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Stahl ML;

Akopian TN, Bard J,

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                                                                                                                                                                                                                                                                                 Beta-secretase, enzyme, cleavage site, amyloid protein precursor, APP, aspartyl protease, neuroprotective, nootropic, beta-secretase inhibitor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel substrates for human aspartyl protease useful for identifying modulators of beta secretase activity of aspartyl protease for treating
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    DB 5,
1.4e+06;
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 Length 9;
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   DB 5;
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95.0%; Score 19; DB 100.0%; Pred. No. 1.4
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                                                                                                                                                                 ABB06593 standard; peptide; 10 AA.
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12-MAR-2001; 2001US-0275251P.
                                                                                                                                                                                                                            (first entry)
                               Conservative
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Alzheimer's disease.
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                                                           2 VAEF
                                                                                                                                                                                                                          31-MAY-2002
                                                                                                                                                                                                                                                                                                                                               sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                        24-JAN-2002,
                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                               ABB06593;
    Query Match
                                                                                                                                      RESULT 11
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Sequence 9 AA;

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15-NOV-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                 Koelsch G,
                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-619088/66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 VAEF 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12 AA;
                                                                                                                                                                                           WO200253594-A2.
                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                           11-JUL-2002
                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                 Tang JJN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADD35467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disease
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   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         쉱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes an isolated peptide (I) comprising a sequence of at least four amino acids, where the peptide is a substrate for conducting aspartyl protease assays. (I) has neuroprotective and notropic activities, and can be used as an inhibitor of beta-secretase activity. A beta-secretase modulator from the present invention can be used for inhibiting beta-secretase activity in vivo, and in the manufacture of a medicament for the treatment of Alzheimer's disease. Pharmaceutical compositions from the present invention can be used for treating a disease or condition characterised by an abnormal beta-corretase activity. (I) is useful for identifying agents that modulate the activity of human hap2 aspartyl protease (Hu-Asp2). (I) is useful as a core structure to construct derivatives. ABL49914 to ABL49925 and ABB06409 to ABB06593 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                         Beta-secretase; enzyme; cleavage site; amyloid protein precursor; APP; aspartyl protease; neuroprotective; nootropic; beta-secretase inhibitor; Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel substrates for human aspartyl protease useful for identifying modulators of beta secretase activity of aspartyl protease for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bienkowski MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95.0%; Score 19; DB 5; L. 100.0%; Pred. No. 1.5e+02; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Emmons TL,
                                                                                                                                                              Beta-secretase related peptide SEQ ID NO:196.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 188; 188pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tomasselli AG, Gurney ME,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABG78404 standard; peptide; 12 AA.
                                                                 ABB06592 standard; peptide; 12 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PHAA ) PHARMACIA & UPJOHN CO
                                                                                                                                                                                                                                                                                                                                                                                                     19-JUL-2000; 2000US-0219795P.
12-MAR-2001; 2001US-0275251P.
                                                                                                                                                                                                                                                                                                                                                                       19-JUL-2001; 2001WO-US023035.
                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-216995/27
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                                                                                                                                                                                                                                                                                                          WO200206306-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Heinrikson RL;
                                                                                                                                                                                                                                                             Homo sapiens.
Synthetic.
                                                                                                                                31-MAY-2002
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ABG78404
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ABG78404;

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The invention relates to an inhibitor of catalytically active memapsin 2 (an aspartic protease which can cleave at beta secretase sites), which binds to the active site of memapsin 2 defined by the presence of two catalytic aspartic residues and substrate binding cleft. Also included is a method of determination of the substrate side-chain preference in memapsin 2 sub-sites comprising: (a) reacting a mixture of memapsin 2 substrates with memapsin 2, and determining the sub-site preference of mixture of memapsin 2 substrates; or (b) preparing a combinatorial inhary of memapsin 2 inhibitors containing a base sequence taken from OM99-2 (Glu-Val-Asn-Leu-Ala-Ala-Glu-phe), probing the library of inhibitors with memapsin 2 inhibitors containing a base sequence taken from OM99-2 (Glu-Val-Asn-Leu-Ala-Ala-Glu-phe), probing the library of inhibitors with memapsin 2 and detecting the bound memapsin 2 with an antibody raised to memapsin 2 and an alkaline phosphatase conjugated secondary antibody. The inhibitors may be used in the manufacture of a medicament for the treatment of Alaheimer's disease since memapsin 2 may be involved in the cleavage of amyloid precursor protein (APP), and for determining the substrate side-chain preference in memapsin 2 sub-sites.

The present sequence represents a subsite variant peptide used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New memapsin 2 activity inhibitor useful in treatment of e.g. Alzheimer's
                                                  Human, memapsin 2, aspartic protease, beta secretase, degenerative disease, Alzheiner's disease, amyloid precursor protein, APP, neuroprotective, nootropic, inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Memapsin 2 substrate specificity determination peptide #10.
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100.0%; Pred. No. 1.5e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (OKLA-) OKLAHOMA MEDICAL RES FOUND. (UNII ) UNIV ILLINOIS FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADD35467 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 5; Page 51; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ghosh AK;
                                                                                                                                                                                                    substrate side-chain preference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-DEC-2001; 2001WO-US050826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-DEC-2000; 2000US-0258705P.
14-MAR-2001; 2001US-0275756P.
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ADD35467
ID ADD354
XX
AC ADD354
DT 15-JAN
XX
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Power M;

us-09-594-978a-3.rag

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Glutamic acid; glutamine; vaccine; major histocompatibility complex; MHC; immunomodulator; antiallergic; endocrine; neuroprotectant; virucidal; bactericidal; antiparasitic; fungicidal; cytostatic; medicine; prbarmaceutical; immune disorder; immune deficiency; autoimmune; hypersensitivity; allergy; graft rejection; infection; hormonal disorder; central nervous system disease; cancer; melanoma; anti-melanoma vaccine; human immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The specification describes a beta-secretase enzyme. The enzyme cleaves beta-amyloid precursor protein to produce beta-amyloid peptide. This enzyme is therefore implicated in the production of amyloid plaque components which accumulate in the brains of individuals afflicted with Alzhaimer's disease. Inhibitors of beta-secretase are administered to a mammalian subject e.g. with Alzhaimer's disease or Alzhaimer's disease. It ke pathology to test if they maintain or improve cognitive ability or reduce the plaque burden. The compounds are used for the treatment of amyloidogenic diseases e.g. Alzhaimer's disease. The present sequence represents an inhibitor of beta-secretase enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           specification describes a beta-secretase enzyme. The enzyme cleaves
                                                                                                                                                                                                                                                                                                                                                                                                               Purified beta-secretase protein used in assays to discover inhibitors which can be used for the treatment of amyloidogenic diseases e.g. Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95.0%; Score 19; DB 3; Length 13; 100.0%; Pred. No. 1.6e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                          Doane MT, Frigon N, John V,
Tung J, Wang S, Mcconlogue L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vaccine related MHC ligand peptide SEQ ID NO:379,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 33; Page 24; 121pp; English.
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                                                                                                                                                                                                                                                                                                                                   Tung J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%;
watches 4; Conservative 0
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                                                                                                                                                                 2000WO-US003819.
                                                                                                                                                                                                       99US-0119571P.
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                                                                                                                                                                                                                                                                      (ELAN-) ELAN PHARM INC
                                                                                                                                                                                                                                                                                                                 Basi G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium leprae.
                                                                                                                                                                                                                                                                                                                                   Tatsuno G,
                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-533011/48.
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                                                                                WO200047618-A2
                                                                                                                                                                 10-FEB-2000;
                                                                                                                                                                                                       10-FEB-1999;
15-JUN-1999;
                                                                                                                                                                                                                                                                                                                 Anderson JP,
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                                                                                                                           17-AUG-2000
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inhibitor.
                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAM99276;
                                                                                                                                                                                                                                                                                                                                     Sinha S,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention comprises a crystallised recombinant protein that is involved in general metabolism, the recombinant protein may be from staphylococcus arrens, Streptococcus puenoniae, Helicobacter pylori, Eschapition coli or Pseudomonas aeruginosa. The crystallised recombinant protein of the invention is useful in the prevention (vaccine) or treatment of a disease or disorder caused by S. pneumoniae, H. pylori, S. coli or P. aeruginosa. The present amino acid sequence was used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vedadi M, Alam MZ, Awrey D, Beattie B;
, Houston S, Mansoury K, Necakov S, Nethery K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New crystallized recombinant polypeptides from Staphylococcus aureus, Streptococcus pneumoniae, Helicobacter pylori or Pseudomonas aeruginosa involved in general metabolism, useful as drug targets for pathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide; amyloid plaque component; Alzheimer's disease; amyloidogenic disease;
                                        crystallised recombinant protein, metabolism; Staphylococcus aureus; Streptococcus pneumoniae; Helicobacter pylori; Escherichia coli; Pseudomonas aeruginosa; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Wrezel O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                on S, Mansc
Vallee F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure, SEQ ID NO 66; 277pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A beta-secretase inhibitor peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB07889 standard; peptide; 13 AA.
  Escherichia coli DnaK peptide #3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Edwards A, Dharamsi A, Vedadi
Canadien V, Domagala M, Houst.
Ng I, Pinder B, Sheldrick B,
                                                                                                                                                                                                                                                                                        21-NOV-2001; 2001US-0332160P.
27-NOV-2001; 2001US-0333661P.
27-NOV-2001; 2001US-0333665P.
18-DEC-2001; 2001US-0341554P.
19-DEC-2001; 2001US-0341554P.
20-DEC-2001; 2001US-0342542P.
21-DEC-2001; 2001US-0342542P.
28-DEC-2001; 2001US-0343500P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-DEC-2001; 2001US-0343679P
                                                                                                                                                                                                                                                       21-NOV-2002; 2002WO-CA001768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AFFI-) AFFINIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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Best Local Similarity
Matches 4; Conserv
                                                                                                                           Escherichia coli.
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                                                                                                                                                                      WO2003044185-A2
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AAB07889;

15 RESULT 15 AAB07889

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Gaps ö

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10-FEB-2000; 2000WO-US003819
  23-MAR-2000; 2000FR-00003711
                                                                                                                          Query Match
Best Local Similarity 100.
                     WPI; 2001-611470/70
               Klinguer-Hamour C,
                                                                                                                                           2 VAEF 5
                                                                                                                                                 4 VAEF 7
                                                                                                                       Sequence 13 AA;
                                                                                                                                                                                                               WO200047618-A2.
                                                                                                                                                                                                                                  10-FEB-1999;
15-JUN-1999;
                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                        AAB07888;
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Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic; eurorpordective; antimicrobial; gene therapy; vaccine; amylase; cancer; amyloid protein; angiopoletin, apoptosis related protein; cadherin; cyclih; polymerase; oncogene; histone; kinase; colony stimulating factor; complement related protein; cytochrome; kinase; cytokine; interferon; interleukin; G-protein coupled receptor; thiossie; cytokine; interferon; interleukin; d-protein coupled receptor; thiossierase; inflammation; multifactorial disease; autoimmune disease; infection;
                                                                                                                                                                                                                                                                                                                        The specification describes a beta-secretase enzyme. The enzyme cleaves beta-amyloid precursor protein to produce beta-amyloid peptide. This enzyme is therefore implicated in the production of amyloid plaque components which accumulate in the brains of individuals afflicted with Alzheimer's disease. Inhibitors of beta-secretase are administered to a mammalian subject e.g. with Alzheimer's disease or Alzheimer's disease. Is they maintain or improve cognitive ability or reduce the plaque burden. The compounds are used for the treatment of amyloidogenic disease e.g. Alzheimer's disease. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
                                                                                                                                                                    Purified beta-secretase protein used in assays to discover inhibitors which can be used for the treatment of amyloidogenic diseases e.g. Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    represents a peptide derived from beta-amyloid precursor protein
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                                                 Power M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.0%; Score 19; DB 3; Length 14; 100.0%; Pred. No. 1.8e+02; ive 0; Mismatches 0; Indels
                                                 Doane MT, Frigon N, John V,
Tung J, Wang S, Mcconlogue L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human peptide #735 encoded by a SNP oligonucleotide.
                                                                                                                                                                                                                                                                                  Disclosure; Page 12; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM97460 standard; peptide; 14 AA.
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27-DEC-2000; 2000US-00173419.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nervous system disease
(ELAN-) ELAN PHARM INC
                                                 Basi G,
                                              Anderson JP, Basi G,
Sinha S, Tatsuno G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-465210/50.
                                                                                                                           WPI; 2000-533011/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200147944-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a pharmaceutical compound (I) that
contains an N-terminal glutamic acid (Glu) or glutamine (Gln) residue in
the form of an addition salt with a strong, physiologically acceptable
acid (II). Also described are: (a) a pharmaceutical composition
containing at least one (I); (b) a vaccine containing at least one (I)
where this is a major histocompatibility complex (Marc) ligand (Ia); (c) a
method for in vitro diagnosis of diseases associated with the presence of
(Ia); (d) a kit for method (c) that includes a (Ia); and (e) a process
(Ia); (d) a kit for method (c) that includes a (Ia); and (e) a process
(Ia); (d) a kit for method (c) that includes a (Ia); and (e) a process
(Ia); (d) a kit for method (c) that includes a (Ia); and (e) a process
(Ia); (d) a kit for method (c) that includes a (Ia); and (e) a process
(Ia); (d) a kit for method (c) that includes a (Ia); and (e) a process
(Ia); (d) a kit for method (c) that includes a (Ia); and (e) a process
(Ia); (d) a kit for method (c) that includes a (Ia); in vaccines for reatment or prevention of: (i) viral; bacterial; parasitic or fungal
infections; or (ii) of cancers. A particular application is in anti-
melanoma vaccines. (I) are also useful for in vitro diagnosis of diseases
associated with interactions between MHC and (I); e.g. melanoma and human
immunodeficiency virus infection. AAM98898 to AAM95592 represent invention
immunodeficiency virus infection compounds from the present invention
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                                                                                                                                                                                                                           Stabilized pharmaceutical containing N-terminal glutamic acid or glutamine, useful e.g. in anti-melanoma vaccines, is an addition salt with strong acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide; amyloid plaque component; Alzheimer's disease; amyloidogenic disease; inhibitor.
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1.6e+02;
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                                                                                                                              Goetsch L;
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                                                                                                                              Corvaia N, Beck A,
                                                                         (FABR ) FABRE MEDICAMENT SA PIERRE.
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                                                                                                                                                                                                                                                                                                                                      Claim 9; Page 96; 149pp; French.
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99US-0139172P.
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us-09-594-978a-3.rag

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The present invention relates to oligonucleotides (see AAL26793-AAL34659)
encoding polymorphic variants of proteins related to amylases, amyloid
complement selected proteins, apptobes related proteins, cadharin, cyclin,
polymerase, oncogenes, histones, kinases, colony stimulating factors,
complement related proteins, cytchromes, kinesins, cytchrines,
interferons, interleukins, G-protein coupled receptors and thioesterases.
The present sequence is a peptide encoded by one such oligonucleotide.
The oligonucleotides and the peptides encoded by them may be used in the
prevention, diagnosis and treatment of diseases associated with
inappropriate expression of the proteins listed above. Disorders that may
be prevented, diagnosed and/or treated include multifactorial diseases
with a genetic component, such as autoimmune diseases (e.g. rheumatoid
arthitis, multiple solerosis, diabetes, systemic lupus erythromatosus
conditions, breast, colon and kidney, leukaemia), diseases of the nervous
system and an infection of pathogenic organisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genomic database; mass spectrometer; proteomic business; pharmaceutical; nuclear transport; signalling pathway; cellular organelle.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying coding sequence in genomic databases for conducting proteomics business, by using polypeptide sequence information obtained from peptide sequencing projects, especially those using mass spectrometers.
                                                                                                                                                                                                                                                                                                                                                                                                                                              95.0%; Score 19; DB 4; Length 14; 100.0%; Pred. No. 1.8e+02; ive 0; Mismatches 0; Indels
                                   Disclosure; Page 3829; 4143pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana S11 peptide #6.
autoimmune diseases and infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 41; 100pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE32223 standard; peptide; 15 AA.
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20-APR-2001; 2001US-0285362P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 14 AA;
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Gaps ö

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also used for establishing a distribution system for distributing the pharmacutical preparation for sale, and may optionally include establishing a sales group for marketing the pharmacutical preparation. It is also used for predicting the gene structure, such as intron/exon boundaries; for searching genomic databases for sequences derived from multi-protein complexes e.g. assemblies with a particular function such as splicing, transport or nuclear import or export; for elucidating transfer than structural complexes (that are involved in signalling pathways) and for identifiang proteins in cellular organales. The present sequence is Arabidopsis thaliana peptide used to illustrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptides AAW42943-46 are immunogenic peptides corresponding to immunogenic epitopes of the Hepatitis A virus (HAV). The peptides are ubstantially shinlar to a portion of the amino acid sequence of the P3A protein of HAV corresponding to amino acids 1423-1496. The present peptide is derived from amino acids 1430-1449 and has a reactivity of 58.5% with acute sera. Compositions containing the peptides can be used to induce an immune response to HAV in a mammal. The peptides can also be used to detect the presence of antibodies against HAV in mammalian serum. The peptides can also be used to make an antibody against HAV by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunogenic Hepatitis A Virus (HAV) peptide(s) - used to induce an immune response to HAV in a mammal or to detect the presence of antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunogenic peptide; immunogenic epitope; P3A protein; immune response; antibody.
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                                                                                                                                                                                                                                                 95.0%; Score 19; DB 6; Length 15; 100.0%; Pred. No. 1.9e+02; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunogenic Hepatitis A virus peptide YK-1369.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 33; Page 115; 140pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW42944 standard; peptide; 20 AA.
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                                                                                                                                                                                the method of the invention
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                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                                                   Sequence 15 AA;
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Hepatitis A virus.
Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 21 AA;
                                                                                                                 WO200105824-A2
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Matches
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                                                                                                                                                                                                                                  Immunogenic peptide; immunogenic epitope; P3A protein; immune response;
             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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 100.0%; Pred. No. 2.6e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                           Immunogenic Hepatitis A virus peptide YK-1368.
                                                                                                                                                                                                                                                                                                                                                                                                                         (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 33; Page 115; 140pp; English.
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(D AAB69462 standard; peptide; 21 AA.
(X AAB69462;
(X 20-APR-2001 (first entry)
                                                                                                                             AAW42943 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                      97WO-US006891
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                                                                                                                                                                                 28-APR-1998 (first entry)
            4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fields HA, Khudyakov YE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              against HAV in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-535831/49.
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                        Hepatitis A virus.
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                                                            4 VAEF 7
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                                                                                                                                                                                                                                                                                                                                                                      18-APR-1997;
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                                                                                                                                                                                                                                                                            Synthetic.
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The present sequence is one of a number of synthetic peptides which are immunoreactive with hepatitis A virus (HAV) antibodies. The peptides comprise antigenic epitopes of the major structural capsid polypeptides or non-structural polypeptides of HAV with one or more glutamine or non-structural polypeptides of HAV with one or more glutamine correct the presence of antibodies against HAV in mammalian serum, to detect the presence of HAV in a human or animal through the binding of the peptide to an antibody, to detect acute phase infection by detecting ISM antibodies in mammalian serum and detecting convalescence in a mammalian serum and detecting convalescence in a mammalian serum and detecting convalescence in a samples in clinical or research-based assays using immunoblotting, fluorescence in situ hybridisation analysis, gel-mobility shift assays, tracking of radioactive or bioluminescent markers, chromatography or lelectrophoresis. The peptides are used to induce an immune response to HAV when administered to a human or animal. Glutamine at the carboxy end the peptides enhances the ISM antibody reactivity
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                                                                                Hepatitis A virus; HAV; immunogen; immunostimulant; virucide; vaccine; antigen; major structural capsid polypeptide; HAV antibody detection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic peptides used as antigen sources for enzyme immunoassays detecting anti-hepatitis A virus and as vaccines.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic HAV P3A peptide, SEQ ID NO: 63.
Synthetic HAV P3A peptide, SEQ ID NO: 62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 22; Page 108; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB69463 standard; peptide; 21 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-JUL-2000; 2000WO-US019267.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1999; 99US-0144412P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fields HA, Khudyakov YE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-112681/12
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WPI; 1997-535831/49.

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The present sequence is one of a number of synthetic peptides which are immunoreactive with hepatitis A virus (HAV) antibodies. The peptides comprise anigenic epitopes of the major structural acasid polypeptides or or non-structural polypeptides of the peptide. The peptides are used to detect the presence of antibodies against HAV in mammalian serum, to detect the presence of AT in a human or animal through the binding of the peptide to an antibody, to detect acute phase infection by detecting Ism antibodies in mammalian serum and detecting convalescence in a mammalian serum and detecting convalescence in a mammalian serum and detecting convalescence in a mammalian serum and attentify and inclinated or research-based assays using immunoblotting, fluorescence in situ hybridisation analysis, gel-mobility shift assays, tracking of radioactive or bioluminescent markers, chromatography or electrophoresis. The peptides are used to induce an immune response to HAV when administered to a human or animal. Glutamine at the carboxy end of the peptides enhances the IgM antibody reactivity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunogenic peptide; immunogenic epitope; P3A protein; immune response; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                        Synthetic peptides used as antigen sources for enzyme immunoassays detecting anti-hepatitis A virus and as vaccines.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95.0%; Score 19; DB 4; Length 21; 100.0%; Pred. No. 2.7e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunogenic Hepatitis A virus peptide YK-1832.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                          (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                      Claim 22; Page 109; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW42946 standard; peptide; 25 AA.
                                            14-JUL-2000; 2000WO-US019267
                                                                             99US-0144412P
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                                                                                                                                           Khudyakov YE;
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                                                                                                                                                                          VPI; 2001-112681/12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 21 AA;
                                                                           LS-JUL-1999;
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               25-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-APR-1998
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                                                                                                                                           Fields HA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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AAW42946
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                                                                                                                                             The present immunogenic peptide corresponds to an immunogenic epitope of the Hepatitis A virus (HAV). The peptide is substantially similar to a portion of the amino acid sequence of the PAA protein of HAV corresponding to amino acids 1423-1496. Compositions containing the peptide can be used to induce an immune response to HAV in a mammal. The peptide can also be used to detect the presence of antibodies against HAV in mammalian serum. The peptide can also be used to make an antibody against HAV by administering the peptide to a mammal
                                         Immunogenic Hepatitis A Virus (HAV) peptide(s) - used to induce an immune response to HAV in a mammal or to detect the presence of antibodies against HAV in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is one of a number of synthetic peptides which are immunoreactive with hepatitis A virus (HAV) antibodies. The peptides comprises antispenic epitopes of the major structural capsid polypeptides or non-structural polypeptides of HAV with one or more glutamine molecules at the carboxy end of the peptide. The peptides are used to detect the presence of antibodies against HAV in mammalian serum, to detect the presence of HAV in a human or animal through the binding of the peptide to an antibody, to detect acute phase infection by detecting IgM antibodies in mammalian serum and detecting convalescence in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis A virus; HAV; immunogen; immunostimulant; virucide; vaccine; antigen; major structural capsid polypeptide; HAV antibody detection.
                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic peptides used as antigen sources for enzyme immunoassays detecting anti-hepatitis A virus and as vaccines.
                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                      Length 25;
                                                                                                                                                                                                                                                                                                                                                                      0; Indels
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                                                                                                                                                                                                                                                                                                                                      95.0%; Score 19; DB 100.0%; Pred. No. 3.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                  Claim 33; Page 115; 140pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 22; Page 110; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB69465 standard; peptide; 25 AA.
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                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.v
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-112681/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatitis A virus
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                         2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                           3 VAEF 6
                                                                                                                                                                                                                                                                                                       Sequence 25 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1999;
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AAM33910 standard; protein; 28 AA.

AAM33910 ID AAM3

(first entry)

17-0CT-2001

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Gaps

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AAM33910;

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mammal. The peptides are used to detect or quantify HAV antibodies in samples in clinical or research-based assays using immunoblotting, fluorescence in situ hybridisation analysis, gel-mobility shift assays, tracking of radioactive or bioluminescent markers, chromatography or electrophoresis. The peptides are used to induce an immune response to HAV when administered to a human or animal. Glutamine at the carboxy end of the peptides enhances the IgM antibody reactivity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human mevalonate pyrophosphate decarboxylase coding sequence - used for screening for MPD inhibitors, which regulate and control cholesterol
                                                                                                                                                                                                                                                                                                                                                                             Human mevalonate pyrophosphate decarboxylase peptide NT71.
                                                                                                                                         95.0%; Score 19; DB 4; Length 25; 100.0%; Pred. No. 3.3e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                     Mevalonate pyrophosphate decarboxylase; MPD; cholesterol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; Page 10; 37pp; English
                                                                                                                                                                                                                                                                                              AAW17832 standard; peptide; 28 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96WO-EP004394
                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                     4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Huwyler LR;
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                                                                                                                                         Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                2 VAEF 5
                                                                                                                                                                                                                            3 VAEF 6
                                                                                                                  Sequence 25 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-0CT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9714787-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-APR-1997.
                                                                                                                                                                                                                                                                                                                                                     29-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Toth MJ,
                                                                                                                                                                                                                                                                                                                          AAW17832;
                                                                                                                                                                                                                                                                      RESULT 26
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Peptide NT71 (AAW17832) was obtd. by trypsin digestion of human liver mevalonate pyrophosphate decarboxylase (MPD) (AAW17831), an enzyme of the cholesterol biosynthetic pathway. The sequence of the peptide was used to design PCR primers utilised in the amplification of cDMA from a rat liver cDNA library. A rat MPD partial clone was obtd. and used as a probe to screen a human liver cDNA library. A 1800 bp sequence (AAT66464) coding for human MPD was identified

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Sequence 28 AA;

Gaps ö 95.0%; Score 19; DB 2; Length 28; 100.0%; Pred. No. 3.7e+02; ive 0; Mismatches 0; Indels 4; Conservative Query Match Best Local Similarity Matches 4; Conserv

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RESULT 27

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Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia; coronary heart disease.

WO200157273-A2

Homo sapiens.

Human liver peptide, SEQ ID No 34112.

25-FEB-2003

ABG55464;

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Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta.
                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal disgnosis of
                                                     Peptide #7947 encoded by probe for measuring placental gene expression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95.0%; Score 19; DB 4; Length 28; 100.0%; Pred. No. 3.7e+02; ive 0; Mismatches 0; Indels
                                                                            Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 27; SEQ ID NO 34179; 654pp; English.
                                                                                                                                                                                                                                                                                                                                  Chen W, Rank DR;
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                                                                                                                                                                                                                                                                                                            (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 100.0%; 4; Conservative 0
                                                                                                                                                                                                               04-FEB-2000; 2000US-0180312P.
26-MAY-2000; 2000US-0207456P.
30-UUN-2000; 2000US-0608408.
33-AUG-2000; 2000US-00632366.
                                                                                                                                                                                                                                                             21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                        30-JAN-2001; 2001WO-US000663.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human genetic disorders
                                                                                                                                                                                                                                                                                                                                    Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-488897/53
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Best Local Similarity
Matches 4; Conserv
                                                                                           genetic disorder
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 28 AA;
                                                                                                                                          WO200157272-A2
                                                                                                                     Homo sapiens.
                                                                                                                                                                   09-AUG-2001
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2000US-0180312P

Chen W, Rank DR

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The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver. comprising one of 11109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. Assorbables here seen thuman liver single exon encoded peptides of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                             Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human peptide encoded by genome-derived single exon probe SEQ ID 33266.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary hveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension; hyaline membrane disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, single exon probe, asthma, lung cancer, COPD, ILD, chronic obstructive pulmonary disease; interstitual lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 27; SEQ ID NO 34112; 658pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABG43601 standard; peptide; 28 AA.
                                                                                                             26-MAY-2000) 2000US-0207456P.
30-JUN-2000) 2000US-00608408.
03-AUG-2000) 2000US-00632366.
21-SEP-2000) 2000US-0234687P.
27-SEP-2000) 2000US-0234587P.
04-OCT-2000) 2000GB-00024263.
                                                                                                                                                                                                                                                   (MOLE-) MOLECULAR DYNAMICS INC
                                                       30-JAN-2001; 2001WO-US000664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Conservative
                                                                                                                                                                                                                                                                                       Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                              WPI; 2001-488898/53
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Best Local Similarity
Matches 4; Conserv
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                                                                                               04-FEB-2000;
                  09-AUG-2001
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ABG43601
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0; Gaps

95.0%; Score 19; DB 4; Length 28; 100.0%; Pred. No. 3.7e+02; tive 0; Mismatches 0; Indels

(first entry)

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Complements or the 1287 open reading frames derived from the 12614 probes to probe which hybridise and things the novel set of probes with a properties of the novel set of probes which hybridise at high stringency to a mucleic caid expressed in the human lung; measuring gene expression in a sample carl early efform human lung; measuring gene expression in a sample carl early and (b) measuring the label detectably bound to each probe of the collection of detectably labeled nucleic acids derived from human lung collection of detectably labeled nucleic acids derived from human lung canner in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the enkaryote; and (b) detecting at least one exon from genomic sequences of algorithmically predicting at least one exon from genomic sequences of the enkaryote; and (b) detecting apporting specific hybridisation of detectably contributed and collection and coll
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their
                                                                                                                                                                                                                                                                                                                                                                                                                           Spatially-addressable set of single exon nucleic acid probes, used to measure gene expression in human lung samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 27; SEQ ID NO 33266; 634pp; English
                                                                                                                                                                                                                                                                                                                                       Chen W, Rank DR,
                                                                                                                                                                                                                                                                                           (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                   2000US-0234687P.
2000US-0236359P.
2000GB-00024263.
                                                               30-JAN-2001, 2001WO-US000665
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Matches 4; Conserv
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27-SEP-2000;
04-OCT-2000;
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2000US-0227182P.
2000US-0227009P.
2000US-0228924P.
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2000US-0229343P.
2000US-0229344P.
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2000US-0231413P.
2000US-0231414P.
2000US-0232080P.
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2000US-0232401P.
2000US-0233063P.
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22-AUG-2000; 2000US-0226681P.
22-AUG-2000; 2000US-0226868P.
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                                     17-JAN-2001; 2001WO-US001354
09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus pneumoniae polynucleotides - useful for developing products for diagnosis, prevention and treatment of infections e.g. pneumonia, bacteremia, meningitis or endocarditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence is that of a Streptococcal polypeptide. The polypeptide can potentially be used for the diagnosis and prevention of bacterial infections, especially SP infection. It may be used for the treatment of diseases such as otitis media, conjunctivitis, pneumonia, bacteremia, meningitis, sinusitis, pleural empyema, endocarditis or infection of the cerebrospinal fluid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis.
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                                                                                                                                                                                                                     Polypeptide, ORF, open reading frame; infection; bacterial; streptococcal; bacteremia; diagnosis; prophylaxis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Black MT, Hodgson JE, Knowles DJC,
Reid RH, Zarfos PN;
                                                                                                                                                                                   Streptococcus pneumoniae polypeptide.
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                                                             AAW62760 standard; protein; 30 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
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                                                                                                                                             (first entry)
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Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                  Streptococcus pneumoniae
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                                                                                                     AAW62760;
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AAM82654
                         ESULT 30
                                            AW62760
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08-NOV-2000; 2000US-0246475F

08-NOV-2000; 2000US-0246477F

08-NOV-2000; 2000US-0246477F

08-NOV-2000; 2000US-0246537F

08-NOV-2000; 2000US-0246527F

08-NOV-2000; 2000US-0246527F

08-NOV-2000; 2000US-0246527F

08-NOV-2000; 2000US-0246527F

08-NOV-2000; 2000US-0246528F

08-NOV-2000; 2000US-0246528F

08-NOV-2000; 2000US-0246537F

08-NOV-2000; 2000US-0246611F

17-NOV-2000; 2000US-0249208F

17-NOV-2000; 2000US-0249210F

17-NOV-2000; 2000US-0249211F

17-NOV-2000; 2000US-0249211F
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17-NOV-2000; 2000US-0249216P.
17-NOV-2000; 2000US-0249217P.
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01-DEC-2000;
05-DEC-2000;
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06-DEC-2000;
06-DEC-2000;
08-DEC-2000;
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08-DEC-2000;
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17-NOV-2000;
17-NOV-2000;
01-DEC-2000;
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02-0CT-2000;
02-0CT-2000;
02-0CT-2000;
13-0CT-2000;
13-0CT-2000;
20-0CT-2000;
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17-NOV-2000
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$\;\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\frac{\chi}{\chi}\fr
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Barash SC, Ruben SM; WPI; 2001-483426/52

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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (1)
amino acid sequences given in AAM82170 to AAM91921. (1) have cytostatic
activity, and can be used in gene therapy and vaccine production. (1)
cativity, and can be used in gene therapy and vaccine production. (1)
creatment of diseases associated with inappropriate (1) expression. For
example, they may be used to reat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (1) by expressing inactive proteins or to
cupplement the patients own production of (1). Additionally, (1)
polymucleorides may be used to produce the secreted (1), by inserting the
nucleic acids into a host cell and culturing the cell to express the
protein. (1) proteins and polymucleotides may be used to prevent,
diagnose and treat immune/haematopoietic-related diseases, especially
cancers and cancer metastesses of haematopoietic antigen genomic
to AAK87694 represent human immune/haematopoietic antigen genomic
sequences from the present invention. AAK4942 to AAK54950 and AAM82169
represent sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                               Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, cytokine, cell proliferation, cell differentiation, gene therapy, vaccine, peptide therapy, stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
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                                                                                   Claim 11; SEQ ID NO 10247; 3071pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95.0%; Score 19; DB 4; Length 32; ilarity 100.0%; Pred. No. 4.3e+02; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human polypeptide SEQ ID NO 22916.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA009024 standard; protein; 33 AA.
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18-MAY-2000; 2000US-00577409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tang YT, Liu C, Drmanac RT;
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Best Local Similarity
A; Conserve
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N-PSDB; AAK55435
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The invention relates to human polymucleotides (AA179941-AA193841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to prytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The vacines or polymucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, memunomodilatory activity and activity, issue growth factor activity, immunomodilatory activity and activity, inhibin activity and may be useful in the diagnosis and/or treatment of cancer, laukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pot\_sequences

Sequence 33 AA;

Gaps ö 95.0%; Score 19; DB 4; Length 33; 100.0%; Pred. No. 4.4e+02; tive 0; Mismatches 0; Indels 4; Conservative Local Similarity 2 VAEF 5 3 VAEF 6 Query Match Best Local S: Matches 4 ⋩

AAR77953 standard; peptide; 35 AA. 

09-OCT-1996 (first entry) AAR77953;

Antigenic Tbp2 peptide TBP2-21

Tbp1, Tbp2, transferrin receptor operon, vaccine, antigen, non-typable strain, Haemophilus influenzae, meningitis.

Synthetic.

18-MAY-1995.

WO9513370-A1.

94WO-CA000616. 07-NOV-1994; 93US-00148968. 93US-00175116. 08-NOV-1993;

(CONN-) CONNAUGHT LAB LTD.

LOOSMORE S, Harkness R, Schryvers A, Chong P, Gray-Owen S; Yang Y, Murdin A, Klein M;

WPI; 1995-194089/25.

develop Nucleic acids encoding Haemophilus transferrin receptor - used to prods for detection and in diagnosis, prevention and treatment of Haemophilus infection.

Example 16; Page 72; 231pp; English.

AAR77933-969 are predicted antigenic peptides derived from conserved regions of the TRP2 protein from H. influenzae strains Bagan, MinhA, DL63 and non-typable strain PAK12085. The transferrin receptor (TfR) operon consists of two genes (Tbp1 and Tbp2) arranged in tandem and which are transcribed from a single promoter. H. influenzae TfR is Iron- and/or haemin-regulated and a purative fur-binding site has been identified upstream of tbp2. Antibodies blocking this binding site may prevent bacterial growth. Fragments of the TfR (or its genes) are useful in vaccines to provide protection against, e.g. bacterial meningtis. An advantage of using the TfR is that it shares homology with TfR of other

H. influenzae strains including non-typable strains. According to the specification the present sequence shows residues 449-484 of Tbp2 from the H. influenzae strain Eagan ន្តដូច្ច

Sequence 35 AA;

ö Gaps ö 95.0%; Score 19; DB 2; Length 35; 100.0%; Pred. No. 4.7e+02; ive 0; Mismatches 0; Indels 4; Conservative Sest Local Similarity Query Match Matches

14 VAEF 17 2 VAEF 5 ò

RESULT 34 AAW46146

AAW46146 standard; protein; 35 AA.

AAW46146;

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05-MAY-1998 (first entry)

Predicted antigenic Tbpl peptide TBP2-21.

Transferrin receptor; Haemophilus influenzae type b; iron; human transferrin; iron source; antibody; bacterial growth; vaccine; immunogenic truncated analogue; antigen; Tbp1; Tbp2.

Haemophilus influenzae. Synthetic

WO9640929-A2. 

19-DEC-1996.

96WO-CA000399. 07-JUN-1996;

07-JUN-1995;

95US-00483577. 96US-00649518. 17-MAY-1996;

(CONN-) CONNAUGHT LAB LTD.

Schryvers AB, Chong P, Gray-Owen Klein MH; Harkness RE, Loosmore SM, Harknee Yang Y, Murdin AD,

WPI; 1997-052329/05.

Haemophilus truncated transferrin receptor protein analogue, Tbp2 - uto induce protection against disease caused by transferrin producing pathogens, or as antigen to detect Haemophilus TfR antibodies.

Example 16; Page 70; 228pp; English.

protein of Haemophilus influenzae type b. Thp2 is part of the transferrin receptor, of which Tbp1 and Tbp2 were organic. The deduced amino acid sequences of Tbp1 and Tbp2 were compared, and regions of conservation is defunitied. The above peptides are derived from these regions, the present peptide being derived from residues 449-444. Iron is an essential quirient for the growth of these bacteria, and they can utilise human current for the growth of these bacteria, and they can utilise human cransferrin as a source of iron. Antibodies which block the access of the transferrin receptor to its iron source prevent bacterial growth. The transferrin receptor, or fragments, therefore, are good vaccine cannoidates. An immunogenic composition comprising for encoding) the immunogenic truncated analogue is also useful as an antigen in immunosasays for the detection of Haemophilus transferrin receptor.

The immunosasays for the detection of themophilus transferrin receptor antibodies, while the nucleic acid molecule can be used as a hybridisation probe for the detection of other transferrin receptor genes

Sequence 35 AA;

Human; aquaporin-1; AQP-1; water channel protein; regulation; osmotic change; erythrocyte; dryness; blindness; hydration; asthma;

secretion.

Human aquaporin-1 NH2-terminal amino acid sequence CHIP28.

14-JUL-1998 (first entry)

AAW55788;

AAW55788 standard; peptide; 35 AA.

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RESULT 36
                                     AAW55788
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transferrin receptor; Tbp1; Tbp2; immunogenic; antibacterial; vaccine;
                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haemophilus truncated transferrin receptor protein analogue, Tbp2 - u to induce protection against disease caused by transferrin producing pathogens, or as antigen to detect Haemophilus TfR antibodies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yang Y;
                                 Length 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 95.0%; Score 19; DB 2; Length 35; Best Local Similarity 100.0%; Pred. No. 4.7e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schryvers A, Gray-Owen S,
                      95.0%; Score 19; DB 2; Le
100.0%; Pred. No. 4.7e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H. influenzae antigenic Tbp2 peptide TBP2-21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 16; Col 39-40; 281pp; English
                                                                                                                                                                                                                                                                                                                                                                                                        AAY51751 standard; protein; 35 AA.
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94US-00337483.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CONN-) CONNAUGHT LAB LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-JUN-2000 (first entry)
                                                                                                 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Harkness R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haemophilus influenzae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-052329/05.
                          Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                14 VAEF 17
                                                                                                                                                             2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 35 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US6015688-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY51751;
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                                                                                                                                                                                                                                                                                                                                     RESULT 35
                                                                                                                                                                                                                                                                                                                                                                   AAY51751
AAY
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Polynuclectide(s) encoding water channel protein Aquaporin-1 - are useful for recombinant production of protein for activity studies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents the NH2-terminal amino acid sequence of aquaporin-1 (AOP-1), isolated from human erythrocytes. AQP-1 is a water channel protein. Water channel proteins regulate the passage of water and out of cells, in response to osmotic changes. The DNA encoding AQP-1 is useful for the recombinant production of AQP-1, found in mammalian erythrocytes, and is useful in the study to identify reagents which enhance or inhibit water channel function. This can lead to therapeutics which enhance secretion e.g. in the case of dryness of eyes which can dead to blindness or to hydrate large respiratory airways, as their
                                                                                                                                                                                                             /note= "not specified but is given as Ser in the full
length protein given in AAW55786"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95.0%; Score 19; DB 2; Length 35; 100.0%; Pred. No. 4.7e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; Col 20; 48pp; English.
                                                                                                                                                                                                      label= Unknown
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                                                                                                                                                                                                                                                                                                                                            92US-00930168.
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                                                                                                                                                                              Key
Misc-difference 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 35 AA;
                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                  06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                           17-AUG-1992;
24-FEB-1995;
                                                                                                                                                                                                                                                             US5741671-A.
                                                                                                                                                                                                                                                                                         21-APR-1998.
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                                                                                                                                                                                                                                                                                                                                                                                                               Agre PC;
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Matches
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Gaps

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Disclosure, Col 37-38; 252pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                 AAY80448 standard; peptide; 35 AA.
                                                                                                                           Example 2; Col 20; 47pp; English.
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93US-00175116.
95US-00337483.
92US-00930168.
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                   UNIO ) UNIV JOHNS HOPKINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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Schryvers A;
                                                                                                                                                                                                                                                                                            4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-096387/08.
                                                                                                       recombinant protein
                                                                  WPI; 1999-152100/13
                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tracheobronchitis.
                                                                                                                                                                                                                        present invention
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                                                                                                                                                                                                                                                                                                                  2 VAEF 5
                                                                                                                                                                                                                                              Sequence 35 AA;
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29-DEC-1993;
08-NOV-1995;
17-AUG-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JUN-1995;
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Murdin A, S
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                                                                                                                                                                                                                                                                                                                                                                                                                      AAY80448;
                                              Agre PC;
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                                                                                                                                                                                                                                                                                                                            Peptides AAW53086-W53100 and peptides AAW54100-W54122 are derived from the Tbp2 protein. The Tbp2 protein is one of two proteins with genes found on the transferrin operon. These peptides can be used along with immunisation and sequences and recombinant proteins for diagnosis. They can also be used to protect from bacteria that produce transferrin receptor protein
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                                                                                                                                                                                                                                                                       Purification of recombinant Haemophilus transferrin-binding protein solubilising inclusion bodies separated from cell 1ysate.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rat; aquaporin-5; AQP5; AQP1; transmembrane water channel protein; major intrinsic protein; MIP; CHIP28.
                                                                                                                                                                                                              Chong
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0
                                                                                                                                                                                                               Yang Y,
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Similarity 100.0%; Pred. No. 4.7e+02;
4; Conservative 0; Mismatches 0; Indels
             tbpl; tbp2; vaccine; H. influenzae; antibody; diagnosis; passive immunisation; transferrin receptor operon.
                                                                                                                                                                                                                Loosmore S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human aquaporin-1 (CHIP28) N-terminal peptide.
                                                                                                                                                                                                                                                                                                         Example 16/17; Column 37-38; 261pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "unspecified"
                                                                                                                                                                                                                Harkness R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW94320 standard; peptide; 35 AA
                                                                                                                                          93US-00148968.
93US-00175116.
94US-00337483.
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                                                                                                                                                                                        (CONN-) CONNAUGHT LAB LTD.
                                                                                                                                                                                                               Gray-Owen S, Klein M, Murdin A, Schryvers A;
                                                 Haemophilus influenzae
                                                                                                                                                                                                                                                 WPI; 1998-100410/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VAEF 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 35 AA;
                                                                                                                                          08-NOV-1993;
29-DEC-1993;
08-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-FEB-1995;
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                                                                                                                    1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-APR-1999
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                                                                       US5708149-A
                                                                                             13-JAN-1998
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Matches
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Antibodies specific for transferrin receptor proteins of Haemophilus influenzae, useful for treating otitis media, epiglottitis, pneumonia and
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DNA encoding aquaporin-5 water channel protein - useful for producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to novel antibodies (or monospecific antisera) specific for single transferrin receptor proteins (or immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Klein M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antibacterial; antiinflammatory; auditory; respiratory; antibody; antiserum; transferrin receptor; immunogen; epitope; otitis media; bacterial meningitis; epiglottitis; pneumonia; tracheobronchitis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95.0%; Score 19; DB 2; Length 35; 100.0%; Pred. No. 4.7e+02; rive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H. influenzae transferrin receptor Tbpl epitope TBP2-21.
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The present sequence represents a Staphylococcus aureus protein, that, based on homology with a Bacillus subtilis protein, is believed to be a probable UDP-N-acetylglucosamine 1-carboxyvinyltransferase (encylpyruvate transferase, UDP-N-acetylglucosamine encylpyruvyl transferase). The DNA sequence was isolated from a library of clones of S. aureus WCUH 29 in Escherichia coli. The DNA sequence can be used in the construction of riboxymes and antisense sequences to control the expression of Staphylococcal genes. The DNA sequence is also useful as a source of regulatory elements for the control of bacterial gene expression. The present protein may be used to produce vaccines to enable a host to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus aureus protein; ribozyme; antisense sequence; control; Staphylococcal gene; regulatory element; bacterial gene expression; vaccine; Staphylococcal infection; food poisoning; scaled skin syndrome;
               corresponds to an epitope from the H. influenzae transferrin receptor protein TDp2. The antibodies may be used for preventing and treating infections and disorders caused by H. influenzae, including bacterial meningitis, otitis media, epiglottitis, pneumonia and tracheobronchitis. The antibodies may also be used detect the presence of H. influenzae proteins in samples according to standard methodologies (e.g. enzyme linked immunosorbant assay (ELISA)) and hence diagnose infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                used to
                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel polypeptide(s) from Staphylococcus aureus strain WCUH29 - use isolate antimicrobial compounds, and in vaccines against S. aureus
fragment) from strains of Haemophilus influenzae. This sequence
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, Ward JM;
                                                                                                                                                                                         95.0%; Score 19; DB 3; Length 35; 100.0%; Pred. No. 4.7e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UDP-N-acetylglucosamine 1-carboxyvinyltransferase.
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Rosenberg M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "not specified"
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                                                                                                                                                                                                                                                                                                                                                                                                AAW27782 standard; protein; 36 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96US-0011888P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                 4; Conservative
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Reichard RW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 toxic shock syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-424969/39.
N-PSDB; AAT83751.
                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
Misc-difference
                                                                                                                                                                                                                                                                                                      14 VAEF 17
                                                                                                                                                                                                                                                                    2 VAEF 5
                                                                                                                                                              Sequence 35 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9730070-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Black MT,
Pratt JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                AAW27782;
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produce specific antibodies with antibacterial action. These vaccines and antibodies would protect a host against invasion by S. aureus, and conditions relating to Staphylococcal infection, e.g. Staphylococcal food poisoning, scaled skin syndrome, and toxic shock syndrome
                                                                                                                                                                                                                                                                                                       Human; nootropic, neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antihatlammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisaickling; antianaemic; antiarchritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antidiabetic; antidiabetic; antionallaer; anticonvulsant; antidiagal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine;
                                                                                                      Gaps
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                                                                                Length 36;
                                                                                                      Indels
                                                                       DB 2; Leus.
7. 4.8e+02;
0;
                                                                                                                                                                                                                                                                                   Human excretory related polypeptide SEQ ID NO 570.
                                                                                95.0%; Score 19; DB 100.0%; Pred. No. 4.6:ive 0; Mismatches
                                                                                                                                                                                                              AAM99833 standard; protein; 37 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0190076P.
2000US-0205515P.
2000US-0209467P.
2000US-0215135P.
2000US-0215135P.
2000US-0215135P.
2000US-0215486P.
2000US-0215487P.
2000US-0217487P.
2000US-0217486P.
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2000US-0224518P.
2000US-0224513P.
2000US-0225214P.
2000US-0225214P.
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2000US-0186350P.
2000US-0189874P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-JAN-2001; 2001WO-US001323
                                                                                                                                                                                                                                                            07-JAN-2002 (first entry)
                                                                                                      4; Conservative
                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                           excretory system.
                                                                                                                               2 VAEF 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200155313-A2.
                                                            Seguence 36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-MAR-2000;
16-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-JUL-2000;
11-JUL-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-JUL-2000;
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                                                                                                                                                                                                                                      AAM99833;
                                                                                                       Matches
                                                                                                                                                                                        RESULT 41
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The invention relates to novel excretory system related human polymuclectides (AA198567-AA199503) and the encoded proteins (AAM99594-Dolymuclectides (AA198567-AA199503) and the encoded proteins (AAM99594-AA19913) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy, espeically disorders related to the excretory system. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal prevention of: (a) cancering or uroganital; (b) immume disorders e.g. Addison's disease, allergies, autoimmume haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple solerosis, cheuractoid and ulcerative collitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases equence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO true from free fig. Isolated nucleic acid molecule encoding excretory system antigen is used in preventing, treating or ameliorating a medical condition. Claim 11; SEQ ID NO 570; 574pp + Sequence Listing; English. Rosen CA, Barash SC, Ruben SM, 08-NOV-2000; 2000US-0246613P.
17-NOV-2000; 2000US-0249200P.
17-NOV-2000; 2000US-0249200P.
17-NOV-2000; 2000US-0249210P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249213P.
17-NOV-2000; 2000US-0249214P.
17-NOV-2000; 2000US-0249214P.
17-NOV-2000; 2000US-0249214P.
17-NOV-2000; 2000US-0249216P.
17-NOV-2000; 2000US-024924P.
17-NOV-2000; 2000US-024924P.
17-NOV-2000; 2000US-024924P.
17-NOV-2000; 2000US-024924P.
17-NOV-2000; 2000US-024924P.
17-NOV-2000; 2000US-024926P.
17-NOV-2000; 2000US-025198P.
17-NOV-2000; 2000US-025198P.
18-DEC-2000; 2000US-025186P.
18-DEC-2000; 2000US-025186P.
18-DEC-2000; 2000US-025186P.
18-DEC-2000; 2000US-025186P.
18-DEC-2000; 2000US-025186P. 08-DEC-2000; 2000US-0251990P 11-DEC-2000; 2000US-0254097P (HUMA-) HUMAN GENOME SCI INC WPI; 2001-465569/50. N-PSDB; AAI98806. 

Sequence 37 AA;

Gaps .. o Query Match

95.0%; Score 19; DB 4; Length 37;

Best Local Similarity 100.0%; Pred. No. 5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels

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Human; kidney antigen; immunosuppressive; antiarthritic; antirheumatic; antipolifertative; gytostatic; cardiant; vasotropic; cerebroprotective; nototropic; neuroprotective; antibacterial; virucide; fungicide; opthalmological; antiallergic; hepatocropic; antidiabetic; antiallammatory; antiulcer; vulnerary; anticonvulsant; antiparasitic; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection.
                                                                                                                                                                                                                                                                 Human kidney related polypeptide SEQ ID NO 517
                                                                                                                              AAM42648 standard; protein; 37 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-AUG-2000) 2000US-0180638P-2000-4-FEB-2000) 2000US-0180644P-2000-4-FEB-2000) 2000US-0180644P-2000-4-FEB-2000) 2000US-0180644P-2000) 2000US-0180644P-2000) 2000US-0180644P-2000) 2000US-0180644P-2000) 2000US-0208464P-2000-4-FEB-2000) 2000US-0208464P-2000-4-FEB-2000) 2000US-0218185P-20-4-FEB-2000) 2000US-0218647P-2000-2000US-0218647P-2000-2000US-0218647P-2000-2000US-021864P-2000-2000US-02218P-2000US-2000US-02218P-2000US-2000US-022524P-2000US-2000US-022524P-2000US-2000US-022524P-2000US-2000US-022524P-2000US-2000US-022524P-2000US-2000US-022524P-2000US-2000US-022524P-2000US-2000US-022524P-2000US-2000US-022524P-2000US-2000US-022524P-2000US-2000US-022524P-2000US-2000US-022528P-2000US-2000US-022528P-2000US-2000US-02258P-2000US-202259P-2000US-202259P-2000US-202259P-2000US-202259P-2000US-202259P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-2000US-20225P-200
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01-SEP-2000; 2000US-0229345P-
05-SEP-2000; 2000US-0229359P-
05-SEP-2000; 2000US-0229513P-
06-SEP-2000; 2000US-0230437P-
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                                                                                                                                                                                                                       (first entry)
VAEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                       22-OCT-2001
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                                                                                                                                                                          AAM42648;
                       14
                                                                                                           AAM42648
                                                                                    RESULT
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01-NOV-2000)
08-NOV-2000)
08-NOV-2000) 14-887-2000; 14-887-2000; 14-887-2000; 14-887-2000; 14-887-2000; 14-887-2000; 14-887-2000; 25-SEP-2000; 25-SEP-2000; 26-SEP-2000; 13-0CT-2000, 20-0CT-2000, 20-0CT-2000, 20-0CT-2000, 20-0CT-2000, 20-0CT-2000, 20-0CT-2000, 20-0CT-2000, 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 29-SEP-2000; 

2000US-0249217P

17-NOV-2000;

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(MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                               30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
                                                                                                                                                                                                                                  30-JAN-2001; 2001WO-US000670.
                                                                                                                                                                                                                                                                                                                                                                          27-SEP-2000; 2000US-0236359P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-488901/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40 VAEF 43
                                                                            cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 VAEF 5
                                                                                                                                                        WO200157278-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 43 AA;
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                                                                                                                    Homo sapiens.
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                                                                                                                                                                                                                                                                             04-FEB-2000;
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                                                                                                                                                                                            09-AUG-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to novel kidney related polymucleotides (AAJ62971-AAJ63993) and the encoded polypeptides (AAM2417-AAM45691) collectively known as kidney antigens and the use of such kidney antigens for cancer metastases. The kidney, especially kidney cancer and kidney cancer metastases. The polymucleotides and proteins are also useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The mucleic acids, proteins, antibodies and ant) gancer, e.g. breast and ovarian cancer, and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urgoeintal, (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic ansemia, autoimmune thyroiditis, diabetes mellitus Crohn's disease, multiple sclerosis, rheumatoid any myocardial ischaemias; (d) wound healing; (e) neurological diseases such as wiral, carefiral, fungal and parasitic infections diseases such as viral, carefiral, fungal and parasitic infections. Note: The sequence data for this patent did not form part of the printed specification, but was
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acids and polypeptides, useful for diagnosing, treating and/or preventing human diseases and disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 11; SEQ ID NO 517; 564pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 95.0%; Score 19; DB 4; Length 37; Best Local Similarity 100.0%; Pred. No. 5e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAM17544 standard; protein; 43 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ruben SM
                                                    7.-NOV-2000; 2000US-0249265F.
7.-NOV-2000; 2000US-0249265F.
7.-NOV-2000; 2000US-0249297P.
7.-NOV-2000; 2000US-0249300P.
7.-NOV-2000; 2000US-02591P.
7.-NOV-2000; 2000US-025191P.
10-DEC-2000; 2000US-025193P.
15-DEC-2000; 2000US-025198P.
15-DEC-2000; 2000US-025198P.
16-DEC-2000; 2000US-025186F.
18-DEC-2000; 2000US-025186F.
18-DEC-2000; 2000US-025186F.
18-DEC-2000; 2000US-025186F.
18-DEC-2000; 2000US-025186F.
18-DEC-2000; 2000US-025186F.
18-DEC-2000; 2000US-025186F.
                                                                                                                                                                                                                                                                                                                                                         11-DEC-2000; 2000US-0254097P.
05-JAN-2001; 2001US-0259678P.
                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-488784/53.
N-PSDB; AAI63202.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 37 AA;
                                                                          17-NOV-2000; 2
17-NOV-2000; 2
17-NOV-2000; 2
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Peptide #1978 encoded by probe for measurting cervical gene expression.

**Record Canter.**

**Probe; human intercarray; gene expression; cervical epithelial cell;

**Record Canter.**

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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probes of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They proposing breast disease. Gene expression analysis is useful for prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag information from genomic sequence. The present sequence is a peptide encoded by a single exon mucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed sequence.
                                                                                                                                                                                                                                                                                                      New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein #3903 encoded by probe for measuring heart cell gene expression.
                                                                                                                                                                                                                                                                                                                                                                            Claim 27; SEQ ID NO 14330; 327pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, gene expression, heart, microarray, vascular system;
cardiovascular disease; hypertension; cardiac arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95.0%; Score 19; DB 4; Length 43; 100.0%; Pred. No. 5.9e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                          for measuring gene expression in sample derived from comprises number of single exon nucleic acid probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                 Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB21904 standard; protein; 43 AA
                                                04-FEB-2000; 2000US-0180312P.
26-MX-2000; 2000US-0204465P.
30-UJN-2000; 2000US-00608408.
03-AUG-2000; 2000US-003438F.
21-SEP-2000; 2000US-023468PP.
21-SEP-2000; 2000US-023468PP.
04-OCT-2000; 2000GB-00024263;
                                                                                                                                                                                              (MOLE-) MOLECULAR DYNAMICS INC
               30-JAN-2001; 2001WO-US000662.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100..
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                                                                                                                                                                                                                                 Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                    WPI; 2001-496933/54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 VAEF 5
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The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see PARA1305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                        Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
hypercholesterolaemia; coronary heart disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            h Similarity 100.0%; Score 19; DB 4; Length 43; Similarity 100.0%; Pred. No. 5.9e+02; 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                     Claim 15; SEQ ID NO 23674; 530pp; English.
                                                                                                                                                                      Chen W, Rank DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human liver peptide, SEQ ID No 30062.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABG51414 standard; peptide; 43 AA.
                                       26-MAY-2000; 2000US-0207456F.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687F.
27-SEP-2000; 2000US-0235959.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                         (MOLE-) MOLECULAR DYNAMICS INC
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200005-02068408.
200005-00632366.
200005-0234687P.
200005-0234687P.
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30-JAN-2001; 2001WO-US000666
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                                                                                                                                                                      Hanzel DK,
                                                                                                                                                                                              WPI; 2001-488899/53
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 43 AA;
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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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Chen W, Rank DR,

Hanzel DK,

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Peptide #3896 encoded by probe for measuring breast gene expression
                                                                      Claim 27; SEQ ID NO 30062; 658pp; English
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30-JUN-2000; 2000US-0069408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234559P.
04-OCT-2000; 2000GB-00024263.
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       (MOLE-) MOLECULAR DYNAMICS INC
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Best Local Similarity luv...
A; Conservative
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                                   WPI; 2001-488898/53
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                    Penn SG,
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(first entry)

Chen W, Rank DR;

Hanzel DK,

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The present invention relates to novel single exon nucleic acid probes (see AA100010-AA110067). The present sequence is a peptide encoded by one auch probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic actiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative inflammatory disease and non-carcinoma tumours. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fip.wipo.int/pub/published_pct_sequences
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Novel single exon nucleic acid probe used to measuring gene expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Producing attenuated negative stranded RNA virus vaccines from cloned sequences, useful for immunizing against e.g. respiratory syncytial virus, human parainfluenza virus, Sendai virus Newcastle disease virus, mumps virus and measles virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Negative stranded RNA virus; vaccine; attenuated virus; RSV; PIV; measles; respiratory syncytial virus; parainfluenza virus.
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100.0%; Pred. No. 5.9e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RSV partial protein sequence SEQ ID NO: 26.
                                                                   Claim 27; SEQ ID NO 13954; 322pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (USSH ) US DEPT HEALTH & HUMAN SERVICES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB27178 standard; protein; 47 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-APR-2000; 2000WO-US009695.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-687044/67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40 VAEF 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 43 AA;
                         a human breast.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB27178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Matches
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                                                                                                                                                                                                                                                                                The invention relates to a single exon nucleic acid probe (SENP) (1) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (1) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, myperial proproteinmenta, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. Assay348-Assay3930 represent human liver single exon encoded peptides of the invention. Note: The sequence but was obtained in electronic format directly from WIPO at the printed specification ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                   Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Probe, human, breast disease; breast cancer; development disorder; inflammatory disease; proliferative breast disease; non-carcinoma tumour.
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Length 43; 0; Indels

95.0%; Score 19; DB 4; Le 100.0%; Pred. No. 5.9e+02; tive 0; Mismatches 0;

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RESULT 50
ABB37578
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to human single exon nucleic acid probes (SENP: see AA110068-AA128459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human Hela cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or eraging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.
                                                                                                                                                                                                                      Peptide #4975 encoded by probe for measuring cervical gene expression.
                                            Gaps
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                                                                                                                                                                                                                                            Probe; human; microarray; gene expression; cervical epithelial cell;
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                   95.0%; Score 19; DB 3; Length 47; 100.0%; Pred. No. 6.4e+02; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 27; SEQ ID NO 23367; 487pp; English.
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                                                                                                                                                 AAM18541 standard; protein; 48 AA.
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31-AUG-2000) 2000US-00503266.
21-SEP-2000) 2000US-0234687P.
24-OCT-2000) 2000US-0235399P.
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2000US-0207456P.
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                                                                                                                                                                                               (first entry)
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Best Local Similarity 100.
Matches 4; Conservative
                                            4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-488901/53.
                    Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                          34 VAEF 37
                                                                   2 VAEF 5
Sequence 47 AA;
                                                                                                                                                                                                                                                       cervical cancer
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                                                                                                                                                                                                                                                                                                    WO200157278-A2.
                                                                                                                                                                                                                                                                                Homo sapiens.
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The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human feetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.
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                                                                                                                                                                                                      Human; foetal liver; gene expression; single exon nucleic acid probe.
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                                                                                                                                                     Peptide #5084 encoded by human foetal liver single exon probe.
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95.0%; Score 19; DB 4; L.
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 0; Mismatches 0;
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ABB37578 standard; peptide; 48 AA.
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21-SEP-2000; 2000US-0063356.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236559P.
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                                                                                                    (first entry)
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                                                                                                    04-FEB-2002
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26-MAY-2000;
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                                                   ABB37578;
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measuring human gene expression in a sample derived from human heart (see MBA11535-ABA41305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease. Note: The sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow.
                                                                                                                                                                                                                             The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see
                                                                                                                             Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human bone marrow expressed probe encoded protein SEQ ID NO: 30993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95.0%; Score 19; DB 4; Length 48; 100.0%; Pred. No. 6.6e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                         Claim 15; SEQ ID NO 24638; 530pp; English
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                                                    Chen W, Rank DR;
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              (MOLE-) MOLECULAR DYNAMICS INC.
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26-MAY-2000; 2000US-0207456P.
30-UTN-2000; 2000US-0060408.
31-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
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Best Local Similarity
                                                    Penn SG, Hanzel DK,
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                                                                                         WPI; 2001-488899/53
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ID AAM
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                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid probes useful for analyzing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein #4867 encoded by probe for measuring heart cell gene expression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95.0%; Score 19; DB 4; Length 48; 100.0%; Pred. No. 6.6e+02; ive 0; Mismatches 0; Indels
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gene expression in human placenta.
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30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632566.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234539P.
04-OCT-2000; 2000GB-00024263.
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21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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2000US-00608408.
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                                                                                                                                                                                                                                                                                                                                       Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-488897/53
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Best Local Similarity
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                    WO200157272-A2
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30-JUN-2000;
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The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipidaemia and hypercholesteroleemia which is sesociated with coronary heart disease. ABG47348-ABG59990 represent human liver single exon encoded peptides of the invention. Note: The sequence information for this patent does not appear in the printed specification
                                                             probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human genome-derived single exon nucleic acid probes useful for analyzing
                                                The present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia; coronary heart disease.
             Example 4; SEQ ID NO 30993; 658pp + Sequence Listing; English
                                                                                                                                                                                                            95.0%; Score 19; DB 4; Let 100.0%; Pred. No. 6.6e+02; ative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                ABG52389 standard; peptide; 48 AA.
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26-MAY-2000; 2000US-0207456P.
30-UJN-2000; 2000US-00608408
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234687P.
04-OCT-2000; 2000UG-023659P.
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Best Local Similarity luv...
4; Conservative
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The present invention relates to novel single exon nucleic acid probes (see AA100010-AA110067). The present sequence is a peptide encoded by one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic actiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease and non-carcinoma tumours. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel single exon nucleic acid probe used to measuring gene expression in a human breast.
                                                                                                                                                                                                                                                                                                                                                                                     Probe; human; breast disease; breast cancer; development disorder; inflammatory disease; proliferative breast disease; non-carcinoma tumour.
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                                                                                                                                                                                                                                                                                                                                                    Peptide #4789 encoded by probe for measuring breast gene expression.
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llarity 100.0%; Pred. No. 6.6e+02;
Conservative 0; Mismatches 0; Indels
but was obtained in electronic format directly from WIPO ftp.wipo.int/pub/published_pct_sequences
                                                                               Length 48;
                                                                                                           0; Indels
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                                                                               Query Match 95.0%; Score 19; DB Best Local Similarity 100.0%; Pred. No. 6.6 Matches 4; Conservative 0; Mismatches
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ftp.wipo.int/pub/published_pct_sequences
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2000US-00632366.
2000US-0234687P.
2000US-0236359P.
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ses 4; Conserv
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30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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The invention relates to human polymuclectides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or which may induce production of other cytokines in other cell populations. The polymerides are useful in gene therapy, vaccines or peptide therapy. The polymerides are various cytokine-like activities, e.g. stem cell growth factor activity, hemmatopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activity, inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
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                                                                                                                                                                                    AA010565 standard; protein; 53 AA
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18-MAY-2000; 2000US-00577409.
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Best Local Similarity 100.
Matches 4; Conservative
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N-PSDB; AAI90496.
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VAEF 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to human polymucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to protokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymucleotides and polymetides are useful in gene therapy, vaccines or peptide therapy. The polymetides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, infinial activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                            Human; cytokine; cell proliferation; cell differentiation; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                         vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 20; SEQ ID NO 19139; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immune/haematopoietic antigen SEQ ID NO:14983.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95.0%; Score 19; DB 4; Lv
100.0%; Pred. No. 7.3e+02;
cive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAM87390 standard; protein; 56 AA.
                                                               Human polypeptide SEQ ID NO 19139.
                                                                                                                                                                                                                                                                                                                                                                                                         Fang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                     28-FEB-2000; 2000US-00515126.
18-MAY-2000; 2000US-00577409.
                                                                                                                                                                                                                                                                                     26-FEB-2001; 2001WO-US004927
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                                (first entry)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAI85178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 53 AA;
                                                                                                                                                                                                                     WO200164835-A2.
                                                                                                                                                                                      Homo sapiens
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                                06-NOV-2001
                                                                                                                                                                                                                                                      07-SEP-2001.
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Homo sapiens

AAO05247 standard; protein; 53 AA.

ESULT 57

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Gaps 6

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2001WO-US001354
WO200157182-A2
 17-JAN-2001;
 09-AUG-2001
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2000US-0236327P 2000US-0236367P 2000US-0236369P 2000US-0237037P 2000US-0237037P 2000US-0237037P 2000US-0237037P 2000US-0237037P 2000US-0237037P 2000US-0237037P 2000US-0237038P 2000US-0237038P 2000US-0241886P 2000US-0241886P 2000US-0241886P 2000US-0241886P 2000US-0241886P 2000US-0241886P 2000US-024178P 2000US-024178P 2000US-024178P 2000US-024178P 2000US-024178P 2000US-024178P 2000US-024178P 2000US-024178P 2000US-024178P 2000US-0246528P 2000US-0246528P 2000US-0246528P 2000US-0246528P 2000US-0246528P 2000US-0246528P 2000US-0246528P 2000US-0249204P 2000US-0249204P 2000US-0249214P 2000US-024924P 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 17-NOV-2000; 18-NOV-2000; 18 29-569 29-569 20-669-2000 20-6 3-NOV-2000; 3-NOV-2000; 3-NOV-2000; 3-NOV-2000; 3-NOV-2000; 11-DEC-2000; 05-JAN-2001; 

HUMAN GENOME SCI

(HUMA-)

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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAW82170 to AAW91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polymucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polymucleotides may be used to produce the secreted (I), by inserting the protein. (I) proteins and polymucleotides may be used to produce the secreted diseases, especially diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metaateses of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK5950 and AAM82169 represent sequences used in the exemplification of the present invention
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                                                                                                                                                                                 Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human matrix metalloproteinase 7 cleavage region peptide SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                     claim 11; SEQ ID NO 14983; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            non-vascularised; surgical incision; chronic wound; stroke;
macular degeneration; diabetic retinopathy; cleavage region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95.0%; Score 19; DB 4; Length 56; 100.0%; Pred. No. 7.8e+02; ive 0; Mismatches 0; Indels
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Ruben SM;
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21-DEC-2001; 2001US-00032376.
21-MAY-2002; 2002US-00153185.
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Best Local Similarity 100...
4; Conservative
    Barash SC,
                                                                          WPI; 2001-483426/52.
N-PSDB; AAK60171.
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    Rosen CA,
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Gaps ô

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                                                                                                                              The present invention describes an anti-angiogenic composition (1) for inhibiting expression of vascular endothelial growth factor (VEGF). (1) comprises an effective amount of a peptide inhibitor of matrix metalloproteinase (WMP), where the peptide inhibit the expression of VEGF. (1) has cytostatic, vulnerary, cardiant, cerebroprotective, vertical entitials of the composition of VEGF, and so can be used for inhibiting expression of VEGF, and so can be used for inhibiting growth of tumours and diminishing tumours size. The tumour can be metastatic, non-metastatic, vascularised, non-vascularised, hard or soft. (1) is also useful for treating injuries including wounds, surgical includions, chronic wounds, heart disease and stroke.
                                                                                                                                                                                                                                                                                                                               for treating disorders characterised by excessive angiogenesis e.g. macular degeneration and diabetic retinopathy. The present sequence represents a human MMP cleavage region peptide, which is used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; peptide inhibitor; matrix metalloproteinase-7; MMP-7; cleavage region; proenzyme form; cellular proliferation; fibroblast; keratinocyte; healthy skin development; wound healing; scarring; skin tone; wrinkle; anti-aging; vulnerary.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel peptide inhibitor of proteinase activity of matrix metalloproteinases, e.g. matrix metalloproteinase-2, useful for stimulating cellular proliferation of fibroblasts or keratinocytes.
                                                  vascular
                               Anti-angiogenic composition comprising peptide inhibitor of matrix metalloproteinase, useful for decreasing the expression of vascular endothelial growth factor and treating cancers and tissue injuries.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human matrix metalloproteinase (MMP) peptide inhibitor #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        95.0%; Score 19; DB 6; Le
100.0%; Pred. No. 7.8e+02;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABG76312 standard; protein; 56 AA
                                                                                                        Claim 17; Page 15; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 16; 120pp; English
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21-DEC-2001; 2001US-00032376.
21-MAY-2002; 2002US-00153185.
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WPI; 2003-381408/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 56 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31 VAEF
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The present invention relates to peptide inhibitors of metalloproteinases (MMPs), particularly metalloproteinase-2 (MMP-2). The inhibitors have peptide sequences related to the cleavage regions of the proenzyme forms of the MMPS. The peptide inhibitors are useful for stimulating collisation of fibroblasts or keratinocytes, promoting healthy skin development, treating wounds, preventing scarring, improving skin tone, reducing wrinkling and for simulating the development of smooth, healthy skin. The peptide inhibitors are useful as anti-aging and wound healing compounds. ABG76309-ABG76321 represent peptide inhibitors of MMPs
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Sequence 56 AA;

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95.0%; Score 19; DB 6; Length 56; 100.0%; Pred. No. 7.8e+02; ive 0; Mismatches 0; Indels
             Best Local Similarity 100.
Matches 4; Conservative
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                                                          2 VAEF 5
Query Match
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RESULT 61 **AAW**55888

AAW55888 standard; protein; 58 AA. AAW55888;

(first entry) 22-JUL-1998 

Rat PC12.

Rat; telomerase; human; cancer; screening; inhibitor; elucidation; detection; probe; diagnosis; cell growth; ageing.

Rattus sp.

WO9807838-A1

26-FEB-1998.

97WO-JP002904. 21-AUG-1997;

96JP-00219761. 97JP-00018878 97JP-00031807 17-FEB-1997; 21-AUG-1996;

(MITU ) MITSUBISHI CHEM CORP.

Takahashi K, Fujino Y, Harada N; shikawa F, Nakamura H,

WPI; 1998-169149/15. N-PSDB; AAV25990 Telomerase protein of higher animals and humans and gene encoding it for use in diagnosis of cancer, screening of telomerase inhibitors and elucidation of biological control mechanisms.

Example 1; Page 69-70; 106pp; Japanese.

The present sequence represents rat PC12 which is used in an example of the present invention which describes protein components of telomerase. The DNA or RNA encoding the telomerase protein component or its fragments can be used as a nucleotide probe for the detection of cancer cells and for diagnosis of cancer. Potential telomerase inhibitors can be screened by measuring their effect on the assay of the active form in cells or tissues. The polypeptide and DNA coding for it can be used in the elucidation of biological control mechanisms of, e.g. cell growth or ageing and of the mechanisms of cancer development.

The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 in the specification). ABNI5762 to ABN27252 encode the human ORFX proteins given in ABP00010 to ABP1500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX associated disorder in humans, and in the manufacture of a medicament for treating of gydrome associated with ORFX associated disorder. ORFX polynucleotide syndrome associated in Gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage, of transplantation, cardiovascular diseases, disorders related to organ transplantation, cardiovascular diseases, disorders, infectious costocarthitis, neurodegenerative diseases, disorders, infectious costocarthitis, autoimmune disorders such as multiple sclerosis, rheumatoid diseases, autoimmune infilammatory eye disease. Organ proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from systemic cytokine damage. N.B. The sequence data for this patent did not

Sequence 58 AA;

Query Match

Length 58; 95.0%; Score 19; DB 2;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperpooliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human polypeptides and polymucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders.
   Pred. No. 8.1e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 9690; 1037pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human ORFX protein sequence SEQ ID NO:9690.
                                                                                                                                                                                                                                                                                                                  ABP04854 standard; protein; 58 AA.
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29-AUG-2000; 2000US-0228716P.
      100.0%;
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                                        4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-106308/14.
Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                           49 VAEF 52
                                                                                              2 VARF 5
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990S-0137724P.
990S-0137724P.
990S-0138647P.
990S-0138647P.
990S-0139452P.
990S-014033P.
990S-014033P.
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                                                                                                                                                                                                                                                                                                                                           Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
    form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                      Gaps
                                                                      Query Match 95.0%; Score 19; DB 5; Length 58; Best Local Similarity 100.0%; Pred. No. 8.18+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana protein fragment SEQ ID NO: 77787.
                                                                                                                                                                                                                                 AAG60085 standard; protein; 59 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9905-012180P.
9905-0123180P.
9905-0125788P.
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9905-0125788P.
9905-012674P.
9905-012874P.
9905-0130077P.
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                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana.
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                                                Sequence 58 AA;
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AG60085
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Gaps .

Indels

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95.0%; Score 19; DB 3; Length 59; 100.0%; Pred. No. 8.2e+02;
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9908-0147416P

9908-0147431P

9908-0148111P

9908-0148341P

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Best Local Similarity
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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0; Mismatches
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99US-0123180P.
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99US-01324407P.
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05-MAX-1999;
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990S-0139453P 990S-0139454P 990S-0139455P 990S-0139456P 990S-0139456P 990S-0139451P 990S-0139451P 990S-0139451P 990S-0139461P 990S-0139461P 990S-0139461P 990S-013961P 990S-014033P 990S-014033P 990S-014230P 990S-014231P 990S-014231P 990S-014231P 990S-014433P 990S-014433P 990S-014433P 990S-014433P 990S-014433P 990S-014433P 990S-014433P 990S-014433P 990S-014433P 990S-014433P 990S-014433P 990S-014433P 990S-014433P 990S-014433P 990S-014433P 990S-014433P 990S-014433P 990S-014455P 990S-014458P 990S-014458P 990S-014458P 990S-014458P 990S-014458P 990S-014458P 990S-014458P 990S-014458P 990S-014458P	9US-014192P 9US-0145214F 9US-0145224P 9US-0145216F 9US-0145918P 9US-01459119P 9US-01463818P 9US-01463818P 9US-0147038P 9US-0147038P 9US-0147304P 9US-0147304P 9US-0147304P 9US-0147304P 9US-0147304P 9US-0147304P 9US-0147304P 9US-0147304P 9US-0147304P 9US-0147304P 9US-0147304P 9US-0147304P 9US-0147304P 9US-0147304P
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13-AUG-1999   99US-0149664P.     15-AUG-1999   99US-0149356P.     16-AUG-1999   99US-0149356P.     16-AUG-1999   99US-0149356P.     18-AUG-1999   99US-0149356P.     20-AUG-1999   99US-0149322P.     20-AUG-1999   99US-0149926P.     21-AUG-1999   99US-0149902P.     22-AUG-1999   99US-0149902P.     27-AUG-1999   99US-0149902P.     27-AUG-1999   99US-0149902P.     27-AUG-1999   99US-0151006P.     27-AUG-1999   99US-0151006P.     27-AUG-1999   99US-0151006P.     27-AUG-1999   99US-0151006P.     27-AUG-1999   99US-0151006P.     27-AUG-1999   99US-0151006P.     28-EP-1999   99US-0151006P.     28-EP-1999   99US-0151006P.     28-EP-1999   99US-0151006P.     28-EP-1999   99US-0151006P.     28-EP-1999   99US-015408P.     28-EP-1999   99US-015408P.     4-OCT-1999   99US-0155056P.     4-OCT-1999   99US-0155058P.     4-OCT-1999   99US-0155039P.     4-OCT-1999   99US-0156039P.     4-OCT-1999   99US-016039P.     4-O				B 3; Length 59 .2e+02; s 0; Indels
13.AUG-1999; 99US-0148 17.AUG-1999; 99US-0149 20.AUG-1999; 99US-0149 20.AUG-1999; 99US-0149 20.AUG-1999; 99US-0149 20.AUG-1999; 99US-0149 23.AUG-1999; 99US-0149 23.AUG-1999; 99US-0149 24.AUG-1999; 99US-0159 27.AUG-1999; 99US-0159	வ வ வ வ வ வ வ வ வ வ வ வ	ந் <sub>ல</sub> ் க்	ស់ សំ	Score 19; ; Pred. No. 0; Mismatch
13-AUG-1999; 17-AUG-1999; 17-AUG-1999; 20-AUG-1999; 20-AUG-1999; 20-AUG-1999; 21-AUG-1999; 22-AUG-1999; 23-AUG-1999; 24-AUG-1999; 25-AUG-1999; 26-AUG-1999; 27-AUG-1999; 28-SEP-1999; 28-SEP-1999; 29-SEP-1999; 29-SEP-1999; 21-OCT-1999; 21-OCT-1999; 21-OCT-1999; 22-OCT-1999; 22-OCT-1999; 23-OCT-1999; 24-OCT-1999; 25-OCT-1999; 26-OCT-1999; 26-OCT-1999; 26-OCT-1999; 27-OCT-1999; 28-OCT-1999; 28-OC	90S-0148 90S-0149 90S-0149 90S-0149 90S-0149 90S-0149 90S-0150 90S-0150	09000000000000000000000000000000000000	9008-01599 9008-01599 9008-01699 9008-01609 9008-01609 9008-01609 9008-016199 9008-016199 9008-016199 9008-016199 9008-016199	95.0% ty 100.0 ervative
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nucleic acid probes useful for analyzing
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                                                                                                                                                                                                                                                                                                                                                                                                             claim 27; SEQ ID NO 36115; 654pp; English
                                                                                                                                                                                                                                                                                      Rank DR;
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                                                                                                                                26-MAY-2000; 2000US-0207456P.
30-UUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-023659P.
04-OCT-2000; 2000GB-00024263.
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2000US-00632366.
2000US-0234687P.
2000US-0234687P.
2000US-0236359P.
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              WO200157272-A2
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03-AUG-2000;
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26-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and single exon nucleic acid probes derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.
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                                                                                                                                                                      Human; foetal liver; gene expression; single exon nucleic acid probe.
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                                                                                                                                   Peptide #9550 encoded by human foetal liver single exon probe.
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genetic disorder.
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                                  ABB42044 standard; peptide; 60 AA
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26-MX-2000; 2000US-0201456P.
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03-AUG-2000; 2000US-0053356.
21-SFP-2000; 2000US-023468TP.
04-GCT-2000; 2000US-0236559P.
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                                                                                                      04-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Conservative
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 VAEF 5
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                                                                                                                                                                                                                                            WO200157277-A2.
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                                                                     ABB42044;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99
   RESULT 65
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diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention
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                                                                                                                                                                                                                                                                                                                                                                                       Human liver peptide, SEQ ID No 36123
                                                                                                                                                                                                                                                                                      ABG57475 standard; peptide; 60 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0234687P.
2000US-0236359P.
2000GB-00024263.
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                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                       4; Conservative
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                                                                                                    Query Match
Best Local Similarity
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                                                                                                                                                                       2 VAEF 5
                                                                        Sequence 60 AA;
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04-OCT-2000;
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21-SEP-2000;
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Matches
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                                                                                                                                                                                                     요
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                                                                                                                                                                                    The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention
                                                                                                      Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human brain expressed single exon probe encoded protein SEQ ID NO: 35030.
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                                                                                                                                                       Example 4; SEQ ID NO 36043; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                    Similarity 100.0%; Score 19; DB 4; Length 60; Similarity 100.0%; Pred. No. 8.4e+02; 4; Conservative 0; Mismatches 0; Indels
                                      Rank DR
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                                                                                                                      gene expression in human bone marrow.
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30-JUN-2000; 2000US-0069408.
03-AUG-2000; 2000US-00632466.
27-SEP-2000; 2000US-023468PP.
27-SEP-2000; 2000US-023659P.
04-OCT-2000; 2000GB-00024263.
        (MOLE-) MOLECULAR DYNAMICS INC
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                                      Chen W,
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                                      Penn SG, Hanzel DK,
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                                                                        WPI; 2001-488900/53
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                          Sequence 60 AA;
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                                                                                     Gaps
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hypercholesterolaemia, coronary heart disease.
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Length 60;
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95.0%; Score 19; DB 4; Le 100.0%; Pred. No. 8.4e+02; ive 0; Mismatches 0;
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WO200157182-A2
             Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a human ORF polypeptide, a substrate for extracellular signal-regulated kinase, ERR-6. Substances that modulate the activity of the ORF polypeptide can be used to treat diseases selected from dermatemyositis, polymositis, inclusion body myositis, sarcoid myopathy, AZT myopathy, myocardial infarction, and ischaemia/reperfusion. The probes and antibodies can be used to detect the presence
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                                                                                                                                                                                                                                                        ORF polypeptide; dermatomyositis; polymyositis; inclusion body myositis; sarcoid myopathy; AZT myopathy; myocardial infarction; ischaemia; ERK-6; extracellular signal-regulated kinase; reperfusion.
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                Gaps
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1.7e+02;
ss 0; Indels
100.0%; Pred. No. 8.4e+02; ative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid encoding ORF polypeptide.
                                                                                                                                                                                                                                 HLH domain of drosophila E-spl m5.
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                                                                                                                                            AAY17262 standard; peptide; 62 AA
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Best Local Similarity 100.
Matches 4; Conservative
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Giot J;
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                                                                   VAEF 11
                                          2 VAEF S
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2000US-0226868P.
2000US-0227182P.
2000US-022924P.
2000US-0229344P.
2000US-0229344P.
2000US-0229344P.
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2000US-0239344P.
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2000US-0220963P.
2000US-0220964P.
2000US-0224518P.
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2000US-0217487P.
2000US-0217496P.
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17-JAN-2001; 2001WO-US001354
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(HUMA-) HUMAN GENOME SCI INC.

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000US-0249265P
29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000;
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20-067-2800;
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08-NOV-2000;
08-NOV-2000;
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05-JAN-2001;
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM1921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polymucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased cample, they may be used to treat disorders associated with decreased that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polymucleotides may be used to produce the secreted (I), by inserting the protein cacids into a host cell and culturing the cell to express the protein and polymucleotides may be used to provent, diagnose and treat immune/haematopoietic-felated diseases, especially cancers and cancer mederatess of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention
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                                                                                                                          Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
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Jones R, Carter D;
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                                                                                                                                                                                Claim 11; SEQ ID NO 18840; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95.0%; Score 19; DB 4; Length 62;
100.0%; Pred. No. 8.7e+02;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Propionibacterium acnes immunogenic polypeptide #30343.
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Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR,
Barth B, Vallieve-Douglass J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABM65667 standard; protein; 62 AA.
                                  Ruben SM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 4; Conservative
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                                  Barash SC,
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                                                                   WPI; 2001-483426/52.
N-PSDB; AAK64028.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 62 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-APR-2003.
                                  Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABM65667;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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26-FEB-2001; 2001WO-US004927
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18-MAY-2000; 2000US-00577409.
                                                                                                                                                                                                                                                                  rang YT, Liu C, Drmanac RT;
                                                                                                                             Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC
                                                                                                                      Sequence 62 AA;
                                                                                                                                                                                                                          40200164835-A2.
                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                   06-NOV-2001
                                                                                                                                                                                                                                 07-SEP-2001,
                                                                                                                                                                            AA009517;
                                                                                                                                                             RESULT
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Isolated hucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                                                                                     The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                               Claim 20; SEQ ID NO 23409; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98DE-01011194
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                            WPI; 2001:514838/56
                                                                N-PSDB; AAI89448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                       concoding a Propionibacterium acnes protein. The invention also relates to an isolated purplication. The invention also relates to polypeptides encoded by the polymuclectides (ABM35624-ABM64536) and to immunogenic fragments of P. acnes polypeptides. The invention additionally encompasses expression vectors and host cells comprising a diditionally encompasses expression vectors and host cells comprising a polypeptide of the invention; a method for stimulating an immune response specific for a P. acnes polypeptide and an isolated T cell population comprising T cells prepared via this method; a vaccine composition (comprising P. acnes polypeptides, polymeticotides, antibodies, fusion proteins, T cell populations, or antigen-presenting cells that express the polypeptide); a method and kit for detecting or determining the presence or absence of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a proteins. T cell populations or antigen-presenting cells that express the polypeptides antibodies, fusion proteins, T cell populations or antigen-presenting acne polypeptides antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the polypeptides are useful for diagnosing, preventing or treating acnes protein. The polymucleotides can also be used as probes or primers for nucleic acid hybridisation. The vaccine composition is useful for performing a diagnostic assay. The present and the kit is useful for performing a diagnostic assay. The present contain an immunogenic region. Note The sequence data for this patent did not form part of the printed specification, but was contain an immunoffice.
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polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
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                                                                                                                                                                         to an isolated polymucleotide (ACF64435-ACF64733)
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                                                                                                    Claim 7; SEQ ID NO 30343; 1481pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid expressed at high level in normal prostatic tissue and encoded polypeptides, used to treat cancer and screen for therapeutic
                                                                                                                                                                                                                                                  Expressed sequence tag; EST; prostate; tumor; treatment; gene therapy; cancer; tissue specificity; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes novel nucleic acid sequences (A) that are expressed at high level in normal prostatic tissue. Polypeptides (I) encoded by (A) are used: (a) for identifying agents for treatment of
                          Gaps
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95.0%; Score 19; DB 4; Length 64; 100.0%; Pred. No. 9e+02; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                            Human prostate cancer-associated protein 49.
                                                                                                                                                                                                                                                                                                                                                                                                                           (META-) METAGEN GES GENOMFORSCHUNG MBH.
                                                                                                                                                AAY48352 standard; protein; 67 AA.
                                                                                                                                                                                                                                                                                                                                                                          98DE-01011194.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 22; 143; 194pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  agents.
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prostatic cancer and (b) for therapy of prostate cancer, optionally where expressed by gene therapy methods. (a) is also used to isolate full-length genes (for gene therapy) and for recombinant production of (I), which can be used to raise specific antibodies. (A) are identified by assembly of ESTs (expressed sequence tags) before these are analyzed for expression pattern (tissue specificity). This approach eliminates many of the false results, as regards tissue specificity, associated with known methods that use single (usually short) ESTs. AAY48304-Y48456 represent peptides encoded by the expressed sequence tags described in the method of the invention

Sequence 67 AA;

ö Gaps . Query Match
95.0%; Score 19; DB 2; Length 67;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indele Length 67;

≿ ŏ RESULT 75

ABP31047 standard; protein; 68 AA.

(first entry) 08-JUL-2002 ABP31047;

Human ORF20 protein, SEQ ID NO:40.

Human, ORF; open reading frame; ORPX; drug screening; diagnosis; disease monitoring; cytokine; cell proliferation; cell differentiation; limmune modulation; haematopoiesis regulation; tissue growth, angiogenesis; activin; inhibin; chemotactic; chemokinetic; haemostatic; thrombolytic; tumour inhibition; bodily characteristic; fertility; behaviour; cancer; proliferative disorder; neurological disorder; cardiovascular disease; immune system disorder; organ transplantation; tissue growth disorder; tissue regeneration disorder; diabetes mellitus; hypothyroidism; cholesterol ester storage disease; infection; vulnerary; vasotropic; antipsoriatic; antidiabetic; cytostatic; nostropic; vanciant; hypotensive, antiatherosclerotic; antidoscular; thrombolytic; cardiant; hypotensive, antiatherosclerotic; anticoagulant; thrombolytic; cardiant; hypotensive, antichyroid; antiinflammatory; immunomodulator; dermatological; analgesic; virucide; antibacterial; fungicide.

WO200190366-A2.

29-NOV-2001.

24-MAY-2001; 2001WO-US017076.

24-MAY-2000; 2000US-0206690P

(CURA-) CURAGEN CORP.

Leach MD, Shimkets RA;

WPI; 2002-106200/14. N-PSDB; ABN75073. Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and disorders related to organ transplantation.

Claim 10; Page 280; 2508pp; English.

Sequences ABB31028-ABB35561 represent 4534 novel human proteins designated ORF (open reading frame) 1-4534, and sequences ABN75054-ABN7567 represent cDNAs encoding them. The invention also encompasses 

cc polypeptides at least 80% identical to the ORFI-ORF4534 (collectively cf. referred to as ORFX) proteins, polymucleotides at least 85% identical to the ORFX undered cond sequences, vectors and host cells comprising ORFX polymucleotides, the recombinant production of ORFX proteins, antibodies specific for ORFX proteins, methods of detecting ORFX proteins, antibodies and polymucleotides methods of screening for modulators of ORFX expression or activity, and methods of screening individuals for a predisposition to an ORFX-associated disorder. The ORFX proteins of the invention have a wide crange of biological activities, such as cytokine, cell proliferation, cell differentiation, immune modulation, hadematopolesis regulation, cell differentiation, immune modulation, hadematopolesis regulation, cell differentiation, antiinflammatory activity, thrombolytic activity, named antiinflammatory activity, thrombolytic activity, and may also be involved in the determination of bodily characteristics, fertility and behaviour. ORFX proteins, or the proliferative disorders such as sporiasis and banigh tumours, cother proliferative disorders such as sporiasis and banigh tumours, cother proliferative disorders such as sporiasis and banigh tumours, corpus proliferative disorders such as sporiasis and banigh tumours, corpus proliferative disorders such as epollapsy and Alzheimer's disease, corpus and infectious diseases caused by viral, bacterial, diseases such as epollapsy and Alzheimer's disease, and infectious diseases caused by viral, bacterial, corpus disease, and infectious diseases caused by viral, bacterial, sequences, in penetic diagnosis, and in forensic belongs control of primers and probes, in the detection of ORFX general and in drug screening. The ORFX proteins may be useful for studying the function and/or activity of ORFX protein, and in drug specialic and in free profession and in drug specialic and special and in drug specialic and conditions, treatment and monitoring of ORFX resociated belonged to disages. ö Query Match Best Local Similarity 100... A; Conservative Sequence 68 AA; 

Gaps ö 95.0%; Score 19; DB 5; Length 68; 100.0%; Pred. No. 9.6e+02; ive 0; Mismatches 0; Indels

2 VAEF 5 ઠ g Search completed: May 24, 2004, 17:38:08 Job time : 53.7857 secs

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on 5.1.6 4 Compugen Ltd. 1. 1. 1. 1. 1. (without alignments) 38.477 Million cell updates/sec	283366	chance to l result bei stribution	nding I prote I prote I prote Prothet Prothet Protei I prote I
GenCore versi Copyright (c) 1993 - 200 protein - protein search, using sw mode n on: May 24, 2004, 17:32:13 ; S Lle: ' US-09-594-978A-3	score: 20 C. S.	Database: PIR 78:*  1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:* 6: pir4:* 8: core greater than or equal to the score of the and is derived by analysis of the total score diagram of a score of the and is derived by analysis of the total score diagram of the total score	1 19 95.0 20 233049 3 19 95.0 33 2 G64625 4 19 95.0 33 2 G64618 6 19 95.0 54 2 R64618 7 19 95.0 55 2 A42375 19 95.0 63 2 G64007 10 19 95.0 63 2 G74007 11 19 95.0 63 2 G74007 12 19 95.0 63 2 G74007 13 19 95.0 74 2 D97045 14 19 95.0 77 2 G7277 15 19 95.0 77 2 G7277 16 19 95.0 79 2 T176034 17 19 95.0 89 2 R68118 18 19 95.0 89 2 R68118 19 95.0 89 2 R68118 19 95.0 89 2 R68118 22 19 95.0 100 2 G64490 24 19 95.0 101 2 H6416 25 19 95.0 108 2 G64490 26 19 95.0 111 2 T17582 27 19 95.0 111 2 T17582 28 19 95.0 114 2 A55872

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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  Qy 2 VARF 5              Db 15 VAEF 18  RESULT 3  E64618  hypothetical protein HP0789 - Helicobacter pylori (strain 26695) C;Species: Helicobacter pylori C;Species: Helicobacter pylori C;Species: Helicobacter pylori C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999	C;Accession: E64618 R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.; Khalak, H.G.; Glodek, A.; McKenn Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenn son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Rujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997 A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori. A;Reference number: A64520; MUID:97394467; PMID:9252185 A;Status: prellminary; nucleic acid sequence not shown; translation not shown A;Redetence: DNA A;Redetences: GB:AE000591; GB:AE000511; NID:92313918; PIDN:AAD07847.1; PID:923139	Query Match 95.0%; Score 19; DB 2; Length 48;  Best Local Similarity 100.0%; Pred. No. 1.36+02;  Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  Qy 2 VARF 5  Db 15 VAEF 18	REBULT 4 A42375 hypothetical protein (lon 5' region) - Bacillus brevis C;Bacies: Bacillus brevis C;Bacies: Bacillus brevis C;Bate: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 15-Oct-1999 C;Accession: A42375; 139873 B;Ito, K.; Udaka, S.; Yamagata, H. J; Bacteriol. 174, 2281-2287, 1992 A;Title: Cloning, characterization, and inactivation of the Bacillus brevis lon gene. A;Reference number: A42375; MUID:92202157; PMID:1551846 A;Accession: A42375 A;Accession: A2375 A;Accession: Dreliminary A;Relecule type: DNA A;Residues: 1-52 < ITO> A;Cross-references: GB:D00863; NID:9216293; PIDN:BAA00736.1; PID:g303507	Query Match  Query Match  Best Local Similarity 100.0%; Pred. No. 1.40+02;  Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  Qy 2 VAEF 5  AT VAEF 50  RESULT 5  E85745  Unknown protein encoded within prophage CP-933R [imported] - Escherichia coli (strain O C, Species: Escherichia coli (strain O C, Species: Escherichia coli #text_change 14-Sep-2001 C, Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C, Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C, Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 A; Perna, N. T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayher iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamcusis, K.; Apodaca Nature 409, 529-533, 2001 A; Reference number: A85480; MUID:21074935; PMID:11206551 A; Accession: E85745 A; Accession: E85745
probable calcium c 2990 rapid lysis protei 2990 phenylalanine ammo 4787 phenylalanine ammo 6147 probable Arp-depen 1038 probable membrane 1058 probable membrane 1050 probable membrane 1051 protein	NWENTS	mestic rabbit) on 19-Apr-1996 #text_change 16-Feb-1997 eidolf, R.; Linder, D.	abbit erythrocyte membrane	RESULT 2 GG4625 hypothelical protein HP0847 - Helicobacter pylori (strain 26695) C;Species: Helicobacter pylori C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999 R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Reterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne son, J.D.; Reliev, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997 A;Authors: Wallin, B.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori. A;Reference number: A64520; MuID:97394467; PMID:9282185 A;Accession: G64625 A;Accession: G64625 A;Accession: G64625 A;Accession: G64625 A;Accession: G64626 A;Residues: 1-33 <-TOM> A;Molecule type: DNA A;Residues: 1-33 <-TOM> A;Cross-references: GB:AE000596; GB:AE000511; NID:g2313982; PIDN:AAD07920.1; PID:g231400 Query Match Best Local Similarity 100.0%; Pred. No. 88;
979 19 95.0 724 2 B85045 980 19 95.0 725 1 22BPA4 981 19 95.0 725 2 S52990 983 19 95.0 725 2 G84787 984 19 95.0 726 2 AIO147 985 19 95.0 729 2 AF0808 987 19 95.0 742 2 AF0816 987 19 95.0 742 2 AF0816 988 19 95.0 744 2 T13048 989 19 95.0 744 2 T13048 990 19 95.0 746 2 S31816	19 95.0 754 2 725 19 95.0 761 1 704 19 95.0 763 2 823 19 95.0 763 2 849 19 95.0 768 2 849 19 95.0 768 2 865 19 95.0 772 2 705 19 95.0 772 2 705 19 95.0 781 2 A69	RESULT 1 S39049 cytotoxin-binding protein - rabbit C,Species: Oryctolagus cuniculus (don C,Date: 18-Feb-1994 #sequence_revisic C,Accession: S39049 R,Lutz, F.; Mohr, M.; Grimmig, M.; Le	Eur. J. Blochem. 217, 1123-1128, 1993 A,Title: Pseudomones aeruginosa cytocoxin-binding protein in 1 A,Reference number: S39049; MUID:94039134; PMID:7693466 A,Accession: S39049 A,Status: preliminary A,Molecule type: protein A,Residues: 1-20 <lut> C,Superfamily: lens fiber membrane major intrinsic protein C,Superfamily: lens fiber membrane major intrinsic protein C,Superfamily: lens fiber wembrane ajor intrinsic protein Matches 4; Conservative 0; Mismatches 0; Indels C,YAEF 5 Db 14 VAEF 17</lut>	RESULT 2 G64625 hypothetical protein HP0847 - Helicob C,Species: Helicobacter pylori C,Date: 09-Aug-1997 #sequence_revisic C,Dacession: G64625 R,Tomb, J.F.; White, O.; Kerlavage, J Peterson, S.; Loftus, B.; Richardson son, J.D.; Kelley, J.M.; Cotton, M.D. Nature 388, 539-547, 1997 A,Authors: Wallin, E.; Hayes, W.S.; BA,Title: The complete genome sequence A,Tetle: The complete genome sequence A,Reference number: A64520; MUID:973 A,Accession: G64625 A,Status: preliminary; nucleic acid i A;Molecule type: DNA A,Residues: 1-33 < TOM> A;Residues: 1-33 < TOM> A;Coss-references: GB:AE000596; GB:A Couery Match Best Local Similarity 100.0%; P.

N;Molecule type: DNA N;Residues: 1-54 <STO>

Query Match Best Local Similarity 100.0

7;Genetics: 1;Gene: Z2382

32 VAEF 35

2 VAEF 5

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C;Accession: JC4002

Rivarisawa, A.; Faunekawa, H.; Okamura, K.; Okamoto, R.
Biosci. Biotechnol. Biochem. 59, 582-588, 1995

A;Attle: Nucleothol. Biochem. 59, 582-588, 1995

A;Attle: Nucleothol. Biochem. 59, 582-588, 1995

A;Accession: JC4001; MUID:95290751; PMID:7772821

A;Accession: JC4002

A;Molecule type: DNA

A;Residues: 1-63 <ARI>
A;Cross-references: DDBJ:D30759; NID:9551628; PIDN:BAA06419.1; PID:d1006989; PID:9551629

A;Octe: the source was designated as Streptomyces thermotolerans
C;Genetics:
A;Gene: carA
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A; Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A; Status: nucleic acid sequence not shown; translation not shown
A; Status: nucleic acid sequence not shown; translation not shown
A; Residues: 1-63 <110R3
A; Cross-references: GB:U32728; GB:L42023; NID:g1573425; PIDN:AAC22109.1; PID:g1573437; T
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R;Kvingedal, A.M.
R;Kvingedal, A.M.
A;Title: Characterization of the 5' region of the Atlantic salmon (Salmo salar) transfer A;Reference number: 151350; MUID:95121925; PMID:7821802
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C; Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette
C; Keywords: ATP
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C;Species: Salmo salar (Atlantic salmon)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein H10451 - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999
C;Accession: G64007
                                                                                                                                                             carbomycin resistance protein carA - Streptomyces sp. (fragment)
C;Species: Streptomyces sp.
C;Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 20-Sep-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C:Keywords: ATP
F:1-55/Domain: ATP-binding cassette homology (fragment) <ABC2>
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95.0%; Score 19; DB 2; Length 63;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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VAEF 15
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Matches 4
12
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C; Accession: E71349

R; Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwintsfor, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDq they, L.; Weindah, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-389, 1998

A; Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A; Reference number: A71250; MuID:98332770; PMID:965876
A; Accession: E71349
A; Accession: E71349
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-59 <COL>A; Cross-references: GB:AE001205; GB:AE000520; NID:g3322501; PIDN:AAC65223.1; PID:g332250
A; Experimental source: strain Nichols
C; Genetics:
A; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Accession: A63386
3; Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson S; Klenk, H.P.; Clayton, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, B.F. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Wature 390, 364-370, 1997 Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Venter, J.C.

A; Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaech, Reference number: A69250; MUID:98049343; PMID:9389475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Cross-references: GB:AE001028, GB:AE000782, NID:g2689351, PIDN:AAB90157.1, PID:g264956
C;Superfamily: Methanococcus jannaschii hypothetical protein MJ0975
                                                                 4) Cross-references: GB:AE005174; NID:g12s15374; PIDN:AAG56425.1; GSPDB:GN00145; UWGP:Z23
A:Experimental source: strain 0157:H7, substrain EDL933
3) Genetics:
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C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Species: Archaeoglobus fulgidus
.Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 11-Jan-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            conserved hypothetical protein AF1090 - Archaeoglobus fulgidus
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                                                                                                                                                                                                                                                     95.0%; Score 19; DB 2; Length 54; 100.0%; Pred. No. 1.5e+02; tive 0; Mismatches 0; Indels
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51 VAEF 54

2 VAEF 5

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Query Match Best Loc Matches

A, Accession: A69386

Query Match Best Local Similarity Matches 4; Conserv

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hypothetical protein BH2182 [imported] - Bacillus halodurans (strain C-125)

C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: R93922
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hir:
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
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                                                                                                                                                                            hypothetical protein A532L - Chlorella virus PBCV-1
C;Species: Chlorella virus PBCV-1
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T1803# #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
R;Graves, N.V.; Van Etten, J.L.
submitted to the EMBL Data Library, May 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein ZC477.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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A;Experimental source: specific host Chlorella strain NC64A
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:U40802; PIDN:AAA81506.1; CESP:ZC477.6 C;Genetics:
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text
C;Accession: T27605
R;Du, Z
submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid ZC477.
A;Reference number: Z20392
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100.0%; Pred. No. 2.2e+02;
ive 0; Mismatches 0;
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A;Molecule type: DNA
A;Residues: 1-79 <GRA>
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A,Molecule type: DNA
A,Residues: 1-79 <DUZ>
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Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity
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A;Molecule type: DNA
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Gene: CBSP:ZC477.6
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  2 VAEF
                                                   VAEF
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T27605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein CAC1179 [imported] - Clostridium acetobutylicum
CiSpecies: Clostridium acetobutylicum
CiSpecies: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
CiAccession: D97045
Rivolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, Daly, M.J.; Bennett, G.N.; Koonin, B.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Fitle: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc
A;Reference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: phage 186
C;Date: 28-May-1993 #sequence_revision 28-May-1993 #text_change 17-Mar-1999
C;Accession: 807277; $807277; $815277
Mol. Biol. 191, 199-209, 1986
A;Title: Control of gene expression in the P2-related template coliphages. III. DNA sequence number: 807277; $\text{MUD:87112711}; $\text{PMID:3806670}$
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A; Readdues: 1-75 «XDL.)
A; Cross-references: EMBL:X04449; NID:915549; PID:915550
R; Dibbens, J.A.; Gregory, S.L.; Egan, J.B.
Mol. Microbiol. 6, 2643-2450, 1992
A; Title: Control of gene expression in the temperate coliphage 186. X. The cl repressor
A; Reference number: S25273; MUID:93078618; PMID:1447973
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A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
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A;Molecule type: DNA
A;Residues: 1-64 <KVI>>
A;Residues: 1-64 <KVI>>
A;Crose-references: GB:L26909; NID:g598395; PIDN:AAC42221.1; PID:g598396
C;Genetics:
A;Gene: Tf
A;Introns: 14/1
C;Superfamily: transferrin; transferrin repeat homology
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                                                                                                                                                                                                                  Query Match 95.0%; Score 19; DB 2; Length 64; Best Local Similarity 100.0%; Pred. No. 1.8e+02; Matches 4; Conservative 0; Mismatches 0; Indels
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A;Molecule type: DNA
A;Residues: 1-74 <KUR>
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A; Residues: 1-75 <DIB>
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us-09-594-978a-3.rpr

Page 11

A; Residues: 1-84 <STO>

C;Genetics: A;Gene: BH2182

Query Match Best Local Similarity Matches 4; Conserv

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hypothetical protein Y1103 - Yersinia pestis plasmid pWT1
C;Species: Yersinia pestis
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T15018
R;Lindler, L.E.; Plano, G.V.; Burland, V.; Mayhew, G.F.; Blattner, F.R.
Infect. Immun. 66, 5731-5742, 1998
A;Title: Complete DNA sequence and detailed analysis of the Yersinia pestis KIMS plasmid
A;Reference number: Z18268; MUID:99043898; PMID:9826348
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R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L. R;Wood, D.W.; Setubal, J.C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell; Karp, P.; Romero, P.; Zhang, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C,Accession: F86818
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis se A;Reference number: A86625; WUID:21235186; PMID:11337471
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                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein ypjB (imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
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A;Experimental source: strain IL1403
C;Genetics:
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                                                               Indels
                           Pred. No. 2.5e+02;
Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0;
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A;Molecule type: DNA
A;Residues: 1-89 <LIN>
100.08; Pr.
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Best Local Similarity
Matches 4; Conserv
                      Best Local Similarity
Matches 4; Conserv
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A;Molecule type: DNA
A;Residues: 1-89 <STO>
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A;Genome: plasmid pMT1
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Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

Space: 20-Sep191 #sequence_revision 20-Sep-1991 #text_change 05-Dec-1997

Andreasion: A38725

The Girly G.F.; Achen, M.G.; Aldred, A.R.; Southwell, B.R.; Schreiber, G.

The Biol Chem. 266, 6201-6208, 1991

Antitle: The distribution of cerebral expression of the transferrin gene is species species companies of the 
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C;Superfamily: Escherichia coli ribosomal protein S15; eubacterial ribosomal protein S15
F;23-89/Domain: eubacterial ribosomal protein S15 homology <ES15>
                                             A, Cross-references: GB: AP001514; GB: BA000004; NID: g10174613; PIDN: BAB05901.1; GSPDB: GNOd Bxprimental source: strain C-125
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C;Species: Haemophilus influenzae
C;Species: Haemophilus influenzae
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999
R;Pleistohmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, P. Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.D.; Gocayne, J.D.; Fire, L.D.; Fritchman, J.L.; Glodek, A.; Kellav, J.M.; Weidman, Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Reference number: A64000; MUD:95350630; PMID:7542800
B;Accession: H64116
A;Molecule type: DNA
A;Residues: 1-89 <TILL>
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                                                                                                                                                                                                                                                   DB 2; Length 84; Similarity 100.0%; Pred. No. 2.38+02; 4; Conservative 0; Mismatches
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C)Superfamily: transferrin; transferrin repeat homology
C)Keywords: duplication
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4, Status: preliminary
4, Molecule type: mRNA
4, Residues: 1-87 < TUA>

13 VAEF 16

2 VAEF 5

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Molecule type: DNA Residues: 1-89 <TIG2>

Query Match

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RESULT 25
C64490
hypothetical protein MJI524 - Methanococcus jannaschii
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A,Experimental source: strain PAO1
C,Genetics:
A,Gene: PA3202
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
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A;Molecule type: DNA
A;Residues: 1-99 <STO>
A;Cross-references: GB:AE004744; GB:AE004091; NID:g9949317; PIDN:AAG06590.1; GSPDB:GN001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conserved hypothetical protein lmo2579 [imported] - Listeria monocytogenes (strain EGD-e C; Species: Listeria monocytogenes C; Species: Listeria monocytogenes (c; Species: Listeria monocytogenes (strain EGD-e C; Species: Listeria monocytogenes (strain 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001 C; Accession: AC1397 Rclaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J. Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karft, U. Science 294, 849-852, 2001 A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma A; Authors: Kreft, J.; Simoes, N.; Tierraz, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A; Fitle: Comparative genomics of Listeria species A; A; A; Accession: AC1377; MUID:21537279; PMID:11679669
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K.; Lim,
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A.Accession: E83244
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C;Species: Pseudomonas aeruginosa
C;Species: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: E8324
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brady, L.L.; Coulter, S.N.; Polger, K.R.; Kas, A.; Larbig, K.; Lim, Nature 406, 959-964, 2000
    Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                    ster, E.W.
Ajtile: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CSB.
A;Accession: AB3053
A;Accession: ACCESSION
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A;Molecule type: DNA
A/Residues: 1-97 <GLA>
A/Residues: 1-97 <GLA>
A/Experimental source: GB:NC_003210; PIDN:CAD00657.1; PID:g16412067; GSPDB:GN00177
A/Experimental source: strain EGD-e
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A;Experimental source: strain C58 (Dupont)
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Matches 4; Conserv
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A;Gene: Atu4039
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A;Gene: lmo2579
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Rishe, Q.; Singt, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Char Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, arreft, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: H90297
A;Accession: H90297
A;Molecule type: DNA
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C.Date: 20-85p-1999 #sequence_revision 20-8ep-1999 #text_change 21-Jul-2000

C.Date: 20-86p-1999 #sequence_revision 20-8ep-1999 #text_change 21-Jul-2000

C.Date: 10-80 # Modarnan, J.; Leigh, J.A.

J. Bacteriol. 179, 541-543, 1997

A.THLE: Nitrogenase phylogeny and the molybdenum dependence of nitrogen fixation in NA, Reference number: 216944; MUID:3144542; PMID:8990309
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A,Cross-references: GB:AE006641; NID:g13814625; PIDN:AAK41639.1; GSPDB:GN00155
C,Genetics:
A,Gene: SSO1404
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A;Molecule type: DNA
A;Residues: 1-106 <KES>
A;Residues: 1-106 <KES>
A;Cross-references: EMBL:U75887; NID:g1666882; PIDN:AAC45519.1; PID:g1666890
C;Genetics:
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C.Spsciese Sulfolobus solfataricus
C.Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C.Accession: #90297
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      Length 99;
95.0%; Score 19; DB 2; Le ilarity 100.0%; Pred. No. 2.8e+02; Conservative 0; Mismatches 0;
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4; Conservative
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\(\)\)\)Residues: 1-114 <HOF>
                                                                                                                                     Query Match
Best Local Similarity
Matches 4; Conserv
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Molecule type: DNA
Residues: 1-112 <STO>
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                                                  Sibilt, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, Relative Relative C.J.; White, O.; Olsen, G.J.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Science 273, 1058-1073, 1996

**Authors: Kaine, B.P.; Bordovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.Y.; Titele Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii **Reference number: A64300; MUID:96337999; PMID:8688087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Gross-references: GB.AL021646, GB:AL123456, NID:g3242278, PIDN:CAA16648.1, PID:g282759
A,Experimental source: strain H37Rv
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CjSpecies: Chlorella virus PBCV-1
CjSpecies: Chlorella virus PBCV-1
CjSpecies: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
CjAccession: T1758
RjCraves, M.V.; Van Etten, J.L.
AjReference number: Z18806
AjReference number: Z18806
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|Species: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
Species: Methanococcus jannaschii
Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 12-Jun-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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A.Status: preliminary, translated from GB/EMBL/DDBJ
A.Status: 1-111 - GRRA>
A.Residues: 1-111 - GRRA>
A.Cross-references: EMBL:U42580; NID:g4028896; PIDN:AAC96460.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h Similarity 100.0%; Score 19; DB 2; Length 108; Similarity 100.0%; Pred. No. 3e+02; 4; Conservative 0; Indels
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Superfamily: uncharacterized conserved protein MJ1524
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Best Local Similarity 100.
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Best Local Similarity
Matches 4; Conserv
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Residues: 1-109 <CC
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bubmitted to the Brookhaven Protein Data Bank, June 1994
A;Reference number: A52519; PDB:1AKP
A;Reference number: A52519; PDB:1AKP
A;Contents: annotation; conformation and disulfide bond assignments by (1)H-NMR, residue
A;Contents: annotation; conformation and disulfide bond assignments by (1)H-NMR, residue
B;Zein, N; Casaaza, A,M; DOYJE, T.W; Leet, J.E.; Schroeder, D.R.; Solomon, W.; Nadler
Proc. Natl. Acad. Sci. U.S.A. 90, 8009:8012, 1993
A;Title: Selective proteolytic activity of the antitumor agent kedarcidin.
A;Reference number: A58601; MUID:93376732; PMID:8367457
A;Note: the apoprotein may have proteolytic activity
C;Superfamily: macromomycin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      kedarcidin [validated] - Streptoalloteichus sp. (ATCC 53650)
NyAlernate names: kedarcidin apoprotein
C;Species: Streptoalloteichus sp.
C;Species: Streptoalloteichus sp.
C;Species: Streptoalloteichus sp.
C;Decies: 21-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 15-Sep-2000
C;Accession: A55872
C;Accession: A55872
Apribiot. 45, 1280-1254, 1992
Ayribiot. 45, 1280-1254, 1992
Ayribiot. As a new chromoprotein antitumor antibiotic. II. Isolation, purificati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ristover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradnan, S.; Cuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Alvire 406, 959-964, 2000
A; Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathor A; Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AE004598; GB:AE004091; NID:g9947687; PIDN:AAG05111.1; GSPDB:GN001
A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: pscI; PA1722
C;Superfamily: Yersinia enterocolitica plasmid pYV virC-region hypothetical protein yscI
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R;Constantine, K.L.; Colson, K.L.; Wittekind, M.; Friedrichs, M.S.; Zein, N.; Tuttle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 type III export protein PscI PA1722 [imported] - Pseudomonas aeruginosa (strain PAOI) C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: B83431
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A;Experimental source: specific host Chlorella strain NC64 C;Genetics: A;Gene: A92L C;Superfamily: Chlorella virus PBCV-1 hypothetical protein A92L
                                                                                                                                                                                                     95.0%; Score 19; DB 2; Length 111; 100.0%; Pred. No. 3.1e+02; Live 0; Mismatches 0; Indels
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95.0%; Score 19; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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C;Accession: A01608
R;Hobart, P.M.; Shen, D.P.; Crawford, R.; Pictet, R.L.; Rutter, W.J.
Science 210, 1360-1363, 1980
A;Title: Comparison of the nucleic acid sequence of anglerfish and mammalian insulin mR
A;Title: Comparison of the NUID:81056434; PMID:7001633
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A;Cross-references: GBs.AB006469; PIDN:AAX65184.1; PID:g14523629; GSPDB:GN00165
A;Experimental source: strain 1021, megaplasmid pSymA
A;Experimental source: strain 1021, megaplasmid pSymA
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler
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31-Mar-1981 #sequence_revision 31-Mar-1981 #text_change 16-Jul-1999
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Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-May-2000
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A,Reference number: Z24535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 95.0%; Score 19; DB 1; Length 116
Best Local Similarity 100.0%; Pred. No. 3.38+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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Best Local Similarity
Matches 4; Conserv
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A,Molecule type: mRNA
A,Residues: 1-118 <AAA>
                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 1-116 <HOB>
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Molecule type: DNA
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C,Date: 05-May-2000
C,Accession: T48682
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                                                                                                                                                                                                                                                                                                                           hypothetical protein ACR_C_804 [imported] - Agrobacterium tumefaciens (strain C58, Cered Cispecies: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Species: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C;Accession: D97414
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2321-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C,Accession: D7528
R;anonymous, Genoscope
submitted to the BMBL Data Library, July 1999
A;Reference number: A75001
A;Accession: D75218
A;Molecule type: DNA
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;Cross-references: GB:AJ248283; GB:AL096836; NID:g5457433; PIDN:CAB49195.1; PID:e151508
;Experimental source: strain Orsay
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Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
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                                                                        Length 114;
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Pred. No. 3.2e+02;
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                                                                   Query Match 95.0%; Score 19; DB 2; I
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 3.2e+02
iive 0; Mismatches (
  C;Keywords: antibiotic; pigment binding F;37-47,88-95/Disulfide bonds: #status experimental
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C;Species: Lophius americanus (American goosefish)
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100.0%; Pred. No. ...
0; Mismatches
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Best Local Similarity 100..
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Matches 4; Conserv
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Molecule type: DNA
Residues: 1-114 <KUR>
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Query Match 95.0
Best Local Similarity 100.
Matches 4; Conservative
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Matches 4; Conservative
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A;Molecule type: DNA
A;Residues: 1-126 <PAR>
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A,Gene: Rv3675
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submitted to GenBank, June 2000
M.A.; Remper, G.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Krieger, J.E.; Krieger, J.E.; Marques, M.V.; Martins, E.M.; Mareukuma, M.P.; Marino, C.L.; Marques, M.V.; Martins, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, W.C.; de Oliveira, R.C.; palmieri, D.P.; Authors: da Silva, A.C. & da Silva, M.S.; de Silva, M.S.; da Silva, M.S.; da Silva, M.S.; da Silva, M.S.; Tsuhako, M.H.; Vallada, H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z.; Z.; Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TyAccession: F82861
Stanonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequentianonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequentiature 406, 151-157, 2000
Yeritle: The genome sequence of the plant pathogen Xylella fastidiosa.
Yeritle: The genome sequence of the plant pathogen Xylella fastidiosa.
Yeritle: A82515; MUID: 20365717; PMID: 10910347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         v.Molecule type: DNA
v.Residues: 1-122 <SIM>
v.Cross-references: GB:AE003851, NID:g9112238; PIDN:AAF85575.1; GSPDB:GN00130; XFSC:XFad
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A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
                                  L.; Hyman, R.W.; Jones, T.
idience 293, 668-672, 2001
Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, lebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.; Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
;Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
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2)Species: Xylella fastidiosa
3)Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
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; Pred. No. 3.4e+02;
0; Mismatches 0; Indels
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100.0%; Pred. No. 3.4e+02;
cive 0; Mismatches 0;
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Matches 4; Conservative
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Best Local Similarity 100.
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A; Note: plasmid pXF5.1
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ki, S.; Church, G.M.; Daniels, C.J.; Mang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N. Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997
A.Fitle: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: B69129
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Residues: 1-125 <a href="https://doi.org/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1
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W. Marchell, M. Wreh, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin C.W.; Quall, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel Nature 403, 665-668, 2000

Nature 403, 665-668, 2000

A, Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp A; Reference number: A81250; MUID:20150912; PMID:10688204
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A;Experimental source: serotype O2, strain NCTC 11168
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C.Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
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100.0%; Pred. No. 3.5e+02;
ive 0; Mismatches 0; Indels
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Pred. No. 3.5e+02;
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C,Superfamily: 4-carboxymuconolactone decarboxylase
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100.0%; Pred. No. ...
... 0; Mismatches
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Page 16

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ileal lipid-binding protein - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 05-Nov-1999
C;Accession: A54797
R;Crossman, M.W.; Hauft, S.M.; Gordon, J.I.
J. Cell Biol. 126, 1547-1554, 1994
A;Title: The mouse ileal lipid-binding protein gene: a model for studying axial pattern
A;Reference number: A54797; MUID:94375529; PMID:8089185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable cathepsin B-like cysteine proteinase (BC 3.4.22.-) T15B16.17b - Arabidopsis th C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 26-Fbb-1999 #sequence_revision 26-Feb-1999 #text_change 22-Jun-1999
C;Accession: T02012
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A,Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome se
A,Reference number: A72200; MUID:99287316; PMID:10360571
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C;Species: Thermotoga maritima
C;Species: 11.-011-1999 #sequence_revision 11.-011-1999 #text_change 21.-011-2000
C;Daccession: D72348
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hicke Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.
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A;Residues: L129 <5TO>
A;Cross-references: EMBL:AF104919; NID:g3859590; PIDN:AAC72873.1; PID:g3859607
A;Experimental source: cultivar Columbia
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A;Residues: 1-128 <CRO>
A;Cross-references: GB:U00938; NID:g507143; PIDN:AAC27352.1; PID:g507144
C;Genetics:
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3.6e+02;
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Local Similarity 100.0%; Pred. No. 3.7e+02;
Les 4; Conservative 0; Mismatches 0;
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R;Stoneking, T.; Smith, R.
submitted to the EMBL Data Library, November 1998
A;Description: The sequence of A. thaliana T15B16.
A;Accession: T02012
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95.0%; Score 19; DB
Best Local Similarity 100.0%; Pred. No. 3.6
Matches 4; Conservative 0; Mismatches
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A,Introns: 26/3; 44/3; 71/3
A,Note: 113H: 61/3; Appain
C,Superfamily: papain
C,Keywords: cysteine proteinase; hydrolase
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A;Molecule type: DNA
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C;Superfamily: myelin P2 protein
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C;Species: Mycobacterium tuberculosis
C;Dacies: Mycobacterium tuberculosis
C;Dacession: D70799
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S; Connor, R.; Daviss, R.; Deviln, K.; Feltwell, T.; Gentles, S.; Hanlin, N.; Holroyd, S. Nature 393, 537-54, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295997; PMID:9634230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Status: preliminary; nucleic acid sequence not shown; translation not shown; Molecule type: DNA; Accoustive type: DNA; Accoustive type: DNA; Accoustive type: DNA; Accoustive type: 1-127 Accoustive type: DNA; Accoustive train account to the train H37Rv train H37Rv train H37Rv train H37Rv
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A;Residues: 1-127 <GLA>
A;Cross-references: GB:AL592022; PIDN:CAC97626.1; PID:g16414922; GSPDB:GN00178
A;Experimental source: strain Clip11262
C;Genetics:
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Accession: AB1732
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                                                                            Length 126;
                                                                            95.0%; Score 19; DB 2; Length 120 100.0%; Pred. No. 3.6e+02; Eve 0; Mismatches 0; Indels
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Best Local Similarity 100.
Matches 4; Conservative
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A;Gene: Cj0939c
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conserved hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
R;Accession: H75623
R;White, 0; Eisen, 7.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; KWhite, Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
                                                                                                                                                                                              hypothetical protein alr1525 [imported] - Nostoc sp. (strain PCC 7120)
C; Species: Nostoc sp. PCC 7120
C; Species: Nostoc sp. PCC 7120
C; Species: Nostoc sp. Rtrain PCC 7120
C; Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C; Accession: AG1996
R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch: Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, SDNA, Res. 8, 205-213, 2001
A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Answersence number: AB1807; MUID:21595285; PMID:11759840
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C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C;Accession: AH0137
C;Accession: AH0137
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
deno-Tarraga, A.M.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 521-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
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A;Molecule type: DNA
A;Residues: 1-132 <UNA
A;Cross-references: GB:BA000019; PIDN:BAB77891.1; PID:g17135345; GSPDB:GN00179
A;Experimental source: strain PCC 7120
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A;Residues: 1-133 <KUR>
A;Cross-references: GB:AL590842; PIDN:CAC89963.1; PID:g15979187; GSPDB:GN00175
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95.0%; Score 19; DB 2; Length 132;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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C;Superfamily: 15.5K protein (tolAB operon 5' region)
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C;Superfamily: rbcX protein
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81 VAEF 84
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Cypace: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 06-Jan-2003
Cypace: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 06-Jan-2003
Cypace: 20-Aug-1999 #sequence
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Ayereacted to the BMEL Data Library, July 1999
Ayereacte number: A7501
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Ayereacte number: A7508
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Ayereacte number: A7508
Ayereacte number: BMA
Ayereacte n
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A;Experimental source: strain MSB8
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C;Species: Anabaena sp.
C;Species: Anabaena sp.
C;Species: Anabaena sp.
C;Accession: UQ2270
R;Larimer, F.W.; Soper, T.S.
Sene 126, 85-92, 1993
A;Title: Overproduction of Anabaena 7120 ribulose-bisphosphate carboxylase/oxygenase in A;Reference number: UQ2270; MUD:93231541; PMID:8472962
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A;Gene: TM0655
C;Superfamily: conserved hypothetical protein MJ0315
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Best Local Similarity 100.0%; Pred. No. 3.7
Matches 4; Conservative 0; Mismatches
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A;Residues: 1-13-2 cLAR>
A;Cross.references: DDBJ:U01540
A;Experimental source: strain 7120
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                                              Status: preliminary
Molecule type: DNA
Residues: 1-130 <ARN>
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Dypotherical protein EC80771 [imported] - Escherichia coli (strain O157:H7, substrain F C; Species: Escherichia coli (forcein Ecentrichia coli (forcein Eccherichia coli (forcein Eccherichia coli (forcesion 18-Jul-2001 #text_change 03-Aug-2001 (forcesion 1.001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001 (forcesion 1.001 # forcesion 1.001 # f
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                               A Status: nucleic acid sequence not shown; translation not shown
A; Moteoule type: DNA
A; Moteoule type: DNA
A; Residues: 1-134 «BLAT»
A; Cross-references: GB:AE000177; GB:U00096; NID:g1786955; PIDN:AAC73830.1; PID:g1786957
A; Experimental source: strain K-12, substrain MG1655
C; Comment: This is one of the proteins, encoded by the fii-tolAB gene cluster, that is C; Genetics:
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A;Experimental source: strain 0157:H7, substrain EDL933
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3.8e+02;
hes 0; Indels
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A,Map position: 17 min
A,Start codon: GTG
C,Superfamily: 15.5K protein (tolAB operon 5' region)
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A;Gene: ybgC
C;Superfamily: 15.5K protein (tolAB operon 5' region)
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C;Superfamily: 15.5K protein (tolAB operon 5' region)
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Best Local Similarity 100.0%; Pred. No. 3.6
Matches 4; Conservative 0; Mismatches
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A;Molecule type: DNA
A;Residues: 1-134 <STO>
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A; Accession: G64809
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Gene: ECs0771
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C.Species: Pab-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C.Accesion: A84221
R.MG, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser. B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabld
Jung, K.H.; Alam, M.; Frestas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Athors: Huvu, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accus: preliminary
A;Molecule type: DNA
A;Esidues: 1-133 <STO>
A;Cross-references: GB:AE004437; NID:g10580221; PIDN:AAG19133.1; GSPDB:GN00138
C;Genetics:
A;Gene: ribE
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A;Cross-references: GB:M16489; NID:g148021; PIDN:AAA83918.1; PID:g1128977
A;Cross-references: GB:M16489; NID:g148021; PIDN:AAA83918.1; PID:g1128977
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc. A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453.1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
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C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 15-Oct-1982 #sequence_revision 30-Jun-1988 #text_change 01-Mar-2002
C;Accession: A55980; #sequence R.E.
J. Bacteriol. 169, 2667-2674, 1987
A;Title: Nucleotide sequence of a gene cluster involved in entry of E colicins and single, Reference number: A91835; MUD:8722192; PMID:3294803
A;Accession: A25980
                                                                                                                                                                                                                                                      A;Cross-references: GB:AE001826; NID:g6460827; PIDN:AAF12590.1; PID:g6460886; TIGR:DRB0d
A;Experimental source: strain R1
C;Genetics:
                               A,Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A,Reference number: A75250, MUID:20036896; PMID:10567266
A,Accession: H75623
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A;Reference number: A64720; MUID:97426617; PMID:9278503
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100.0%; Pred. No. 3.8e+02;
iive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 4; Conservative
286, 1571-1577, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Map position: megaplasmid
A, Genome: plasmid
A, Note: plasmid MP1
                                                                                                                                                        A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-133 <WHI>
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8

Query Match

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C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #text_change 03-Jun-2002
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C;Accession: E81355
R;Parkhill, J; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillir: C.W.; Quall, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyr A;Reference number: A81250; MUID:20150912; PMID:10688204
A;Accession: E81355
A;Eature preliminary
A;Molecule type: DNA
A;Residues: 1-137 <PAR>
A;Molecule type: DNA
A;Residues: 1-137 <PAR>
A;Across-references: GB:AL139076; GB:AL111168; NID:g6968128; PIDN:CAB73094.1; PID:g696827
C;Genetics:
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Nature 406, 477-483, 2000
A. Tille: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A, Accession: F82106
A, Status: preliminary
A, Molecule type: DNA
A, Residues: I-138 CHELY
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A.Experimental source: serogroup O1; strain NI6961; biotype El Tor
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95.0%; Score 19; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0;
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A, Map position: 1
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%, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
NA Res. 3, 109-136, 1996
%; Yitle: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
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A;Note: the nucleotide seguence was submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, D., T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
S.; Revens, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Stitle: Complete genome sequence of a multiple drug resistant Salmonella enterica serovit Reference number: AB0502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ionserved hypothetical protein STY0790 [imported] - Salmonella enterica subsp. enterica ;;Species: Salmonella enterica subsp. enterica serovar Typhi ;;Mote: this species has also been called Salmonella typhi this species has also been called Salmonella typhi this sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 ;;Accession: AD0592
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4, Cross-references: GB: AL513382; PIDN: CAD05206.1; PID: g16501976; GSPDB: GN00176
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is pecies: Synechocystis sp.
is pecies: Synechocystis sp.
is pecies: Sc. 4) wariety: PCC 6803
is pate: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
is peciesion: S76416
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                                        Length 134;
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                                        95.0%; Score 19; DB 2; Lt 100.0%; Pred. No. 3.8e+02;
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                                                                                 Similarity 100.0%; Pred. No. 3.8
4; Conservative 0; Mismatches
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\(\text{A}\)\(\text{Molecule type: DNA}\)
\(\text{A}\)\(\text{Residues: 1-136 <KAN>\)
\(\text{ANS}\)
                                                                            Best Local Similarity
Matches 4; Conserv
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1,Gene: STY0790

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Fig. 15.

Fig. 1
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A;Cross-references: GB:AE000957; GB:AE000782; NID:G2689280; PIDN:AAB89124.1; PID:G26484
C;Superfamily: riboflavin synthase beta chain
                                                                                                                                                      low-temperature regulated protein BN115 - rape
C;Species: Brassica napus (rape)
C;Species: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 28-May-1999
C;Accession: JQ2279
R;Weretilnyk, B.; Orr, W.; White, T.C.; Iu, B.; Singh, J.
Plant Physiol. 101, 171-177, 1993
A;Title: Characterization of three related low-temperature-regulated cDNAs from winter A;Reference number: JQ2279; MUID:94105287; PMID:7904076
A;Accession: JQ2279
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C;Species: Brassica napus (rape)
C;Species: 30-58p-1993 #sequence_revision 20-Aug-1994 #text_change 28-May-1999
C;Date: 30-58p-1993 #sequence_revision 20-Aug-1994 #text_change 28-May-1999
C;Accession: J02280
R;Meretilnyk, E; Orr, W.; White, T.C.; Iu, B.; Singh, J.
Plant Physiol. 101, 171-177, 1993
A;Title: Characterization of three related low-temperature-regulated cDNAs from winter
A;Reference number: J02299; MUID:94105287; PMID:7904076
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A,Residues: 1-142 <WER>
A,Cross-references: GB:S68879; NID:g544695; PIDN:AAB29483.1; PID:g544696
C,Comment: This protein is a low-temperature-related protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residuses: 1-142 <MES
A;Cross-references: GBs:S68726; NID:9544693; PIDN:AAB29482.1; PID:9544694
C;Comment: This protein is a low-temperature-related protein.
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100.0%; Pred. No. 4e+02;
tive 0; Mismatches 0; Indels
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C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 24-Nov-1999
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 24-Nov-1999
C;Accession: B6323.
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
S;Klenk, H.P.; Clayton, R.D.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaect A;Reference number: A6220; MUID:98049343; PMID:9389475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein BH2601 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: A83975
R;Takami, H; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: A83975
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A,Molecule type: DNA
A,Rodles: 1-139 < STIO>
A,Cross-references: GB:AP001516; GB:BA000004; NID:g10175192; PIDN:BAB06320.1; GSPDB:GN00
A,Experimental source: strain C-125
                                    A;Cross-references: GB:AE000902; GB:AE000666; NID:g2622500; PIDN:AAB85867.1; PID:g26225d
A;Experimental source: strain Delta H
C;Genetics:
A;Gene: MTH1390
C;Superfamily: riboflavin synthase beta chain
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C;Superfamily: Archaeoglobus fulgidus hypothetical protein AF0586
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95.0%; Score 19; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                          h Similarity 100.0%; Pred. No. 3.9e+02; 4; Conservative 0; Mismatches 0; Indels
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95.0%; Score 19; DB 2; Length 139;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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A;Residues: 1-140 <KLE>
                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 4; Conserv
A, Residues: 1-139 < MTH>
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A;Gene: BH2601
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DNA Res. 3, 109-136, 1996
A,Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocysti
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Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity
Matches 4; Conserv
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A, Residues: 1-147 <STO>
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R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PI
                                                                                                                                                                                                                                                                 robable transposase, truncated section 1 [imported] - Streptomyces coelicolor (fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fibosomal protein L13 [similarity] - Haloarcula marismortui

S.Species: Haloarcula marismortui

S.Species: Haloarcula marismortui

S.Accession: B41715

S.Kroemer, W.J., Arndt, B.

S.Kroemer, W.J., Arndt, B.

Biol. Chem. 266, 24573-24579, 1991

A,Title: Halobacterial S9 operon. Three ribosomal protein genes are cotranscribed with
                                                                                                                                                                                                                                                                                                                                                        tioliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, August 1999
1;Reference number: Z21618
1;Accession: T36978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , Cross-references: EMBL: AL109949; PIDN: CAB52892.1; GSPDB: GN00070; SCOEDB: SCU11.07c
, Experimental source: strain A3(2)
; Comment: A complete transposase sequence can be assembled from three adjacent orfs
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A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                              ;Species: Streptomyces coelicolor
;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000
;Accession: T36978
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A;Residules: 1-15 <KRO.
4;Crose-references: GB:M76567; NID:g148775; PIDN:AAA73097.1; PID:g148777
2;Superfamily: ribosomal protein L13</pre>
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       Length 143
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95.0%; Score 19; DB 2; Length 143
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                  0; Indels
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4;Reference number: A41715; MUID:92105119; PMID:1840597
4;Accession: B41715
     DB 2; Le
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  Query Match

95.0%; Score 19; DB
Best Local Similarity 100.0%; Pred. No. 4.1
Matches 4; Conservative 0; Mismatches
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Best Local Similarity 100..
Best Local 4; Conservative
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hypothetical protein Vng1398c [imported] - Halobacterium sp. NRC-1
CiSpecies: Halobacterium sp. NRC-1
CiSpecies: Halobacterium sp. NRC-1
CiSpecies: G2-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
CiAccession: G64294
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, E
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, E
Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablc
Jung, K.H.; Alam, M.; Freitas, T.
Proc., Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A,Athibras: Hou, S.; Danlabis, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A,Title: Genome sequence of Halobacterium species NRC-1.
A,Reference number: A84160; MUID:20504483; PMID:11016950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C)Species: Staphylococcus aureus
C)Species: Staphylococcus aureus
C)Jace: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C)Jace: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C)Jaccession: F89837
R)Kuroda, M.; Ohta, T.; Tuchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
R; Kuroda, M.; Ohta, T.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A)Filtle: Mhole genome Sequencing of meticillin-resistant Stapylococcus aureus.
A)Reference number: A89758; MUID:21311952; PMID:11418146
                                        A; Accession: S77043
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-145 < KANA
A; Cross-references: EMBL: D64005; GB: AB001339; NID: g1001779; PIDN: BAA10735.1; PID: g10065:
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C; Superfamily: Synechocystis hypothetical protein s110678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        conserved hypothetical protein SA0624 [imported] - Staphylococcus aureus (strain N315)
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A;Experimental.source: strain N315
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A; Reference number: S74322; MUID: 97061201; PMID: 8905231
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Riglaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecke.; Dominguez.Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, F. D.; Jones, L.M.; Karet, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; M.
A;Authors: Kreft, J.; Kuhn, M.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CiSpecies: Agrobacterium tumefaciens (strain C58, Dupont)
CiSpecies: Agrobacterium tumefaciens
CiSpecies: Agrobacterium tumefaciens
CiSpecies: L1.dan-2002 #sequence_revision 11-dan-2002 #text_change 18-Nov-2002
CiAccession: AB2857
Riwood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutryavin, T.; Levy, R.; Li, M.; McClellerage, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ribose 5-phosphate isomerase homolog lmo0498 [imported] - Listeria monocytogenes (strai
R;Zwickl, P.; Fabry, S.; Bogedain, C.; Haas, A.; Hensel, R.
J. Bacteriol. 172, 4329-4338, 1990
A;Title: Glyceraldehyde-3-phosphate dehydrogenase from the hyperthermophilic archaebact
scherichia coli.
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A)Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A)Reference number: AB2577; MUID:21608550; PMID:11743193

A)Accession: AB2857

A)Status: preliminary

A)Molecule type: DNA

A)Residues: 1.150 KURP.

A)Residues: 1.150 KURP.
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A;Molecule type: DNA
A;Rosidues: 1-149 <GLA>
A;Residues: 1-149 <GLA>
A;Cross-references: GB:NC_003210; PIDN:CAC98577.1; PID:g16409874; GSPDB:GN00177
A;Experimental source: strain EGD-e
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C;Accession: AC1137
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                                                                                                                                                 A;Reference number: S10650; MUID:90330536; PMID:2165475
A;Accession: S10655
A;Adscule type: DNA
A;Residues: 1-148 <ZMI>A;Note: the authors translated the codon GGT for residue 54 as Glu
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100.0%; Pred. No. 4.2e+02;
tive 0; Mismatches 0; Indels
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Local Similarity 100.0%; Pred. No. 4.2e+02;
les 4; Conservative 0; Mismatches 0; Indels
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C;Species: OS-May-2000 #sequence_revision OS-May-2000 #text_change O2-Feb-2001
C;Ccession: E81788
R;Parkhill, J; Achtman, M; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
R;Parkhill, J; Achtman, M; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.
A;Reference number: A81775; MUD:20222556; PMID:10761919
A;Accession: E81788
A;Accession: E81788
A;Accession: E81788
A;Accession: E81788
A;Accession: E8188
A;Accession:
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$10655
hypochetical protein X - Pyrococcus woesei (fragment)
C;Species: Pyrococcus woesei
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 18-Jun-1993
C;Accession: $10655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 04-Mar-2000
C;Accession: T34803
R;Murphy, L; Harris, D: Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
B;Accession: T34803
A;Stetus: preliminary; translated from GB/EMBL/DDBJ
A;Stetus: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-147 <MUR>
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;Gene: SCOEDB:SC2E1.35
;Superfamily: Streptomyces coelicolor hypothetical protein SC2E1.35
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95.0%; Score 19; DB 2; Length 147;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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                Length 147;
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95.0%; Score 19; DB 2; Length 148
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                               0; Indels
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                Query Match

95.0%; Score 19; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0;
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Gene: NMA2160

|||| 105 VAEF 108

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,Gene: Atu2283

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C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: H87263
R;Accession: H87263
R;Aisteran, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon n. J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. US.A. 99, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:AB005673; NID:g13421228; PIDN:AAK22108.1; GSPDB:GN00148
                                                                                                                         protein CC0121 [imported] - Caulobacter crescentus
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Matches 4; Conservative
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A, Status: preliminary
A, Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           !;Glasser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, Dominquez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.; Jones, L.M.; Karst, U.; Karst, U.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maik, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, M.; Reference number: AB1077; MUID:21537279; PMID:11679669
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                                                                                                                                                                                                                                                                                                                                                                                              Species: Listeria monocytogenes
Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
Accession: AB1089
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Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
Accession: AI1452
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Similarity 100.0%; Pred. No. 4.3e+02;
4; Conservative 0; Mismatches 0; Indels
                                                                          95.0%; Score 19; DB 2; Length 150; 100.0%; Pred. No. 4.3e+02; tive 0; Mismatches 0; Indels
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Map position: circular chromosome '; Superfamily: plastocyanin
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Matches 4; Conservative
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Best Local Similarity 100.
Matches 4; Conservative
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yMolecule type: DNA
yResidues: 1-150 <GLA>
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NResidues: 1-150 <GLA>
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P27166 stylonychia P02598 tetrahymena P02597 gallus gall P23286 candida alb P04464 triticum ae P06741 homo sapien P02603 oryctolagus P02601 rattus nory P05933 schizosach Q57797 methanococc P02599 dictyosteli Q9nip6 drosophila P13486 rhizobium m P50858 enterobacte	Q87955 fusbbacteri P02585 homo sapien P02587 sus sarofal P02586 oryctolagus P02586 oryctolagus P02586 oryctolagus P02586 oryctolagus P02588 gallus gallus P02589 gallus gall P10246 meleagris g P02589 rana escule Q99wve sulfolobus Q58045 methanococc P80562 anabaena sp P05052 synechocyst Q97328 homo sapien P47759 mus musculu P12986 acidianus a Q8dhrz synechococc P50157 ambyeroma m	949423 drosophila 2949423 drosophila 295678 thermus aqu 292197 homo sapien 200755 homo sapien 200755 homo sapien 260970 mus musculu P42857 homo sapien 262092 mus musculu P37745 escherichia P58008 thermotoga 291122 thermoplasm 22651 methanobact 21172 brugia mala 207792 vibrio mimi 200724 mus musculu P04916 rattus norv 084899 chlamydia t	Q8pvd5 methanosarc Q11063 mycobacteri Q9db76 mus musculu Q942b6 homo sapien P49208 pisum sativ P16631 gracularia Q8tx29 methanopyru Q8G534 piidobacte Q9rej6 arthrobacte P18432 drosophila P47296 mycoplasma P49255 cavia porce P02743 homo sapien P09224 mycoplasma O19063 sus Gcrofa P58654 salmonella Q8ylx9 anabaera sp O26232 methanobact P23680 rattus norv
900.0 900.0 900.0 900.0 900.0 900.0 900.0 900.0 900.0 900.0 900.0 900.0 900.0 900.0 900.0 900.0 900.0 900.0 900.0	18 90.0 155 1 Y463 FUSAN 18 90.0 155 1 TPCS HUMAN 18 90.0 159 1 TPCS HUMAN 18 90.0 159 1 TPCS PIG 18 90.0 169 1 TPCS PABIT 18 90.0 162 1 TPCS RANAN 18 90.0 162 1 TPCS GHCK 18 90.0 162 1 TPCS GHCK 18 90.0 162 1 TPCS MELGA 18 90.0 166 1 Y551 SUBL 19 90.0 166 1 Y551 SUBL 19 90.0 166 1 Y528 METJA 18 90.0 169 1 IPYR ANASP 18 90.0 171 1 NSGZ HUMAN 18 90.0 171 1 NSGZ HUMAN	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	8 8 8 8 9 9000 0 0 0 0 0 0 0 0 0 0 0 0 0
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085064 buchnera ap 007109 enterococcu 093744 pyrococcus Q10612 mycobacteri Q7wdy3 bordetella Q7way3 bordetella Q7vaz0 bordetella P48293 spirulina p P41563 bos taurus P50213 homo sapien	haemophilu corynebact african ho african ho clostridiu methanococ carynebact escherichi lactococu	Q90kb7 pasteurella P3691 neurospora Q8fpd3 corynebacte P45391 schizosacch P45513 citrobacter Q8nd0 fusobacteri Q8nd0 fusobacteri P5626 rhizobium s P31273 saccharomyc P16622 saccharomyc P16632 saccharomyc Q67781 aquifex aeo Q51801 pyrococcus O5443 pyrococcus O59421 pyrococcus	P82487 streptococc 067213 aquifex aeo 030027 archaeoglob 089419 buchnera ap P54355 bacteroides 058282 methanococc 080104 agrobacteri 09247 rhizobium m P46113 escherichia 013883 schlizosacch 050700 mycobacteri 028564 mus musculu P20828 drosophila P20828 drosophila P52093 alcaligenes 085718 acinetobact	940038 saccharomyc 024458 drosophila 026458 drosophila 066841 aquifex aeo 058992 methanococc p35531 shigella fl P4687 salmonella P4093 1111um long 09007 rescherichia P4093 1111um long 09007 1111um long 09007 111um long 091498 candida alb P34948 candida alb P34948 candida alb P34948 cacharomyc 08388 treponema p P57351 buchnera ap 098166 lacanobia o 05847 methanococc P37197 escherichia P57191 methanococc 05847 methanococc 05847 methanococc 05846 rana catebb 057918 methanococc 05898 rickettsia
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Q98v31 arabidopsis Q08451 lycopersico Q39196 arabidopsis Q8laa6 arabidopsis P43286 arabidopsis Q92v07 arabidopsis P25794 pisum sativ Q8y680 listeria mo Q9ff53 arabidopsis	Q80xxv1 arabidopsis Q82xv1 archaeoglob Q82113 chlamydophi Q10298 orgyia pseu Q9j540 fowlpox vir P18773 acinefobact G9nyv9 homo sapien Q44185 agrobacteri Q9yve6 staphylococ	Ogykt rattus norv Ogykt rattus norv Ogykt neisseria m Ogyyt neisseria m P47248 mycoplasma P88238 saccharowyc P59625 enterococcu P20498 vaccinia vi P2299 variola vir O86937 streptomyce O66698 aquifex aeo O6698 aquifex aeo O6698 pan troglod O90ua4 pan troglod	086276 aquifex aeo O66105 aquifex aeo O59phu0 campylobact P55539 bacillus su P55839 arabidopsis Q8e6a9 streptococc Q9ens streptococc Q9ens streptococc Q95755 homo sapien Q8ex54 mycoplasma P2347 vibrio chol Q92jq6 rickettsia P80558 scenaromyc O66576 aquifex aeo	992ed2 rickettsia P30632 caenorhabdi Q09275 caenorhabdi Q0875 caenorhabdi Q8876 thermoanaer Q5877 lactococcus Q04457 lactococcus Q58941 methanococc Q26460 macaa fasc Q43681 homo sapien O54984 mus musculu Q9291 arabidopsis Q9295 rhizobium m P14582 synechococc Q960X1 sulfolobus P50728 bacillus su Q92794 chlamydia p P7437 synechococc P53522 proteus mir P5852 anabaena sp P14167 anabaena sp P14167 anabaena va Q57288 haemophilus P565397 salmonella
2000 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	20000000000000000000000000000000000000	3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	141 1 DUS RICPR 142 1 ARSA CAREL 143 1 HRCA THETN 143 1 HRCA THETN 143 1 HRCA THETN 144 1 ABIC LACLA 145 1 YF46 METJA 146 1 DHA, MACPA 147 1 DHA, MACPA 148 1 ARSI HUMAN 148 1 ARSI HUMAN 148 1 ARSI HUMAN 159 1 RECA SYNPS 150 155 1 ARGC SULSO 155 1 RECA SYNPS 150 155 1 RECA SYNPS 150 155 1 RECA SYNPS 151 1 RECA SYNPS 152 1 RECA SYNPS 153 1 RECA SYNPS 154 1 RECA SYNPS 155 1 RECA SYNPS 155 1 RECA SYNPS 156 1 RECA SYNPS 157 1 RECA SYNPS 158 1 RECA SYNPS 158 1 RECA SYNPS 159 1 RECA SYNPS 150 151 1 RECA SYNPS 150 151 1 RECA SYNPS 150 151 1 RECA SYNPS 151 1 RECA SYNPS 152 1 RECA SYNPS 153 1 RECA SYNPS 154 1 RECA SYNPS 155 1 RECA SYNPS 155 1 RECA SYNPS 156 1 RECA SALIY 157 1 RECA SALIY 158 1 RECA SALIY 158 1 RECA SALIY 159 1 REPERS SALIY 150 151 151 151 151 151 151 151 151 151
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YA90_ARCEU
ID YA90_ARCEU
DT 16-OCT
DT 16-OCT
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DB HyPOTH
GN AF1090
OC Archae
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Q82yd8 pyrobaculum
P4259 escherichia
P19487 xanthomonas
P19487 xanthomonas
P21885 bacillus au
O52351 mycoplasma
P5763 thermoplasm
Q5763 termoplasm
Q5642 caenorhabdi
P26288 arabidopsis
Q68912 and and and p2651 drosophila
P72245 thodobacter
P40051 saccharomyc
Q92d12 rickettsia
Q92d12 rickettsia
Q92d12 rickettsia
Q92d14 rypanosoma
P38140 saccharomyc
P49109 cavia porce
Q8xbv3 escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=H37Rv;
Prasad H.K., Annapurna P.S.;
Submitted (DEC-1997) to Swiss-Prot.
Submitted (DEC-1997) to Swiss-Prot.
-!- SIMILARITY: STRONG, TO THE N-TERMINALS OF C.ELEGANS F20A1.4
AND H.INFLUENZAE H10967.
-!- CAUTION: We are unable to find this protein in the translation of the geneme of strain H37Rv.
NON_TER 19 19
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083263;
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Preprotein translocase secE subunit.
SECE OR TPO235.
Treponema pallidum.
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
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MEDLINE-98332770; PubMed=9665876;
Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis.
atteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95.0%; Score 19; DB 1; Length 19; 100.0%; Pred. No. 35; 0; Indels ive 0; Mismatches 0; Indels
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19 AA; 2211 MW; ABC1854BFIFFIF70 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NS2 MYCTU STANDARD; PRT; 19 AA. P81136; 15-JUL-1999 (Rel. 38, Created) 15-JUL-1999 (Rel. 38, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) 30 kDa non-secretory protein 2 (Fragment).
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Beat A; Conservative
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     11 VAEF 14
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       SEQUENCE
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D NS2 M
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Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
Katchum K.A., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
Katchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
Kirkness B.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001901; SecE.
InterPro; IPR001907; SecE.
Pretarro; IPR005097; SecE.
TIGRFAMS; TIGR00964; 3a0501806; 1.
PR051TE; PS01067; SECE SEC61G; 1.
PR051TE; PS01067; SECE SEC61G; 1.
TRANSMEM 39 POTENTIAL.
SEQUENCE 59 AA; 6789 WAT.
Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A., Sodergren B., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., Khalak H., Richardson D., Howell J.K., Chidambaram M., Uterback T. McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.
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Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                   "Complete genome sequence of Treponema pallidum, the syphilis
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Archaeoglobaceae; Archaeoglobus.
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16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Hypothetical UPF0165 protein AF1090.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 AA.
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us-09-594-978a-3.rsp

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Rd / KW20 / ATCC 51907;
MEDLINE=95550630; PubMed=7542800;
Pleischmann R.D., PubMed=7542800;
Rerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
McKenney K., Sutton G., Fitzhugh W., Kelley J.M.,
Weidman J.F., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
Utterback T.R., Hamna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 269:496-512(1995).
--- FUNCTION: This protein is one of the 16S ribosomal RNA binding proteins (By similarity).
--- SIMILARITY: Belongs to the S15P family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1995 (Rel. 32, Last sequence update)
28-REB-2003 (Rel. 41, Last annotation update)
308 ribosomal protein S15.
(RPSO-A OR RPSIS-A OR HI1328) AND (RPSO-B OR RPSIS-B OR HI1468)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria, Proteobacteria, Gammaproteobacteria, Pasteurellales,
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Length 63;
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Probom; PD157043; R&HS bacr; 1.
TRGRPAMS; TIGRO0552; RIBOGOMAL S15; 1.
PROSITE; PS00362; RIBOGOMAL S15; 1.
Riboscmal protein; rRNA-binding; Complete proteome.
BY SINILARITY.

BY SINILARITY 3. CREATING A CREATI
    Score 19; DB 1; L, Pred. No. 1.1e+02; 0; Mismatches 0;
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H3SP; P05766; 1A32.
TIGR; H11328; --
TIGR; H11468; --
TIGR; H11469; --
TIGR; H11469; Ribosomal_S15.
InterPro; IPR005299; Ribosomal_S15.
Pfam; PP00312; Ribosomal_S15.
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    95.0%; 2
100.0%;
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                                                                                           4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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Best Local Similarity
Matches 4; Conserv
Query Match
Best Local Similarity
Matches 4; Conserv
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SEQUENCE FROM N.A.
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P44389;
01-NOV-1995 (
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                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDINE-95550630; PubMed=7542800; Richines B.F., Richines B.F., Relakanan R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Ferlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hechlow E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Venter J.C., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.;
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Pasteurellaceae; Haemophilus.
NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.0%; Score 19; DB 1; Length 59; 100.0%; Pred. No. 1.1e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR008203; DUF104.
InterPro; IPR008204; DUF104_N.
Pfam; PF01954; DUF104; 1.
ProDom, PD005964; DUF104_N; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 59 AA; 6887 MW; B72E847382B2B6B6 CRC64;
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SEQUENCE 63 AA; 7047 MW; 36B14E60AC306B67 CRC64;
         SIMILARITY: Belongs to the UPF0165 family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
48-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein H10451.
                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE001028; AAB90157.1; -.
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TIGR; AF1090; -.
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51 VAEF 54
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Archaea; Euryarchaeota; Methanococci; Methanococales;
Methanocaldococcaceae; Methanocaldococcus.
NCBI_TaxID=2190;
Methanococcus jannaschii
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                A Sheazev A.I., Mezhevapa K.V., Makarova K.S., Polushin N.N.,
A Shcharbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
A Shcharbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
A Matale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
Matykh A.G., Koonin E.V., Kozawkin S.A.,
The complete genome of hyperthermophile Methanopyrus kandleri AV19
and monophyly of archaedl methanogens."; Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649 (2002).
I chomosome, suggesting a role in chromatin architecture. However, it does not significantly compact DNA (By similarity).
I chose not significantly compact DNA (By similarity).
I sumilarity themotetramer (By similarity) thereby repressing transcription. Regulation of DNA-based activities is therefore achieved at the chromatin level (By similarity).
C.I. SIMILARITY: Belongs to the archaeal histone-like Alba family.
                                                                                                                                    No.0CT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-3003 (Rel. 42, Last annotation update)
ANA-binding protein Alba 2.
Methanopyrus kandleri.
Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
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TIGREAMS; TIGR00285; 1.
DIA-binding; Acetylation; Complete proteome.
MOD RES
SEQUENCE 93 AA; 10142 MW; E11D650FD5F63169 CRC64;
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(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
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                                                                                                93 AA
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MEDLINE=21927647; PubMed=11930014;
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16-0CT-2001 (Rel. 40, Last st
16-0CT-2001 (Rel. 40, Last at
Hypothetical protein MJ1524.
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InterPro; IPR002775; DUF78.
Pfam; PF01918; DUF78; 1.
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                                                                                                STANDARD;
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SEQUENCE FROM N.A.
STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
BULT C.J., White O., Olean G.J., Zhou L., Fleischmann R.D.,
Bult C.J., White O., Olean G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirhenss E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.M., Ennna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klanh H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
Jannaschii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=ATCC 53650 / L585-6;

MEDLINE=93015257; PubMed=1399845;

Hoferead S.J., Matson J.R., Malacko A.R., Marquardt H.;

"Kedarcidin, a new chromoprotein antitumor antibiotic. II. Isolation,

purification and physico-chemical properties.";

J. Antibiot. 45:1250-1254(1992).
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MEDLINE=93376732; PubMed=8367457;
Zein N., Casazza A.M., Doyle T.W., Leet J.E., Scheoeder D.R.,
Solomon W., Nadler S.G.;
Solomon W., Nadler S.G.;
Selective proteolytic activity of the antitumor agent kedarcidin.";
Proc. Natl. Acad. Sci. U.S.A. 90:8009-8012(1993).
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Actinomycete sp. (strain L585-6 / ATCC 53650).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales.
NCBI_TaxID=38989;
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InterPro; IPR003793; DUF190.

Pfam; PF02641; DUF190; 1.

Hypothetical protein; Complete proteome.

REQUENCE 108 AA; 12398 MW; D3E286AFB9D4AF9B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 273:1058-1073(1996).
-!- SIMILARITY: BELONGS TO THE UPF0166 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
KEDA ACTSL STANDARD; FRT; 114 AA.
AC P41249;
DT 01-FRB-1995 (Rel. 31, Created)
DT 01-FRB-1995 (Rel. 31, Last sequence update)
DT 01-FRB-2003 (Rel. 41, Last annotation update)
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PIR; C64490; C64490.
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MEDLINE-95001848; PubMed=7918389;

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Zehin N., Tuttle J., Langley D.R., Leet J.B., Schreeder D.R., Lam K.S.,

Zehin N., Tuttle J., Langley D.R., Leet J.B., Schreeder D.R., Lam K.S.,

Remer B.T. II, Metzler W.J., Bruccoleri R.E., Mueller L.;

"Sequential IH, 13C, and 15N NMR assignments and solution

conformation of apokedarcidin.";

Biochemistry 33:11438-11452(1954).

-!- FUNCTION: BINDS NON-COVALENTLY TO AN ENEDIYNE CHROMOPHORE WHICH IS

THE CYTOTOXIC AND MUTAGENIC COMPONENT OF THE ANTIBIOTIC. THE

CHROMOPHORE CLEAVES DUPLEX DNA SITE-SPECIFICALLY IN A SINGLE-

STRANDED MANNER. THE APOPROTEIN CLEAVES PROTEINS SELECTIVELY, IN

PARTICULAR HIGHLY BASIC HISTONES, WITH HI PROTEINS BEING CLEAVED

-!- DOWAIN: THIS PROTEIN CONSISTS OF AN IMMUNGGLOBULIN-LIKE SEVEN-

STRANDED ANTIPRAALLEL BERA-BARREL DOMAIN LINKED TO A SUBDOMAIN

-!- SIMILARITY: Belongs to the neocarzinostatin family.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
Pleuronectoidei; Pleuronectidae; Verasper.

NCBI_TAXID=98923;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95.0%; Score 19; DB 1; Length 114; 100.0%; Pred. No. 2e+02; ive 0; Mismatches 0; Indels
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16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                 -!- SIMILARITY: Belongs to the neocarz PDB; 1AKP; 31-AUG-94.
InterPro; IPR002186; Neocarzinostat.
Pfam; PF00960; Neocarzinostat, 1.
Probom; PD012709; Neocarzinostat, 1.
Antibiotic; DNA-binding; 3D-structure.
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Matches 4; Conser
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Andoh T., Nagasawa H.;
"Two molecular forms of insulin from barfin flounder, Verasper moseri, are derived from a single gene.";
acod. 15:931-937(1598)
-!- FUNCTION: Insulin decreases blood glucose concentration. It increases cell permeability to monosaccharides, amino acids and fatty acids. It accelerates glycolysis, the pentose phosphate cycle, and glycogen synthesis in liver.
-!- SUBCINIT: Heterodimer of a B chain and an A chain linked by two
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MEDLINE=81056434; PubMed=7001633;
Hobbart P.M., Shen L.-P., Crawford R., Pictet R.L., Rutter W.J.;
"Comparison of the nucleic acid sequence of anglerfish and mammalian insulin mRNA's from cloned CDNA's.";
Science 210:1360-1363(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lophius piscatorius (Allmouth goosefish) (Anglerfish), and Lophius americanus (American goosefish) (Anglerfish).
Bukaryota Metazoa, Chordate, Craniata, Vertebrata; Euteleostom;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Acanthomorpha; Paracanthopterygii; Lophiiformes; Lophiidae; Lophius.
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INSULIN A CHAIN.
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
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HSSP; PO1315; 1MPJ.
InterPro; IPR004825; Ins/IGF/relax.
Pfam; PF00049; Insulin; 1.
PRINTS; PR0077; INSULIN; 1.
PROSTE; PS0027; INSULIN; 1.
PROSTE; PS00262; INSULIN; 1.
Insulin family; Hormone; Glucose metabolism; Signal.
SIGNAL
CHAIN 23 53 INSULIN B CHAIN.
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                                                                                                                                                                                                                                                                           disulfide bonds.
-!- SUBCELLUTAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the insulin family.
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21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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SEQUENCE OF 25-54 AND 96-116.
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56
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115 AA;
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2 VAEF 5
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GTR2_PIG
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                                                                                                                                           -!- SUBCELLUIAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the insulin family.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                       Hoppe-Seyler's Z. Physiol. Chem. 350:1286-1288(1969).

-!- FUNCTION: Insulin decreases blood glucose concentration. It increases cell permeability to monosaccharides, amino acids and fatty acids. It accelerates glycolysis, the pentose phosphate cycle, and glycogen synthesis in liver.

-!- SUBUNIT: Heterodimer of a B chain and an A chain linked by two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adams M.D., Celniker S.E., Hölt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelifer B.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
 SPECIES=L.piscatorius;
MEDILNE=70036620; PubMed=5389298;
Neumann P.A., Koldenhof M., Humbel R.E.;
"Amino acid sequence of insulin from the angler fish (Lophius piscatorius).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.0%; Score 19; DB 1; Length 116; 100.0%; Pred. No. 2.1e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12737 MW; C686P8EF8183BEFE CRC64;
                                                                                                                                                                                                                                                                                         HSSP; PO1308; 1LPH.
InterPro; IPRO04825; Ins/IGF/relax.
Pfan; PPO049; Insulin; 1.
PRINTS; PR00277; INSULINB.
SWART; SW00078; InSF; 1.
PROSITE; PS00262; INSULIN; 1.
INSULIN family; Hormone; Glucose metabolism; Signal.
SIGNAL
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010-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
UPF0279 protein CG14505.
                                                                                                                                                                                                                                                                                                                                                                                                      INSULIN B CHAIN.
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INSULIN A CHAIN.
INTERCHAIN.
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PIR; A01608; IPAF.
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Best Local Similarity
Matches 4; Conserv
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STRAIN=Berkeley;
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DISULFID
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U279_DROME
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RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Rallawin D., Ra allaw R.M., Baul A., Barandale J., Bayarkarogolu C., Baldwin D., Baslew R.M., Baul A., Bandari D., Bayarkarogolu L., Basaley E.M., Beeson K.Y., Bencos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Broktein P., Brottier P., Andrews D., Botchan M.R., Buller H., Cadieu E., Center A., Chandra I., R. Cherry J.M., Cawley S., Dahler C., Davenport L.B., Davies P., Durbin K.J., Evangelista C.C., Rerraz C., Perraz C., Perras S., Dunkov B.C., Dunn P., Boslen D. B., Downes M., Diegan-Rocha S., Dunkov B.C., Dunn P., RA Dodson K., Doup L.B., Garg N.S., Gelbart W.M., Glasser K., A., Golog F., Gorrell J.H., Gu Z., Kenrisch S., Pleischmann W., R. Andren R.B., Garnell J.H., Gu Z., Kenrisch W., Garser K., A., Havlen F., Karpen G.H., Ke Z., Kenniscon J.A., Ketchum K.A., Harris N.L., Harvey D.A., Heiman T.J., Wal M. H., Ibegwam C., Lei Y., Levitzk A.A., Howland T.J., Wal M. H., Ibegwam C., Lasko P., Lei Y., Levitzk A.A., Machan G.H., Ke Z., Kenniscon J.A., Katchum K.A., Lasko P., Lei Y., Levitzk A.A., Moland G.H., Ke Z., Kenniscon D., Lasko P., Lei Y., Matteri B., McIntosh T.C., Morris J., Morherson D., Lu X., Matteri B., McIntosh T.C., Morris J., Morherson D., A., Nelson K.A., Nixon K., Nucskern D.R., Palazcolo M., Pittuan G.S., Pan S., Pollard J., Puri V., Reese M. A., Nixon K., Nucskern D.R., Palazcolo M., Pittuan G.S., Pan S., Pollard J., Puri V., Smith T., Rayles R., Tector C. Turner R., Venter E., Wang A.H., Wang X., Rang S., Yehn S., Zhong K., Zhong G., Zhao Q., Zhao Q., Zhao Q., Zhao G., Zhao G.
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MEDLINE=2245066; PubMed=12537569;
Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
George R.A., Guarin H., Kronmiller B., Pacleb J.M., Park S., Wan K.H.,
Rubin G.M., Celniker S.B.;
"A Drosophila full-length cDNA resource.";
Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
-1- SIMILARITY: Belongs to the UPF0279 family.
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SEQUENCE 119 AA; 13534 MW; 83FA23FCCCE389AA CRC64;
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100.0%; Pred. No. 2.1e+02;
ive 0; Mismatches 0;
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062786;
28-FEB-2003 (Rel. 41, Created)
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InterPro, IPR007967; DUF727.
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us-09-594-978a-3.rsp

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                                                                                                                                                                                                                                            Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
                                                                                                                           SEQUENCE FROM N.A.
STRAIN=IM2 / ATCC 51768 / DSM 7523;
MEDLINE-21664397; PubMed=11792869;
Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
Miller J.H.;
                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
-!- SIMILARITY: Belongs to the L18E family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSUTE; PSO1106; RIBOSOMAL_L18E; FALSE_NEG.
Ribosomal protein; Complete proteome.
SEQUENCE 122 AA; 13252 MW; 88F3DB732C4E0394 CRC64;
                                 Thermoprotei; Thermoproteales;
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100.0%; Pred. No. 2.2e+02;
tive 0; Mismatches 0;
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InterPro; IPR001199; Ribosomal_L15.
InterPro; IPR000039; Ribosomal_L18e.
Ffam; PF00256; L15; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21145866; PubMed=11248100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE009779; AAL62941.1; -.
HAMAP; MF_00329; -; 1.
                                 Archaea; Crenarchaeota; Thermoproteaceae; Pyrobaculum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity luv...
Section 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
            Pyrobaculum aerophilum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pasteurella multocida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                  NCBI_TaxID=13773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35 VARF 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WCBI_TaxID=747;
                                                                                                                                                                                                                                                                             aerophilum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Pm70
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            à
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                   Canty J.M., Young R.F., Fallavollita J.A.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
-!-TMYCTION: Facilitative glucose transporter. This isoform likely mediates the bidirectional transfer of glucose across the plasma membrane of hepatocytes and is responsible for uptake of glucose by the beta cells; may comprise part of the glucose-sensing mechanism of the beta cells, may comprise part of the glucose-sensing mechanism of the beta cell. May also participate with the Na(+)/glucose corransporter in the transcellular transport of glucose in the small intestine and kidney (By similarity).
-!- SUMCELULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to the sugar transporter family. Glucose transporter subfamily.
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-Oute carrier family 2, facilitated glucose transporter, member 2 (Glucose transporter type 2, liver) (Fragment).
51C2A2 OR GLUT2.
                                                                                                                                     Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
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InterPro; IPR007114; MFS.
InterPro; IPR00528; Sugiransporter.
InterPro; IPR00529; Sugiransporter.
InterPro; IPR00563; Sugar_transpt.
Pfam; PR00013; Sugar_tr; 1.
PR0S1TE; PS00101; SUGRTPANSPORT.
PROSITE; PS00216; SUGAR_TRANSPORT.
PROSITE; PS00216; SUGAR_TRANSPORT.
ITANSEMBATIAL.
TRANSEMBATIAL.
TRANSEMBATIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95.0%; Score 19; DB 1; Length 120; 100.0%; Pred. No. 2.18+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13503 MW; D5F73168DBF03203 CRC64;
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EXTRACELLUTAR (POTENTIAL)
10 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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18E PYRAB
D RIBE PYRAE STANDARD; PRT; 122 AA.
T 28-FEB-2003 (Rel. 41, Created)
T 28-FEB-2003 (Rel. 41, Last sequence update)
T 28-FEB-2003 (Rel. 41, Last annotation update)
E 50S ribosomal protein LiBe.
N RPLISE OR PAE0672.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 4; Conservative
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57
78
85
106
120
120 AA;
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                   NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46 VAEF 49
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DOMAIN
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SEQUENCE
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Gaps

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Length 122; 0; Indels

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                                                                                                                                                                                                                                                                                                May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.; "Complete genomic sequence of Pasteurella multocida Pm70."; proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
-i- SIMILARITY: Belongs to the cytochrome b562 family.
                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Pasteurella.
                                      28 FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
124 AA
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SPEH THEMA Q9WZC3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Crossman M.W., Hauft S.M., Gordon J.I.;
"The mouse ileal lipid-binding protein gene: a model for studying axial patterning during gut morphogenesis.";
J. Gell Biol. 126:127-1564(1994).
-:- FUNCTION: ILEAL PROTEIN WHICH STIMULATES GASTRIC ACID AND PEPSINOGEN SECRETION. SEEMS TO BE ABLE TO BIND TO BILE SALTS AND
                                                                                                                                                                                                                                                                                                                                                                    FABP6 OR ILLBP.
Nouses).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BILIRUBINS. SUBCELLULAR LOCATION: Cytoplasmic. SUBCELLULAR LOCATION: Cytoplasmic. SIMILARITY: Belongs to the fatty-acid binding protein (FABP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                              Score 19; DB 1; Length 124;
Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tam; PR00178; FABP; 1.

PROSITE; PS00214; FABP; 1.

Transport; Lipid-binding; Acetylation.

Transport; Lipid-binding; Acetylation.

INIT_MET 1 1 ACETYLATION (BY SIMILARITY).

ACETYLATION (BY SIMILARITY).

1 ACETYLATION (BY SIMILARITY).
Hypothetical protein; Signal; Complete proteome.
SIGNAL
1 24 124
CHAIN
24 HYPOTHETICAL PROTEIN PM0670.
SEQUENCE 124 AA; 13746 MW; D7B2B485C7B51B9A CRC64;
                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                 01-0cT-1996 (Rel. 34, Created)
01-0cT-1996 (Rel. 34, Last sequence update)
10-0cT-2033 (Rel. 42, Last annotation update)
Gastrotropin (GT) (Ileal lipid-binding protein) (ILBP).
                                                                   95.0%; Scor.
100.0%; Pred. No. ...
                                                                                                                                                                                                                                                                   127 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD; MGI:96565; Fabp6.
InterPro; IPR000463; Fatty acid_BP.
InterPro; IPR000566; Lipocin_cytFabP.
Pfam; PF00061; lipocalin; 1.
PRINTS; PR00179; FATTYACIDBP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-DBA/2J; TISSUE-Liver;
MEDLINE-94375529; PubMed-8089185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U00938; AAC27352.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1]
SEQUENCE FROM N.A.
TISSUE=Liver;
                                                                                                                  4; Conservative
                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A54797; A54797.
                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                 45 VAEF 48
                                                                                                                                                  2 VAEF 5
                                                                                                                                                                                                                                                                   MOUSE
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VAEF 94

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                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDIANE=99287316; PubMed=10360571;

MEDIANE=99287316; PubMed=10360571;

Melson K.B., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

Melson K.B., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

Melson K.B., Sutton G.M., Peterson J.D., Melson W.C., Katchium K.A.,

McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,

Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

Mathora S. Sutton G.G., Pleisenhann R.D., Essen J.A., White O.,

Salzberg S.L., Smitch H.O., Venter J.C., Fraser C.M.;

"Evidence for lateral gene transfer between Archaea and Bacteria from

"Evidence for lateral gene transfer between Archaea and Bacteria from

"Evidence for lateral gene transfer between Archaea and Bacteria from

"Evidence for lateral gene transfer between Archaea in Bacteria from

"Evidence for lateral gene transfer between Archaea in Govinson From Nature 339:323-329(1999).

"I EUNCTION: Decarboxylation of S-adenosylmethionine provides the

multopropyl modety required for spermidine biosynthesis from

putressine (By similarity).

"I CATALYTIC ACTIVITY: S-adenosyl-L-methionine alt + CO(2).

adenosyl (3-aminopropyl) methylsulfonium salt + CO(2).

-I - CORACTOR: Pyruvoyl group (By similarity).

-I - SIMILARITY: Belongs to the prokaryotic AdometDC family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN (BY SIMILARITY).

CHAIN (BY SIMILARITY).

CHAIN (BY SIMILARITY).

CLEAVAGE (NONHYDROLYTIC) (BY SIMILARITY).

CLEAVAGE (NONHYDROLYTIC) (BY SIMILARITY).

SIMILARITY).

7659F220A2019928 CRC64;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50) (AdoMetDC)
(SambC) [Contains: S-adenosylmethionine decarboxylase beta chain; S-adenosylmethionine decarboxylase alpha chain].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gabs
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HAMAP; MF 00464; -; 1.
Interpro. IPR003826; SAMDC.
Pfam; PPF02675; AdoMetDC; 1.
Spermidine biosynthesis; Lyase; Decarboxylase; Zymogen; Pyruvate;
                                                                                                                                                                                                                                                                                                       Thermotoga maritima.
Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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95.0%; Score 19; DB 1; Length 130;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            131 AA.
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PIR; D72348; D72348.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14785 MW;
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                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=2336;
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Y194 PYRAB
ID _Y194_PYRAB
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Gaps ö Score 19; DB 1; Length 131; Pred. No. 2.3e+02; 0; Indels

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SEQUENCE FROM N.A.
MEDLINE=20504483; PubMed=11016950;
MEDLINE=20504483; PubMed=11016950;
MG W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D., 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
6,7-dimethyl-8-ribityllumazine synthase (BC 2.5.1.9) (DMRL synthase)
(Lumazine synthase) (Riboflavin synthase beta chain).
RIBH OR RIBE OR VNG0630G. Halobacterium sp. (strain NRC-1 / Arcc 700922 / JCM 11081). Archaea, Buryarchaeota, Halobacteria, Halobacteriales, Halobacteriaceae; Halobacterium NCBI\_TaxID=64091;

Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;

RT "Genome sequence of Halobacterium species NRC-1.";

Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).

- Tabley Mart. Acad. Sci. U.S.A. 97:12176-12181(2000).

- Tabley Lenino-2.4 (1H,3H) - Pyrimidinedione and L-3.4-dibydrohy-2
catalyzing the formation of riboflavin from 5-amino-6-(1'-D)
catalyzes the condensation of 5.7-dimethyl = lumazine. The beta subunit

catalyzes the condensation of 5.4-dihydrohy-2-butanone-4
phosphate yielding 6.7-dimethyl-8-lumazine. Ho beta subunit

catalyzes the condensation of 5-amino-6-(1'-D)-ribityl-amino
2,4(1H,3H)-pyrimidinedione with L-3,4-dihydrohy-2-butanone-4
phosphate yielding 6,7-dimethyl-8-lumazine (By similarity).

catalyzes the condensation of 5-amino-2,6-dihydroxypyrimidine.

catalyzes the formatic for the DML synthese family.

cipharmax: Babolavin biosynthesis; last step.

condensation the DML synthese family.

condensation and the EMBL outstation the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its conservant in settlement is not removed. Usage by and for commercial conficied and this statement is not removed. Usage by and for commercial conficied and this statement is not removed. Usage by and for commercial conficience agreement (See http://www.isb-sib.ch/announce/conficience-display. ö Sun T.-P., Webster R.E.; "Nucleotide sequence of a gene cluster involved in entry of E colicins and single-stranded DNA of infecting filamentous bacteriophages into Gaps SPECIES-E.COLI, STRAIN-KI2 / MG1655, MEDLINE-97426617; PubMed-9278503; MEDLINE-97426617; Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Shigella flexneri. Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales; ö Protein ybgC. YBGC OR B0736 OR C0815 OR Z0904 OR ECS0771 OR SF0561 OR S0574. Bscherichia coli, 95.0%; Score 19; DB 1; Length 133; 100.0%; Pred. No. 2.4e+02; ative 0; Mismatches 0; Indels PIR; A84221; A64221.
HASSP; O66529; 1HQK.
HAMAP; MF 00170; 101008; DMRL synthase.
InterPro; IRR02180; DMRL synthase; 1.
Prodom; PD003664; DMRL synthase; 1.
Riboflavin biosynthesis; Transferaes; Complete proteome.
SEQUENCE 133 AA; 13719 MW; B9724DC24660DGCD CRC64; 01-NOV-1988 (Rel. 09, Created) 01-NOV-1988 (Rel. 09, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) 134 AA. Enterobacteriaceae, Escherichia. NCBI\_TaxID=562, 217992, 83334, 623; Bacteriol. 169:2667-2674 (1987). SPECIES=E.coli; MEDLINE=87222192; PubMed=3294803; EMBL; AE005011; AAG19133.1; -. Escherichia coli O6, Escherichia coli O157:H7, and 4; Conservative STANDARD; Best Local Similarity SEQUENCE FROM N.A. SEQUENCE FROM N.A. Escherichia coli 2 VAEF 5 YBGC\_ECOLI P08999; Query Match YBGC\_BCOLI Matches RESULT 19 ACCOS OS SERVICES SER ઠે 유

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MEDLINE-21156231; PubMed=11258796; Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Tobe T., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; Sasakawa C., Ogasawara N., Yasunaga T., Romara S., Shiba T., Hattori M., Shinagawa H.; Sasakawa C., Olasawara N., Tasunaga T., Romara S., Shiba T., Hattori M., Shinagawa H.; Sasakawa C., Olasawara N., Yasunaga T., Monagawa H.; Sasakawa C., Olasawara M., Sasakawa C., Sasakawa C., Olasawara N., Yasunaga T., Monagawa H.; Sasakawa C., Sasakawa C., Olasawara N., Yasunaga T., Monagawa H.; Sasakawa C., Olasawa M., Sasakawa C., Olasawa N., Yasunaga T., Monagawa H.; Sasakawa C., Olasawa N., Yasunaga T., Monagawa H., Sasakawa C., Olasawa N., Yasunaga T., Monagawa H.; Sasakawa C., Olasawa N., Yasunaga T., Monagawa H.; Sasakawa C., Olasawa N., Yasunaga T., Monagawa H.; Sasakawa C., Olasawa M., Yasunaga T., Monagawa H., Sasakawa M., Yasunaga T., Monagawa M., Yasunaga 
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                                                                                                                                                              SEQUENCE FROM N.A.
SPECIES-E.coli; STRAIN-K12;
MEDLINE=97061202; Pubbed=8905232;
MEDLINE=97061202; Pubbed=8905232;
MEDLINE=97061202; Pubbed=8905232;
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
Sampel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPECIESE Coli; STRAIN-06:H1 / CFT073 / ATCC 700928;
MEDINE-2238024; PubMed=12471157;
Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
MayNew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnanberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence
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MEDLINE-22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
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SPECIES.E coli; STRAIN=0157:H7 / BDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551; Mau B., Glasner J.D.,
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Grosfei G., Hackett J., Kilnk S., Boutin A., Shao Y., Miller L.,
Grocbeck E.J., Davis N.W., Lim A., Dimalanta B.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
"Genome sequence of enterchaemcrhagic Escherichia coli 0157:H7.",
Nature 409:529-533(2001).
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Yano M., Horiuchi T.;
"A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map.";
DNA Res. 3:137-155(1996).
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SPECIES-E.coli, STRAIN-K12 / MG1655,
Kim K., Allen E., Araujo R., Aparicio A.M., Botstein D.,
Kherry M., Chung E., Dietrich F., Duncan M., Federspiel N.,
Kalman S., Komp C., Lashkari D., Lew H., Lin D., Namath A.,
                                Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
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Submitted (UUL-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
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SEQUENCE FROM N.A.
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16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
6,7-dimethyl-8-ribityllumazine synthase (EC 2.5.1.9) (DMRL synthase)
(Lumazine synthase) (Riboflavin synthase beta chain).
SPECIES-S.flexneri; STRAIN=2457T / ATCC 700930 / Serotype 2a; MEDLINE=22590274; PubMed=12704152; Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W., Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A., Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S., Schwartz D.C., Blattner F.R.; "Complete genome sequence and comparative genomics of Shigella
                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99420866; PubMed=10493123; Perndt P., Langen H., Takacs B.; Fountoulakis M., Takacs M.-F., Berndt P., Langen H., Takacs B.; Fountoulakis M., Takacs M.-F., Berndt P., Langen H., Takacs B.; Modroxyapatite chromatography."; Pactrophoresis 20:2181-2195(1999).
-1- SIMILARITY: BELONGS TO THE 4-HYDROXYBENZOYL-COA THIOESTERASE PAMILY. STRONG, TO H. INPLUENZAE H10386.
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Archaea; Buryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae; Methanothermobacter.
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134 AA; 15562 MW; C44582B6EC3BE999 CRC64;
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InterPro; IPR008272; 4HBCoA_thiost_AS.
InterPro; IPR006684; 4HBCoA_thiostrae.
InterPro; IPR006683; ThioseTr_supf.
Pfam; PF03061; 4HBT; IIGR00651; 1.
IIGRPAMS; TIGR00051; IIGR00651; 1.
PROSITE; PS01328; 4HBCOA_THIOESTERASE; 1.
                                                                                                                                                                                                                                                                                                                                       IDENTIFICATION BY MASS SPECTROMETRY.
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                                                                                                                                                                                                                                    flexneri serotype 2a strain 2457T."
Infect. Immun. 71:2775-2786(2003).
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EMBL; AE000177; AAC73830.1; -.
EMBL; AE00713; BAA35402.1; -.
EMBL; AE016757; AAN79288.1; -.
EMBL; AE00552; AAG55072.1; -.
EMBL; AP002553; BAB34194.1; -.
EMBL; AE016979; AAA72398.1; -.
EMBL; AE016979; AAP16078.1; -.
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ACT_SITE 18
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PIR; C90725; C90725.
PIR; D85576; D85576.
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O27443;
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PRT;
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100.08; Pro-
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PIR; B69323; B69323.
TIGR; AF0586; -.
                                                                                                                                         Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                         Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                            2 VAEF 5
                                                                                                        Venter J.C.;
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028152;
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Matches
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MEDLINE=98049343; PubMed=9389475;
Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95.0%; Score 19; DB 1; Length 139; 100.0%; Pred. No. 2.5e+02; ive 0; Mismatches 0; Indels
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139 AA; 15464 MW; B640D8D12EE2A862 CRC64;
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Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
                                                                                                                                                                                                                                                                                             SIMILARITY: Belongs to the DMRL synthase family.
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein AF0586.
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HSSP, P11998; IRVV.
HAMAP: MF 00178; -; 1.
InterPro; IPR002180; DMRL synthase.
Pfam: PF00885; DMRL synthase; 1.
ProDon; P0003664; DMRL synthase; 1.
TIGRPAMS; TIGR00114; ribH; 1.
                                  STRAIN=Delta H;
MEDLINE=98037514; PubMed=9371463;
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Best Local Similarity
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NCBI_TaxID=187420;
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ribityl-amino-2.4 (1H.3H)-pyrimidinedione and L-3,4-dihydxohy-2-butanone-4-phosphate via 6,7-dimethyl-8-lumazine. The beta subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
6,7-dimethyl-8-ribityllumazine synthase (BC 2.5.1.9) (DWRL synthase)
(Lumazine synthase) (Riboflavin synthase beta chain).
RIBH OR RIBE OR AF2128.
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Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D., Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C., Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S., Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou Overbeek R., Gacayne J.D., Weidman J.F., McDonald L., Utterback T. Cotton M.D., Spriggs T.P., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The complete genome sequence of the hyperthermophilic, sulphate-
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100.0%; Pred. No. 2.5e+02;
tive 0; Mismatches 0; Indels
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SEQUENCE 140 AA; 16175 MW; D3B1FE3A62A05901 CRC64;
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Archaeoglobaceae; Archaeoglobus.
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Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                            2 VAEF 5
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catalyzes the condensation of 5-amino-6-(1'-D)-ribityl-amino-2,4(14,3H-)-yrimidinedione with L-3,4-dihydrohy-2-butanone-4-phosphate yielding 6,7-dimethyl-8-lumazine (By similarity).
-!- CATALYTIC ACTIVITY: 2 6,7-dimethyl-8-(1-D-ribityl)lumazine = riboflawin + 4-(1-D-ribityl)amino-2,6-dihydroxypyrimidine.
-!- PATHWAY: Riboflavin blosynthesis; last step.
-!- SIMILARITY: Belongs to the DWRL synthase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=AFCC 43049;
MEDLINE=2036544;
MEDLINE=2036544;
BAN N. Nissen P., Hansen J., Moore P.B., Steitz T.A.;
"The complete atomic structure of the large ribosomal subunit at 2.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A resolution.";
Science 289:905-920(2000).
-!- SIMILARITY: Belongs to the L13P family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=92105119; PubMed=1840597; Kroemer W.J., Arndt E.; "Halobacterial S9 operon. Three ribosomal protein genes are cotranscribed with genes encoding a tRNA(Leu), the enclase, and putative membrane protein in the archaebacterium Haloarcula (Halobacterium) mariamortui."; J. Biol. Chem. 266:24573-24579(1991).
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HAMAP; ME_00178; -; 1.
HAMAP; ME_00178; -; 1.
InterPro; IPR02180; DWRL synthase.
Pfam; PF00885; DWRL synthase; 1.
ProDom; PD003664; DWRL synthase; 1.
TIGRPAMS; TIGR00114; rIbH; 1.
Ribbflavin biosynthesis; Transferase; Complete proteome.
Ribbflavin biosynthesis; Transferase; Complete proteome.
Promewre 143 AA; 15645 WW; BBA3141206905410 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haloarcula marismortui (Halobacterium marismortui).
Archaea; Buryarchaeota; Halobacteria; Halobacteriales;
Halobacteriaceae; Haloarcula.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-BR2-2004 (Rel. 43, Last annotation update)
50S ribosomal protein L13P (Hmal13).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
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TIGR; AF2128; -.
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Best Local Similarity
Matches 4; Conserv
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P29198;
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RX MEDLINE-21085660; PubMed=11217851;

RX MEDLINE-21085660; PubMed=11217851;

RX MARAWA T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Azawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Azawa T., Hara A., Pukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Azawa T., Saino T., Saito T.,

RA Azawa T., Saito R.,

RA Schrim L.,

RA Schrim L.,

RA Brownstein M.,

RA Browns
                                      (See http://www.isb-sib.ch/announce/
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-!- FUNCTION: Implicated in the early stage of ectopic ossification.
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                                                                                                                                                                                                                                                                    Length 145;
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Pred. No. 2.6e+02;
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100.0%; Pred. No. ...
0; Mismatches
modified and this statement is not removed. entities requires a license agreement (See h or send an email to license@isb-sib.ch).
                                                                                                                                                 EMBL; M76567; AAA73097.1; -.
PIR; B41715; B41715.
PDB; IFFK; 26-SEP-01.
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Best Local Similarity 100.0
----hes 4; Conservative
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Local Similarity
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115 VAEF 118
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                                                                                                                                                                                                                                                                                                                                                    RIBH OR PAE3296.
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P11418;
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QBZTE3;
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                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Archaea; Buryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zwickl P., Fabry S., Bogedain C., Haas A., Hensel R.;
"Glyceraldehyde-3-phosphate dehydrogenase from the hyperthermophilic archaebacterium Pyrococcus woesei: characterization of the enzyme, cloning and sequencing of the gene, and expression in Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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    -!- SIMILARITY: Contains 3 EF-hand calcium-binding domains.

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E -> V (IN REF. 2; BAB22914).
M -> V (IN REF. 2; BAB22914).
VEN -> I (IN REF. 1).
ZAB22BC738ADZF9D CRC64;
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95.0%; Score 19; DB 1; Length 148;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein in GAPDH 3'region (ORF X) (Fragment).
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EF-HAND 2 (POTENTIAL)
EF-HAND 3 (POTENTIAL)
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MEDLINE=90330536; PubMed=2165475;
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PRINTS; PR00450; RECOVERIN.
PRODOM; PD000011; E-hand; 2.
SMART; SM00054; EF, 4.
PROSITS; PS00018; EF_HAND; 3.
Calcium-binding; Repeat.
CA_BIND 51 89 EF.
CA_BIND 57 68 EF.
CONFLICT 124 124 M-CENFLICT 124 124 W-DENCENFLICT 124 124 W-DENCENFLICT 146 148 W-DENCENFLICT 146 W-DE
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InterPro; IPR002048; EF-hand.
InterPro; IPR001125; Recoverin.
                                                                                                                                                                                                                                                                    EMBL, AB036744; BAA95412.1; -. EMBL; AK009995; BAB26608.1; -. EMBL; AK009664; BAB2645.1; -. EMBL; AK003648; BAB22914.1; -.
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146 148 VJ
148 AA; 16767 MW;
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Best Local Similarity luv...
4; Conservative
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Hypothetical protein.
NON TER
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P20298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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DRX_PYRWO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C. Natl. Acad. Sci. U.S.A. 99:984-989(2002).

C. Natl. Acad. Sci. U.S.A. 99:984-989(2002).

C. Natl. Suboflavin synthase is a bifunctional enzyme complex catalyzing the formation of riboflavin from 5-amino-6-(1'-D)-ribityl-amino-2,4(1H,3H)-pyrimidinedione and L-3,4-dihydrohy-2-butanone-4-phosphate via 6,7-dimethyl-8-lumazine. The beta subunit amino-2,4(1H,3H)-pyrimidinedione with L-3,4-dihydrohy-2-butanone-4-phosphate yielding 6,7-dimethyl-8-lumazine (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity).

CATALYTIC ACTIVITY: 2 6,7-dimethyl-8-(1-D-ribityl)lumazine = riboflavin + 4-(1-D-ribitylamino)-5-amino-2,6-dihydroxypyrimidine.

PATHWAY: Riboflavin blosynthesis; last step.

SIMILARITY: Belongs to the DMRL synthase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                 10-OCT-2003 (Rel. 42, Last sequence update)
LOCT-2003 (Rel. 42, Last annotation update)
6,7-dimethyl-8-ribityllumazine synthase (EC 2.5.1.9) (DMRL synthase)
(Lumazine synthase) (Riboflavin synthase beta chain).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRALT=NZ / ATCC 51768 / DSM 7523;
MEDLINE=21664397; PubMed=11792869;
Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Riboflavin biosynthesis; Transferase; Complete proteome.
SEQUENCE 150 AA; 16474 MW; 73751C1363A8AD8D CRC64;
                                                                                                                                                                                                                                              Pyrobaculum aerophilum.
Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
Thermoproteaceae; Pyrobaculum.
NCBI_TaxID=13773;
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(Rel. 12, Last sequence update)
(Rel. 42, Last annotation update)
150 AA.
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InterPro; IPR002180; DMRL synthase.
Pfam; PF00885; DMRL synthase; 1.
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TIGRFAMS; TIGR00114; ribH; 1.
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                                                                    .0-OCT-2003 (Rel. 42, Created)
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STANDARD;
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01-OCT-1989
10-OCT-2003
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                                                                                                                                                                                                         SUBCLENCE.

MEDLINE=89290032; PubMed=2500367;

A Calabrese L., Polticelli F., O'Neill P., Galtieri A., Barra D.,
Schinia M.E., Bossa F.;

T. Substitution of arginine for lysine 134 alters electrostatic
as schinia M.E., Bossa F.;

T. Substitution of arginine for lysine 134 alters electrostatic

T. Substitution of arginine for lysine 134 alters electrostatic

T. Substitution of arginine for lysine 134 alters electrostatic

T. Substitution of arginine for lysine 134 alters electrostatic

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T. Substitution bestroys radicals which are normally per subunit.

T. Substitution of arginine for lysine 13 and 12 inc ion per subunit.

T. Substitution of arginine for lysine 13 and 12 inc ion per subunit.

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10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
10-0CT-2003 (Rel. 42, Last annotation update)
6.7-dimethyl-8-ribityllumazine synthase (EC 2.5.1.9) (DWRL synthase)
(Lumazine synthase) (Riboflavin synthase beta chain).
RIBH OR SSO0400.
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STRAIN=ATCC 35092 / DSM 1617 / P2;

STRAIN=ATCC 35092 / DSM 1617 / P2;

STRAIN=ATCC 35092 / DSM 1617 / P2;

SED Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,

Awayez M.J., Chan-Weiher C.C.Y., Clausen I.G., Curtis B.A.,

De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,

Heikamp-de Jong I., Jeffens A.C., Kozera C.J., Medina N., Peng X.,

Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,

Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland I.,
Superoxide dismutase [Cu-Zn] (EC 1.15.1.1).
Prionace glauca (Blue shark).
Briaryyota: Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes; Elasmobranchii; Galeonorphii; Galeoidea; Carcharhiniformes; Carcharhinidae; Prionace.
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Sulfolobus.
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6617642A4F23C5AE CRC64;
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COPPER AND ZINC.
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55 1
152 AA;
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Matches 4; Conserv
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                                                                                                                                       NCBI_TaxID=7815;
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RISE SULSO
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Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
"The complete genome of the crenarchaeon Sulfolbous solfataricus P2.";
Proc. Natl. Acad. Sci. U. S.A. 98:735-7840[2001].

-I- FUNCTION: Riboflavin synthase is a bifunctional enzyme complex catalyzate the formation of riboflavin from 5-amino-6-(1'-D)-
ribityl-amino-2.4 (1H.3H)-pyrimidinhedione and L-3.4 d-dipydrohy.2-
butanone-4-phosphate via 6,7-dimethyl-8-lumazine. The beta subunit catalyzes the condensation of 5-amino-6-(1'-D)-ribityl-
amino-2,4 (HH.3H)-pyrimidinedione with L-3,4-dihydrohy.2-
butanone-4-phosphate yielding 6,7-dimethyl-8-lumazine (By
                                                                                                                                                                                                                                                                                                                                                                                                   -!- CATALYTIC ACTIVITY: 2 6,7-dimethyl-8-(1-D-ribityl)lumazine = riboflavin + 4-(1-D-ribitylamino)-5-amino-2,6-dihydroxypyrimidine.ribATHWAY: Riboflavin biosynthesis; last step. -!- PATHWAY: Riboflavin biosynthesis; last step. -!- SIMILARITY: Belongs to the DWRL synthase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIINE-88115138; PubMed-2828309; Deich R.A., Metcalf B.J., Finn C.W., Farley J.E., Green B.A.; Deich R.A., Metcalf B.J., Finn C.W., Farley J.E., Green B.A.; Cloning of genes encoding a 15,000-dalton peptidoglycan-associated outer membrane lipoprotein and an antigenically related 15,000-dalton J. Bacteriol. 170:489-498 (1988).
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STRAINERA ( FW20 / ATCC 51907;
STRAINERAD ( FW20 / BUDMeda-7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness B.F.,
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.I., Glodek A., Kelley J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Outer membrane lipoprotein PCP precursor (15 kDa lipoprotein) (PAL cross-reacting lipoprotein).
PCP OR LPP OR HI1579.
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Pasteurellaceae; Haemophilus.
NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 154;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Riboflavin biosynthesis; Transferase; Complete proteome.
SEQUENCE 154 AA; 17247 MM; ADFA9E6A2C723210 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 19; DB 1; L. Pred. No. 2.7e+02;
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100.0%; Pred. No. ...
0; Mismatches
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PIR; B90184; B90184. -; 1.
InterPro; IPR002180; DMRL_synthase.
Pfam; PF00885; DMRL_synthase; 1.
ProDom; PD003664; DMRL_synthase; 1.
TIGRFAMS; TIGR00114; TISH; 1.
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Best Local Similarity
'...a 4; Conserve
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                                                                                                                                                                                                                                                                                                                                                                            similarity)
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us-09-594-978a-3.rsp

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Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Geoghagen N.S.M., Geoghagen N.S.M., Vencer J.C., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Vencer J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Viridiplantae, Srreptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta; eudicotyledons, core eudicots, asterids,
campanulids, Asterales, Asteraceae, Cichorioideae, Cichorieae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                              Science 269:496-512(1995).
-!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000437; Prok lipoprot S.
PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.
Outer membrane; Lipoprotein; Signal; Complete proteome; Palmitate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-palmitoyl cysteine.
S-diacylglycerol cysteine.
CSLVABEVF -> VAGRRVRI (IN REF.
D7880327FCF0C985 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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TISSUE=Root;
Xu X.-Y., Bewley J.D., Greenwood J.S.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
-!- ALLERGEN: Causes an allergic reaction in human.
-!- SIMILARITY: Belongs to the BetVI family.
                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: TO E.COLI AND S.TYPHIMURIUM SLYB AND TO Y.ENTEROCOLITICA PCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.0%; Score 19; DB 1; Le 100.0%; Pred. No. 2.7e+02; Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY_2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Roct allergen protein (RAP).
Taraxacum officinale (Common dandelion).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 157 AA
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155 AA; 15425 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, M18677, AAA24938.1; -.
EMBL, 1012832, AAC23228.1; -.
PIR, 164130, 164130.
TIGR, H11579, -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            138 VAEF 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4;
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049065;
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATALYTIC ACTIVITY: 2 6,7-dimethyl-8-(1-D-ribityl)lumazine = riboflavin + 4-(1-D-ribitylamino)-5-amino-2,6-dihydroxypyrimidine. PATHWAY: Riboflavin biosynthesis; last step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S., Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y., Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A., Oshima T., Kikuchi H.,
                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                         10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last synthase (EC 2.5.1.9) (DMRL synthase)
(Lumazine synthase) (Riboflavin synthase beta chain).
RIBH OR ST0394.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
                                                                                                                                                                                        ;
0
                                                                                                                                                         Length 157;
                                        Interpro; IPR000916; Bet v I.
Pfam; PF00407; Bet v I; I.
PRINTS; PR00634; BETALLERGEN.
PROSITE; PS00451; PATHOGENESIS_BETVI; 1.
Allergen; Plant defense; Pathogenesis-related protein.
SEQUENCE 157 AA; 17040 MW; 5892AB8593ABA7E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: Belongs to the DMRL synthase family.
                                                                                                                                                       95.0%; Score 19; DB 1; Le
100.0%; Pred. No. 2.8e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                      157 AA.
                                                                                                                                                                                                                                                                                                                                      PRT;
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InterPro; IPR00218; DMRL_synthase.
InterPro; IPR00218; DMRL_synthase, 1.
ProDom; PD003664; DMRL_synthase; 1.
TIGRFAMS; TIGR00114; rIbH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=JCM 10545 / 7;
MEDLINE=21456156; PubMed=11572479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AP000982; BAB65375.1; -.
HAMAP; MF_00178; -; 1.
             EMBL; AF036931; AAB92255.1; -.
HSSP; O24248; 1E09.
                                                                                                                                                                                        4; Conservative
                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sulfolobus tokodaii
                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                     3 VAEF 6
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RISB_SULTO
ID RISB_SULTO
AC Q975M5;
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Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=2019606; Punded=1073132;

MEDLINE=2019606; Punded=1073132;

Amanatides P.G., Scherer S.E., It P.W., Evans C.A., Gocayne J.D.,

Amanatides P.G., Scherer S.E., Holt R.A., Evans C.A., Gocayne J.D.,

B. Sutton G.G., Workman J.R., Yandell M.D., Zhang Q., Chen L.X.,

B. Staton G.G., Workman J.R., Yandell M.D., Zhang Q., Chen L.X.,

B. Brandon R.C., Rogers Y.-H.C., Blaze? B.G., Change M., Pfeiffer B.D.,

April J.F., Apbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,

Ballew R.M., Basu A., Baxendale J., Baytaktaroglu L., Beasley B.M.,

Ballew R.M., Basu A., Baxendale J., Baytaktaroglu L., Beasley B.M.,

Ballew R.M., Basu A., Butler H., Cadlew B., Center A., Chandra I.,

Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

Borkova D., Botcher A., Deng Z., Mays A.D., Den P. Brottier P.,

Cherry J.M., Cawley S., Dahlke C., Pavengort L.B., Davies B.,

Borkova D., Botcher A., Deng S., Mays A.D., Den P.,

Borkova D., Botcher A., Deng S., Mays A.D., Denter S.,

Bodson K., Doup L.E., Downes M., Dugan-Rocha S., Punkov B.C.,

Bodson K., Doup L.E., Downes M., Dugan-Rocha S., Punkov B.C.,

Bodson K., Deug L.E., Mornel M.F., Gu Z., Guan P., Harris M.,

Hortin D., Hauvey D.A., Helman T.J., Hernandez J.R., Houck J.,

Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Houttei B.E., Kodira C.D., Kraft C., Kravitz S., Kalp D., Laiz Z.,

Liu X., Mattei B., Morntosh T.C., McLeod M.P., Mornes D.L.,

Mount S.M., Moy M., Murphy B., Murphy L., Muzry D.M., Nebsen D.L.,

Rolles D.R., Nelson K.A., Punkor, S., Paul W., Pacleb J.M.,

Shue B.C., Siden-Kiamos I., Simpson M., Strong R., Smith T.,

Shue B.C., Siden-Kiamos I., Sungson M., Weisenbach J.,

Wang Z.-Y., Wassarman D.A., Weiner E., Wang A.H., Wang X.,

Wang Z.-Y., Wassarman D.A., Weiner K., Zhan M., Zhou Y., Zhou Y., Zhou Y., Zhou Y., Zhou Y., Zhou Y., Zhon Y., Zhon Y., Zhou X., Zhou X., Zhou X., Zhou X., Zhou X., Zhou X.,
                                                                           ö
                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Cregon-R;
MEDLINE=87086754; PubMed=3098981;
Shore E.M., Guild G.M.;
"Larval salivary gland secretion proteins in Drosophila structural analysis of the Sgs-5 gene.";
J. Mol. Biol. 190:149-158(1986).
                                                                           ô
                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Erachycera; Muscomorpha;
Psphydroidea; Drosophilidae; Drosophila.
                                          Length 157;
                                         Query Match

95.0%; Score 19; DB 1; Length 157

Best Local Similarity 100.0%; Pred. No. 2.8e+02;

Matches 4; Conservative 0; Mismatches 0; Indels
Riboflavin biosynthesis; Transferase; Complete proteome.
SEQUENCE 157 AA; 17501 MW; 529558077E164A18 CRC64;
                                                                                                                                                                                                                            01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Salivary glue protein Sgs-5 precursor.
                                                                                                                                                                                                                 PRT; 163 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                     14 VAEF 17
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                                                                                                         2 VAEF 5
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GSS_DROME
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                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the "FMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=94016558; PubMed=8411151;
Melnick L., Sherman F.;
Melnick L., Sherman R.;
Melnick L., Sherman R.;
of Sacharomyces cerevisiae share a common ancestry.";
J. Mol. Biol. 233:372-388(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=S2886 / AB972;
MEDIATRE=973264; PubMed=9169868;
MEDIATRE=973264; PubMed=9169868;
Araujo R., Awiliga E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M., Garman E., Hartzell G.,
Hunicke-Gmith S., Hyman R.W., Kayeer A., Komp C., Lashkari D., Lew H.
Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P.,
Oh C., Petel F.X., Roberte D., Sehl P., Schrama S., Shogren T.,
Sanith V., Taylor P., Wei Y., Botstein D., Davis R.W.;
"The nucleotide sequence of Saccharomyces cerevisiae chromosome V.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL 1 18 POTENTIAL.
CHAIN 19 163 SALIVARY GLUE PROTEIN SGS-5.
SEQUENCE 163 AA, 18821 MW; 3A476FID3B06D864 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h Similarity 100.0%; Score 19; DB 1; Length 163 Similarity 100.0%; Pred. No. 2.9e+02; 4; Conservative 0; Mismatches 0; Indels
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
10-0CT-2003 (Rel. 22, Last amnotation update)
UTRS protein (Unknown transcript 5 protein).
UTRS OR YEL035C OR SYGP-ORF27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, X04269; CAA27820.1; -.
EMBL, AR003719; AAF55436.1; -.
PIR, A24504; A24504.
Flykase; FBGN0003375; Sg85.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 387:78-81(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4932;
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P32630;
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(Rel. 31, Created)

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01-FEB-1995 (Rel. 31, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Bcl-2-related protein A1 (BFL-1 protein) (Hemopoietic-specific early
response protein) (Al-A).
BCL2A1 OR BCL2A1A OR BFL1 OR A1.
                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                     01-FEB-1995
                               SOLITE SO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                          MSRYGKNLVHYIIVEHDDQR -> MRDSNVKISVFPCALYN
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
-!- FUNCTION: This protein is essential for replication of the chromosome. It is also involved in DNA recombination and repair (By similarity).
-!- SIMILARITY: Contains 1 SSB domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T., Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R., Schlesner H., Amann R., Reinhardt R., "Complete genome sequence of the marine planctomycete Firellula sp. strain 1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSB RHOBA STANDARD; PRT; 169 AA.
P59532; Q7UKX3;
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Single-strand binding protein (SSB) (Helix-destabilizing protein)
SSB OR RB917.
Rhodopirellula baltica.
Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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DNA-binding; DNA repair; DNA replication; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.0%; Score 19; DB 1; Length 169; 100.0%; Pred. No. 3e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                Score 19; DB 1; Length 166;
Pred. No. 2.9e+02;
                                                                                                                                                                                                                                       RGNTTIN (IN REF. 1).
166 AA; 19335 MW; ASBEEBDOFA6D3DEA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             169 AA; 18108 MW; AA8F93E0FA51F287 CRC64;
                                                                                                                                                                                                                                                                                                      95.0%; Scor.
100.0%; Pred. No. ...
... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=1;
MEDLINE=22735913; PubMed=12835416;
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EMBL; 122173; AAA34936.1; -.
EMBL; 865864; AAD13970.1; -.
EMBL; 866120; AAB28442.1; -.
EMBL; U18779; AAB5807.1; -.
PIR; S50509; S50509.
Germonline; 139039; -.
GED; S000761; UTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Planctomycetaceae; Pirellula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95.0%;
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                                                                                                                                                                                                                                                                                                                                                                                         4; Conservative
                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92 VAEF 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=117;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genes, Al."

Int. Immunol. 10:631-637(1998).

Int. Immunol. 10:631-637(1998).

Int. Immunol. 10:631-637(1998).

Int. Immunol. Retards apoptosis induced by IL-3 deprivation. May function in the response of hemopoietic cells to external signals and in maintaining endothelial survival during infection.

Interest and interacellular.

Interest English Expressed in hemopoietic tissues, including bone marrow, spheen and thymus.

Induction: By granulocyte-macrophage colony-stimulating factor and LPS in macrophages.

Induction: By granulocyte-macrophage colony-stimulating factor and LPS in macrophages.

Induction: By granulocyte-macrophage colony-stimulating factor and LPS in macrophages.

Induction: By granulocyte-macrophage colony-stimulating factor and LPS in macrophages.

Induction: BRILLARITY: Contexing 1 BCl-2 homology 2 (BH1) domain.

Induction: SIMILARITY: Belongs to the BCl-2 family.
                                                                                                             STRAIN=CBA/J; TISSUE=Bone marrow;
MEDLINE=93346743; PubMed=8345191;
Lin E.Y., Orlofsky A., Berger M.S., Prystowsky M.B.;
"Characterization of Al, a novel hemopoietic-specific early-response gene with sequence similarity to bcl-2.";
J. Immunol. 151:1979-1988(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'Multiple gene duplication and expression of mouse bcl-2-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-29/Sv, TISSUE=Liver;
MEDLINE-29307518; PubMed-9645611;
Hatakeyama S., Hamasaki A., Negishi I., Loh D.Y., Sendo F.,
Nakayama K., Nakayama K.-I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37AD35818E756488 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALA/PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L16462; AAA16886.1; -.
EMBL; U23774; AAB97953.1; -.
EMBL; U23773; AAB97953.1; JOINED.
PIR; 149449; 149449.
HSSP; Q07817; IMAZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00337; BCL; 1.
SMOSTER; PSS0062; BCL2 PAMILY; 1.
PROSITE; PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD; MGI:102687; Bcl2ala.
InterPro; IPR000712; Bcl2 BH.
InterPro; IPR002475; BCL2_family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 33 ALA
77 97 BH:
132 147 BH:
172 AA; 19914 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 4; Conserv
                                                                               SEQUENCE FROM N.A.
NCBI_TaxID=10090;
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VAEF 31

SULT 35

2 VAEF S

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SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. NCBI\_TaxID=9606; rissum=r-cell HUMAN Lang J.C.; T 36 HUMAN PUFFFFFFFFFYVVX4FFF774VX4FFF379VX4FFF379VX44FF ŏ

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ALA/PRO-RICH.
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BH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50062; BCL2 FAMILY; 1.
PROSITE; PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, BC016281, AAH16281.1; -. PIR, I39055, I39055. HSSP, PS3563; IAF3. Genew; HGNC:991; BCL2A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20132 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U29680; AACS0438.1; -. EMBL; U27467; AACS0288.1; -. EMBL; Y09397; CAA70566.1; -.
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97
147
72
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77
132 1
72
107 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 VAÈF 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 VAEF 5
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P07798;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Apoptosis.
DOMAIN
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Matches
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A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

B Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Horg L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Horg L.,

B Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Romstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

B Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Rohards S.W., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

B Richards S.W., McTay D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Richards S.W., Netwenn M., Madan A., Rodrigues S., Sanchez A.

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Tucchman J.W., Green E.D., Dickson M.C.,

B Blakesley R.W., Tucchman J.W., Green E.D., Dickson M.C.,

B Blakesley R.W., Tucchman J.W., Green E.D., Dickson M.C.,

B Blakesley R.W., Tucchman J.W., Green E.D., Dickson M.C.,

B Blakesley R.W., Tucchman J.W., Green E.D., Dickson M.C.,

B Rodriguez A.C., Grimwood J., Schmutz J., Marra M.A.,

B Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

B Cheneration and initial analysis of more than 15,000 full-length

Thuman and mouse cDNA sequences "."

FUNCTION: Retards apoptosis induced by IL-3 deprivation. May

Gand in the response of hemopoietic cells to external signals

and in maintaining endothelial survival during infection (By

similarity.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "GRS, a novel member of the Bcl-2 gene family, is highly expressed in multiple cancer cell lines and in normal leukocytes."; Oncogene 14:997-1001(1997).
                                                                                                                                                                                                                           TISSUE-Liver;
MEDLINE=96068895; PubMed=7478596;
MEDLINE=96068895: PubMed=7478596;
MEDLINE=9.068895: Park I.-C., Yun J.W., Sung Y.C., Hong S.-I., Shin H.-S.;
"A novel Bcl-2 related gene, Bfl-1, is overexpressed in stomach cancer and preferentially expressed in bone marrow.";
Oncogene 11:1693-1698 (1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97203281; PubMed=9050999;
Kenny J.J., Knobloch T.J., Augustus M., Carter K.C., Rosen C.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Karsan A., Yee E., Kaushansky K., Harlan J.M.; "Cloning of human Bcl-2 homologue: inflammatory cytokines induce human Al in cultured endothelial cells."; Blood 87:3089-3096(1996).
                                                                                                                                                                                                              175 AA
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SUBCELLULAR LOCATION: Intracellular,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Skin;
MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Umbilical vein;
MEDLINE=96184764; PubMed=8605321;
                                                                                                                                                                                                              STANDARD;
                                                          122 VAEF 125
2 VAEF 5
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-i- TISSUE SPECIFICITY: Seems to be restricted to the hematopoietic compartment. Expressed in peripheral blood, spleen, and bone marrow, at moderate levels in lung, small intestine and testis, a minimal levels in other tissues. Also found in vascular smooth muscle cells and hematopoietic malignancies.
-i- INDUCTION: By phorbol ester and inflammatory cytokines, such as TNP-alpha, or IL-1-beta, but not by growth factors:
-i- SIMILARITY: Conteains 1 Bcl-2 homology 1 (BH1) domain.
-i- SIMILARITY: Belongs to the Bcl-2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01.AUG-1988 (Rel. 08, Created)
01.AUG-1988 (Rel. 08, Last sequence update)
10.0CT-2003 (Rel. 42, Last annotation update)
Ferritin, middle subunit (Ferritin M) (Ferritin X) (Ferritin H').
Rana catesbelana (Bull frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      kana caresberana (Bull Irog).
Bukaryota; Metazoa; Chordia; Craniata; Vertebrata; Buteleostomi;
Amphibia; Barrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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Q -> H (IN REF. 3).
329D98AF2BE07AOD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIM; 601056; -.
GO; GO:0008189; F:apoptosis inhibitor activity; TAS.
GO; GO:0006916; P:anti-apoptosis; TAS.
InterPro; IPRO007012, Bol2_BH.
InterPro; IPRO04715; BCL2_EAMILY.
PF00452; BCl-2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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100.0%; Pred. No. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-11, MADMED PubMed=11248100; MEDLINE-1145866; PubMed=11248100; M.L., Whittam T.S., Kapur V.; May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.; "Complete genomic sequence of Pasteurella multocida Pm70."; Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
                                                                                                                                                                                                                                                                                                                                                                                 DSBB_PASMU STANDARD; PRT; 178 AA.
Q9LGB1; PS7804;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Disulfide bond formation protein B (Disulfide oxidoreductase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fuller T.E., Kennedy M.J., Lowery D.E.; "Identification of Pasteurella multocida virulence genes in a septicemic mouse model using signature-tagged mutagenesis."; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria, Proteobacteria, Gammaproteobacteria, Pasteurellales.
Pasteurellaceae, Pasteurella.
                                                                                                                                                                                                            Thermoanserobacter tengcongensis.
Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 177;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00466; Ribosomal L10; T.
PROSITE; PS01109; RIBOSOWAL L10; FALSE NBG.
Ribosomal protein; Complet proteome.
SEQUENCE 177 AA; 19591 MW; 50DDCF896EF6F4E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 19; DB 1; Le
Pred. No. 3.1e+02;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
50-FEB-2003 (Rel. 41, Last annotation update)
50S ribosomal protein L10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95.0%; Scor.
100.0%; Pred. No. s...
                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Clostridia; Thermoanaer
Thermoanaerobacteriaceae; Thermoanaerobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HAMAP; MF 00362; -; 1.
Interpro; IPR001790; Ribosomal L10.
Interpro; IPR002363; Ribosomal L10eub.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE013173; AAM25445.1; -.
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Best Local Similarity 100...
---- 4; Conservative
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                NCBI_TaxID=119072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 VAEF 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 VAEF 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DSBB OR PM0046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Pm70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HAMAP; MF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DSBB_PASMU
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                 SO WERE THE DESCRIPTION OF THE PROPERTY OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAT TAY REPARE THE TAY OF THE TAY OF THE TAY OF THE TAY AND THE TA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EVBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
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                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            core is deposited.
MISCELLANEOUS: THERE ARE THREE TYPES OF FERRITIN SUBUNITS: L, M
AND H CHAINS IN AMPHIBIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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Pred. No. 3.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: Belongs to the ferritin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20592 MW; A9F0F5BEB8584D46 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IRON (BY SIMILARITY).
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PROSITE; PS00540; FERRITIN 1; 1.
PROSITE; PS00204; FERRITIN 2; 1.
PROSITE; PS00204; FERRITIN LIKE; 1.
INO SCROPE; Inon; Metal-binding; 3D-structure.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95.0%; Scor.
100.0%; Pred. No. 3...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR, C27805; C27805.
PDB; 1MFR; 22-JUN-99.
InterPro; 1PR001519; Ferritin.
InterPro; 1PR008331; Ferritin Dps.
InterPro; 1PR009040; Ferritin like.
Pfam; PF00210; ferritin 1.
the first processed in amphibia.";
J. Biol. Chem. 262:7901-7907(1987)
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; J02724; AAA49525.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 4; Conserv
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510 THETN
7 RL10 THETN
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SEQUENCE
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HELIX TURN HELIX

METAL METAL

177 AA.

PRT;

STANDARD;

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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                   SUBCELLULÂR LOCATION: Integral membrane protein. Inner membrane
FUNCTION: Required for disulfide bond formation in some periplasmic proteins. Acts by oxidizing the dsbA protein (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                        Oxidoreductase, Redox-active center, Transport, Electron tra
Chaperone, Transmembrane, Inner membrane, Complete proteome.
DOMAIN 14 (POTENTIAL).
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REDOX.-ACTIVE (BY SIMILARITY).
REDOX.-ACTIVE (BY SIMILARITY).
D2C45BB73B31F0BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 178;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PERIPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 19; DB 1; Le
Pred. No. 3.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95.0%; Scort
100.0%; Pred. No. J.
                                                                                          (By similarity). SIMILARITY: Belongs to the dsbB family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                                               EMBL; AF237925; AAF68411.1; -. EMBL; AE006038; AAK02130.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MW;
                                                                                                                                                                                                                                                                                                                                                                           HAMAP; MF 00286; -; 1.
InterPro; IPR003752; DsbB.
Pfam; PF02600; DsbB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity luv.
4, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41
105
178 AA;
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DOMAIN
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TRANSMEM
DOMAIN
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DISULFID
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108 VAEF 111

PRT; 178 AA.

PRT; 178 AA.

PRT; 178 AA.

PRT3096; Q9VB18;

10.-JAN-1990 (Rel. 13, Last sequence update)

11.-JAN-1990 (Rel. 13, Last sequence update)

11.-JAN-1990 (Rel. 143, Last annotation update)

11.-JAN-1990 (Rel. 13, Last annotation update)

11.-JAN-1990 (Rel. 13, Last sequence update)

12.-JAN-1990 (Rel. 13, Last sequence update)

13.-JAN-1990 (Rel. 13, Last sequence update)

14.-JAN-1990 (Rel. 13, Last sequence update)

15.-JAN-1990 (Rel. 13, Last sequence update)

16.-JAN-1990 (Rel. 13, Last sequence update)

17.-JAN-1990 (Rel. 13, Last sequence update)

18.-JAN-1990 (Rel. 13, Last sequence update)

19.-JAN-1990 (Rel. 13, Last sequence update)

19.-JAN-1990 (Rel. 13, Last sequence update)

10.-JAN-1990 (Rel. 13, Last sequence update)

11.-JAN-1990 (Rel. 13, Last sequence update)

11.-JAN-1990 (Rel. 13, Last sequence update)

12.-JAN-1990 (Rel. 13, Last sequence update)

13.-JAN-1990 (Rel. 13, Last seq DHHHMZWUUUXZAX4HHHZAUX4444

MEDLINE-89231619; PubMed-2540957;
MEDLINE-89231619; PubMed-2540957;
"Closely related transcripts encoded by the neurogenic gene complex enhancer of split of Drosophila melanogaster."; SEQUENCE FROM N.A.

EMBO J. 8:203-210(1989)

STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., SEQUENCE FROM N.A.

Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
And K.H., Doyle C., Baxter E.G., Helt G., Nalson C.R., Miklos G.L.G.,
Ballium R.M., Basu A., Baxendale J., Bayraktaroglu L., Beaaley E.M.,
Balluw R.M., Basu A., Baxendale J., Bhandari D., Bolshakov S.,
Balluw R.M., Basu A., Baxendale J., Bhandari D., Bolshakov S.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Durkes P.,
Cherry J.M., Brangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
R.Durbin K.J., Brangelista C.C., Ferraz C., Ferriera S., Plaischmann M.,
Rodon K., Gong F., Gorgen M., S., Gelbart W.M., Jlaschman C.,
Allakin M., Helman T.J., Hernandez J.R., Harris M.,
Hostin D., Harry D.A., Heiman T.J., Hernandez J.R., Houck J.,
Allako P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., Mopherson D.,
RA Alazzolo M., Pittuan G.S., Pan S., Pollart W. N., Nelson D.L.,
RA Balazzolo M., Pittuan G.S., Pan S., Nouris J., Moshrefi A.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Ray Reinert K., Remington K., Stapleron M., Skupski M.P., Smith T.,
Sheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Sher S., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Ray Sher S., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Ray Sher S., X., Zaveri J.S., Zhan M., Zhou X., Zhu S., Zhou X., Smith H.O.,
RA Sheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
Ray Sheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
Ray Science 287:2185-2195(2000). MEDLINE=95094252; PubMed=8001118; Paroush Z., Finley R.L. Jr., Kidd T., Wainwright S.M., Ingham P.W., Paroush Z., Finley R.L. Jr., Kidd T., Wainwright S.M., Ingham P.W., Ish-Horowicz D.; Redt R., Ish-Horowicz D.; "Groucho is required for Drosophila neurogenesis, segmentation, and sex determination and interacts directly with hairy-related bHLH proteins."; Cell 79:805-815(1994). 

Hairy-related proteins.

SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain. SIMILARITY: Contains 1 orange domain.

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AE003754; AAF56552.1; EMBL; X16552; CAA34552.1; EMBL; AE003754; AAF! PIR; S03629; S03629

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178 AA; 19319 MW; 378A4F200240D924 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                      APT HAEDU
          SEQUENCE
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                                                                       Query Match
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Matches
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APT_HAEDU
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SEQUENCE FROM N.A.

STRAIN=VC-16 / DSM 4304 / ATCC 49558;

MEDLINE=98049343; PubMed=9389475;

KRIENK H.-P., Clayton R.J., Tomb J.-F., White O., Nelson K.E.,

KRIENK H.-P., Clayton R.J., Gwinn M., Hickey E.K., Peterson J.D.,

Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,

Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,

Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,

Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.

Overbeek R., Gocayne J.D., Waidham J.F., McDonald'L., Utterback T.,

Cotton M.D., Spriggs T., Artiach P., Käine B.P., Sykes S.M.,

Sadow P.W., D'Andrea K.P., Bowman C., Fujil C., Garland S.A.,

Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                       CONTROL OF STATE STAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95.0%; Score 19; DB 1; Length 178; 100.0%; Pred. No. 3.1e+02; tive 0; Mismatches 0; Indels
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PIR; E69389.
TIGR; AF118; -.
Hypothetical protein; Signal; Complete proteome.
SIGNAL
1 20 HYPOTHETICAL PROTEIN AF1118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Archaea; Buryarchãeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
NCBI_TaxID=2234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            88 129 CRANGE.
175 178 WRPW MOTIF.
178 AA; 19923 MW; 19363D0F6043C84F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                               BASIC DOMAIN.
HELIX-LOOP-HELIX MOTIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein AF1118 precursor.
                                                                                                                                                                                                                                                                                                                                                                Transcription regulation, Repressor.

DNA BIND 19 33 BASIC DOMAIN 34 HELIX-L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Conservative
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Best Local Similarity
Matches 4; Conserv
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18 ARCFU
7818 ARCFU
029147;
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SEQUENCE FROM N.A.

STRAIN=35000HP / ATCC 700724;

STRAIN=35000HP / ATCC 700724;

STRAIN=35000HP / ATCC 700724;

SUBMISSON L., Ray W.C., Mahairas G., Sabo P., Mungur R.,

Authoson L., Nguyen D., Wang J., Forst C., Hood L.;

The complete genome sequence of Haemophilus ducreyi.";

Submitted (UTN-2003) to the EMBL/GenBank/DDBJ databases

L. FUNCTION: Catalyzes a salvage reaction resulting in the formation of AMP, that is energically less costly than de novo synthesis.

C. I. CATALYTIC ACTIVITY: AMP + diphosphate = adenine + 5-phospho-alpha-

C. I. PATHWAY: Purine salvage.

C. I. STRUMYT: Homedimer (By similarity).

C. SUBUNT: Homedimer (By similarity).

C. SUBUNT: Belongs to the purine/pyrimidine

phosphoribosyltransferase family.
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InterPro; IPR005764; Ade_phspho_trans.

InterPro; IPR002375; Pr/Py_rp_transf.

InterPro; IPR002375; Pr/Py_rp_transf.

Pfam; PF00156; Pribosyltran; 1.

TIGRPAMS; TIGR01090; apt; 1.

PROSTIE; PS00103; PUR, PYR PR TRANSFER; 1.

Transferase; Glycosyltransferase; Purine salvage; Complete proteome. SEQUENCE 179 AA; 19315 MW; 13AlDAFDC13560DF CRC64;
                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
NCBI_TaxID=730;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.0%; Score 19; DB 1; Length 179; 100.0%; Pred. No. 3.1e+02; ative 0; Mismatches 0; Indels
Length 178;
95.0%; Score 19; DB 1; Length 178
100.0%; Pred. No. 3.1e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          E-MRR-2004 (Rel. 43, Created)
15-MRR-2004 (Rel. 43, Last sequence update)
15-MRR-2004 (Rel. 43, Last amotation update)
43-Manine phosphoribosyltransferase (EC 2.4.2.7) (APRT)
APT OR HD1818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE017156; AAP96568.1; -.
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                                    Local Similarity 100.
ses 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45 VABF 48
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                                                                                                                              2 VAEF 5
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RETB BOVIN
ID RETB BOVIN
AC P18902;
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SIMILARITY. SIMILARITY. SIMILARITY.

DISULPID DISULPID HELIX TURN

TURN STRAND

SEN CHE

STRAND

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
MEDLINE-93266508; PubMed=8496140;
Zanotti G., Berni R., Monaco H.L.;
Carottal structure of liganded and unliganded forms of bovine plasma retinol-binding protein.";
J. Biol. Chem. 268:10738-10738 (1993).
J. Biol. Chem. 268:10738-10738 (1993).
J. FUNCTION: Delivers retinol from the liver stores to the peripheral tissues. In plasma, the RBP-retinol complex interacts with transthyretin, this prevents its loss by filtration through the
                                                                                                                                                                                                                                                                                                                       "The bovine plasma retinol-binding protein. Amino acid sequence, interaction with transthyretin, crystallization and preliminary X-ray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Expression and cellular localization of retinol-binding protein messenger ribonucleic acid in bovine blastocysts and extraembryonic membranes.";
                                                                                                        Bos taurus (Bovine).
Wakaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Cetarriodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-9232903; PubMed=1623143;
Monaco H.L., Zanotti G.;
Three-diamensional structure and active site of three hydrophobic
molecule-binding proteins with significant amino acid sequence
similarity.";
Blopolymers 32:457-465(1992).
                                                                                                                                                                                                                                                                                                                                                                                                           [2]
SEQUENCE OF 52-183 FROM N.A.
MEDLINE=93385352; PubMed=8373966;
Liu K.H., Dore J.J. Jr., Roberts M.P., Krishnan R., Hopkins F.M.,
Godkin J.D.;
                                                                                                                                                                                                                                                          MEDLINE=91006139; PubMed=2209607;
Berni R., Stoppini M., Zapponi M.C., Meloni M.L., Monaco H.L.,
Zanotti G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             kidney glomeruli.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the lipocalin family.
01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Plasma retinol-binding protein (PRBP) (RBP).
                                                                                                                                                                                                                                                                                                                                                                                       Eur. J. Biochem. 192:507-513 (1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biol. Reprod. 49:393-400(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, S65585; AAB28336.1; -. PIR, 146955; 146955. PIR, 513186; S13186. PIR, 118P; 31.7AN-94. PDB; 1HBP; 31.7AN-94. PDB; 1HBQ; 31.7AN-94. PDB; 1FEL, 01.NOV-94. PDB; 1FEN; 01.NOV-94.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY
                                                                                                                                                                                            NCBI_TaxID=9913;
                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                     data."
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MEDLINE=95202115; PubMed=7894745;
MEDLINE=95202115; PubMed=7894745;
MEDLINE=95202115; PubMed=7894765;
MEDLINE=95202115; PubMed=789476 P., Savakis C.;
Ingect and extoplasmic incompatibility among laboratory strains.";
Insect Mol. Biol. 3:131-142(1994).
Insect Mol. Biol. 3:131-142(1994).
Insect Mol. Biol. 3:131-142(1994).
Insect Mol. Biol. 3:131-142(1994).
Insect Mol. Biol. 3:171-142(1994).
Insect Mol. 3:171-
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Rickettsiaceae, Wolbachieae, Wolbachia.
NCBL_TaxID=956;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 183;
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01-JTN-1994 (Rel. 29, Last sequence update)
01-JTN-1994 (Rel. 21, Last amontation update)
28-FEB-2003 (Rel. 41, Last amontation update)
Chromosomal replication initiator protein dnaA (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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100.0%; Pred. No. 3.2e+02;
cive 0; Mismatches 0;
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               Local Similarity
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P35907;
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PRINTS; PRO0179; LIPOCALIN. PROSITE; PS00213; LIPOCALIN; 1. Plasma; Vitamin A; Retinol-binding; Transport; Liver; Lipocalin;

InterPro, IPR002345; Lipocalin. InterPro, IPR000566; Lipocln\_cytFABP. Pfam; PF00061; lipocalin; 1.

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Gaps

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(BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).

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Pfam; PF00355; Rieske; 1.

PRINTS; PR00162; RIESKE.

TIGRPAMS; TIGR01405; Rieske proteo; 1.

TIGRPAMS; TIGR01409; TAT signal_seq; 1.

PROSITE; PS00199; RIESKE_1; 1.

PROSITE; PS00200; RIESKE_2; 1.

Electron transport; Inner membrane; Transmembrane; Metal-binding; Iron-sulfur; Iron; 2Fe-28; Oxidoreductase.

TRANSMEM 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95.0%; Score 19; DB 1; Length 190; 100.0%; Pred. No. 3.3e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                    154 BY SIMILARITY.
20299 MW; F83F5D9A9C1FBEE4 CRC64;
                                                                                                                                                                                                                                                                      IRON-SULFUR (2FE-2S)
IRON-SULFUR (2FE-2S)
IRON-SULFUR (2FE-2S)
IRON-SULFUR (2FE-2S)
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STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
MEDLINE-96337999; Pubmed-8688087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last seq
10-OCT-2003 (Rel. 42, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Methanococcus jannaschii.
        InterPro; IPR006311; Tat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                          137 1
190 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NTPA METUA
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MEDLINE-88007612; PubMed=2820981;
MIDLINE-88007612; PubMed=2820981;
Midline-88007612; PubMed=2820981;
Midline-88007612; Midline-880;
Midline-88007612; Midline-88007612;
Midline-88007612; Midline-88007612;
Midline-88007612; Midline-88007612; Midline-88007612;
Midline-88007612; Midline-88007612; Midline-88007612; Midline-88007612; Midline-88007612; Midline-88007612; Midline-88007612; Midline-88007612; Midline-88007612; Midline-88007612; Midline-88007612; Midline-88007612; Midline-88007612; Midline-88007612; Midline-88007612; Midline-88007612; Midline-88007612; Midline-88007612; Midline-88007612; Midline-88007612; Midline-88007612; Midline-88007612; Midline-88007612; Midline-8800762; Midline-88007
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01-NOV-1988 (Rel. 09, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Ubiquinol-cytochrome C reductase iron-sulfur subunit (EC 1.10.2.2)
(Rieske iron-sulfur protein) (RISP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBUNIT: The main subunits of complex b-cl are: cytochrome b, cytochrome cl and the Rieske protein.
-!- SUBCELLULAR LOCATION: Membrane-bound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ferrocytochrome c.
COFACTOR: Binds 1 2Fe-2S iron sulfur cluster per subunit (By
                                                                                                                                                                                                                                                                                                                                                                                          ö
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Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales,
                                                                                                                                                                                                                                                                                                                                   Length 186;
                                                                                                                                                                                                                                                                               186 AA; 21283 MW; C423C06CEFFB0459 CRC64;
                                                                                                                                                                                                                                                                                                                             95.0%; Score 19; DB 1; Le
100.0%; Pred. No. 3.3e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein. SIMILARITY: Belongs to the Rieske family.
EMBL, Z28981; CAA82285.1; -.
PIR; S39317; S39317.
HAMPE, MF-00377; -!
InterPro; IPR001957; Bac_DnaA.
Pfam; PF00308; bac_dnaA; 1.
PRINTS; PR0051; DNAA.
PROSITE; PS01008; DNAA.
DNA replication; DNA-binding; ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         190 AA
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InterPro; IPR005805; Rieske, dom.
InterPro; IPR005806; Rieske dom.
InterPro; IPR006317; Rieske_proteo.
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EMBL; X05799; CAA29243.1; -.
PIR; A29413; A29413.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rhodobacteraceae; Paracoccus
NCBI_TaxID=266;
                                                                                                                                                                                                                                                                                                                                                                                          4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                              2 VAEF 5
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UCRI PARDE
P05417;
                                                                                                                                                                                                                                                                            SEQUENCE
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-!- FUNCTION: CAN EFFICIENTLY HYDROLYZE NONSTANDARD NUCLEOTIDES SUCH
AS XTP TO XMP ON ITP TO IMP, BUT NOT THE STANDARD NUCLEOTIDES. XTP
IS THE BEST SUBSTRAITE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D., Rerlavage A.R., Dougherty B.A., Tomb. J.-F., Adams M.D., Reich C.I., Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A., Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D., Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M., Klenk H.-P., Fraser C.M., Smith H.O., Woses C.R., Venter J.C., Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
MEDLINE=99332061; PubMed=10404228;
Hwang K.Y., Chung J.H., Rim S.-H., Han Y.S., Cho Y.;
Hunture-based identification of a novel NTPase from Methanococcus jannaschii.";
                                                                                                                        01-NOV-1997 (Rel. 35, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Nucleoside-triphosphatase (BC 3.6.1.15) (Nucleoside triphosphate
phosphohydrolase) (NTPase).
                                                                                                                                                                                                                                                                                                                                                                                      Archaea, Buryarchaecta; Methanococci; Methanococcales; Methanocaldococcaceae; Methanocaldococcus.
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193 AA
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us-09-594-978a-3.rsp

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InterPro; IPR006120; HTH 7.
                                                                                                                                                       Query Match
Best Local Similarity
4, Conserve
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                      Escherichia coli.
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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=C-125 / JCM 9153;
MEDLINE22512582; Pubmed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
Horikoshi K.;
                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                           95.0%; Score 19; DB 1; Length 193; 100.0%; Pred. No. 3.4e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus halodurans.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                              22202 MW; 3570565E007D3DAC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-203 (Rel. 41, Last annotation update)
HAM1 protein homolog 2.
                                                                                                                                                                                                                                                                                                                                                                                     194 AA
                                                                                                                                                                                                                                                                                                                         4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                        191
193 AA;
                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                   53 VAEF 56
                                                                                                                                                                                                                                                                                                                                      2 VAEF 5
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Q9K8D9;
                                                                                                                                                                                                                                                                                              SEQUENCE
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TURN
STRAND
TURN
STRAND
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HELIX
TURN
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                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=87109049; PubMed=3027041;
Michiels T., Cornelis G., Ellis K., Grinsted J.;

of a new category of class II transposable elements.";
J. Bacteriol. 169:624-631(1987).
I. FUNCTION: RESOLUTION CA SITE-SPECIFIC RECOMBINATION) OF THE COINTEGRATED REPLICON TO YIELD THE FINAL TRANSPOSITION PRODUCTS.
INSCELLANBOUG: TRANSPOSION TOOST TRANSPOSON FOUND AS PART OF THE LACTOSE TRANSPOSON TNOSI.
I. SIMILARITY: Belongs to the site-specific recombinase resolvase
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Enterobacteriaceae; Escherichia,
NCBI_TaxID=562;
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100.0%; Pred. No. 3.4e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hydrolase, Complete proteome.
SEQUENCE 194 AA; 21868 MW; BBCSA0C4F19A04B3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOOLI STANDARD; PRT; 194 AA.
TURGO_ECOLI STANDARD; PRT; 194 AA.
1905323;
01-NOV-1988 (Rel. 09, Last sequence update)
01-NOV-1988 (Rel. 04). Last amnotation update)
Transposon Th2501 resolvase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AP001517; BAB06786.1; -. PIR; C84033; C84033. BSP; O57679; 1B78. HAWAP; MF 01405; -; 1. InterPro; IPR002637; Hamlp_like. Pfan; PP01725; Hamlp_like; 1. ProDom; PD004952; Hamlp_like; 1. TIGRFAM9; TIGRO0042; TIGRO0042; 1.
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Gaps

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InterPro; IPR066120; HTH 7.
InterPro; IPR066118; Recombinase.
InterPro; IPR006119; Recombinase.
InterPro; IPR006119; resolvase_N.
Pfam; PF02796; HTH 7; 1.
Pfam; PF02796; HTH 7; 1.
Pfam; PF02196; RECOMBINASES 1; FALSE_NEG.
PROSITE; PS00397; RECOMBINASES 2; 1.
Hypochetical protein; DNA recombination; DNA-binding; DNA invertase; Complete proteome.
                                                                                                                                                                                                                                                TRANSIENT COVALENT LINKAGE TO DNA DURING STRAND CLEAVAGE AND REJOINING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE 97251357; PubMed=9097039;
Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
Kasai H., Rashimoto K., Kitakawa M.,
Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N.,
Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J.,
Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
"A S70-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 28.0-40.1 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=06:H1 / CFT073 / ATCC 700928;
MEDLINE=22388234; PubMed=12471157;
MEDLINE=22388234; PubMed=12471157;
MEDLINE=22388234; PubMed=12471157;
Melch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coll.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
I- SIMILARITY: Belongs to the site-specific recombinase resolvase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SERVAIN-KI2 / MG1655;
MEDLINE=97426617; PubMed=9278503;
MEDLINE=97426617; PubMett G. III, Bloch C.A., Perna N.T., Burland V.,.
Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F.,
Riley M., Collado-Vides J., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Ragregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=562, 217992;
                                                                                                                                                                                                                                                                                                                                                                             95.0%; Score 19; DB 1; Length 196; 100.0%; Pred. No. 3.4e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                7CF47F6D88DBD497 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FBB-2003 (Rel. 41, Last amotation update)
Putative DNA-invertase from lambdoid prophage Rac.
PINR OR B1374 OR C3146.
Escherichia coli, and
Escherichia coli 06.
                                                                                                                                                                                                                                                                                                                                     SEQUENCE 196 AA; 21852 MW;
                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0%;
Matches 4; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=K12
                                                                                                                                                                                                                                                          ACT SITE
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PINR ECOLI
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        STTTTS
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MIDLINE=97251357; PubMed=9097039;

Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
Kasai H., Kashimoto K., Kimura S., Kitakwa M., Kitagawa M.,
Kasai H., Kashimoto K., Mizobuchi K., Mori H., Mori T., Motomura K.,
Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N.,
Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J.,
Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.,
Takemoto K., Dawa sequence of the Escherichia coli K-12 genome
corresponding to the 28.0-40.1 min region on the linkage map.";
DNA Res. 3:363-377(1996).

-! SIMILARITY: Belongs to the site-specific recombinase resolvase
InterPro; IPR006118; Recombinase.
InterPro; IPR006119; resolvase_N.
Pfam; PF00219; HTH 7; 1.
PR0219; FS0039; RECOMBINASES_1; 1.
PROSITE; PS00397; RECOMBINASES_2; 1.
DNA recombination; DNA integration; DNA-binding; Transposable element.
ACT_SITE 11 11 TRANSIENT COVALENT LINKAGE TO DNA DURING STRAND CLERVAGE AND REJOINING STRAND CLERVAGE AND REJOINING STRAND LAY H MOTIF (PROBABLE).
SEQÜENCE 194 AA; 21420 MW; DEDPC0BA6406EAD1 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                  95.0%; Score 19; DB 1; Length 194; 100.0%; Pred. No. 3.4e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-PEB-2003 (Rel. 41, Last annotation update)
Putative DNA-invertase from lambdoid prophage Qin.
PINQ OR B1545.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     196 AA
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                                                                                                                                                                                                                                                                                                                                                           Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 VAEF 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                   2 VAEF 5
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PINQ ECOLI

NO ECOLI

Query Match Best Local S: Matches 4

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MEDLINE=93315143; PubMed=7686882;
EMBL; ABC74456.1; -.

R EMBL; ABC74456.1; -.

R EMBL; AE016764; AAN81596.1; -.

R EMSP; AGG888; AG688.

R PIR; AG6888; AG688.

R INCEPPO; IPR006120; HTH 7.

R INCEPPO; IPR006120; HTH 7.

R INCEPPO; IPR006119; resolvase.N.

R PEm; PF00239; resolvase; 1.

R PROSITE; PS00397; RECOMBINASES 1; FALSE NEG.

R PROSITE; PS00397; RECOMBINASES 2; 1.

R PACSITE; PS00399; RECOMBINASES 2; 1.

R PACSITE; PS00399; RECOMBINASES 2; 1.

R PACT_SITE 11 11 TRENGET ON A INCEPTATION; DNA-binding; TACT_SITE 11 TRENGET ON A TRENGET ON A TRENGET ON TRENGET ON
                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this etatement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shigella flexneri.
Bacteria, Protecobacteria, Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae, Becharichia.
NCBI_TaxID=562, 217992, 83334, 623;
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01-070-1989 (Rel. 11, Last sequence update)
10-071-2003 (Rel. 42, Last annotation update)
17-anscriptional regulatory protein uhpA.
UHPA OR B1669 OR C4593 OR Z5159 OR ECS4606 OR SF3792 OR S3976.
Bscherichia coli,
Bscherichia coli (06,
Escherichia coli (0157:H7, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPECIES=E.coli;
MEDLINE=87279903; PubMed=3301805;
Friedrich M.J., Kadner R.J.;
Filedrich M.J., Kadner R.J.;
Filedrich B.G., Radner F.J.;
J. Bacteriol. 169:3556-3563 (1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSIENT COVALENT LINKAGE TO STRAND CLEAVAGE AND REJOINING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 19; DB 1; Length 196;
Pred. No. 3.4e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         643A62BC940B29A9 CRC64;
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SPECIES=E.coli; STRAIN=K12 / MG1655;
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100.0%; Pred
0; N
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MEDLINE=92234930; PubMed=1569007;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           196 AA; 21908 MW;
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nes 4; Conserv
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D _UHPA_ECOLI
C P10940;
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Handrand V.D., Pilmiest G. III, Daniels D.L., Blatter F.R.,

Will Requence and analysis of 136 Kilobaes of the Escherichia coli

RY Genome: organizational symmetry around the origin of replication.;

Genome: organizational symmetry around the origin of replication.;

Genome: organizational symmetry around the origin of replication.;

RECURSE. OLI, STRAING. HIL (CF073 / ARCC 70022)

RECURSE. COLI, STRAING. HIL (CF073 / ARCC 70022)

RECURSE. CROSS D.J., Fose D
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EMBL, M89480; AAA27243.1; ---
EMBL, AEG08876; AAL22648.1; ---
PIR; A41853, A41853.
HSSP, P10957; 1RNL.
Stydene; SG10406; uhpA.
INTERPO; IPR001799; HTH_LUXR.
INTERPO; IPR001799; RESPONSE_rEG.
Pfam; PF00196; GerE; 1.
PRINTS; PR00039; HTHLUXR.
ProDom; PD000030; HTHLUXR.
ProDom; PD000039; HTHLUXR; 1.
PRODOm; PD000039; HTHLUXR; 1.
SMART; SM00421; HTH_LUXR; 1.
SMART; SM00421; HTH_LUXR; 1.
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                                                                                                                                                                                   Nature 413:852-856(2001)
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE-21534948; PubMed=11677609;
McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR0019; HTH LuxR.
InterPro; IPR00192; HTH LuxR.
InterPro; IPR00192; Response_reg.
Pfam; PF001092; Tesponse_reg; 1.
Pfam; PF000030; Tesponse_reg; 1.
PRINTS; PR00030; HTH_LuxR; 1.
PRODOM; PD000030; Response_reg; 1.
PRODOM; PD000030; Response_reg; 1.
PROSTTS; SW00421; HTH_LUXR; 1.
PROSTTE; PS00421; HTH_LUXR; THH_LUXR; 1.
PROSTTE; PS00422; HTH_LUXR_FAMILY; 1.
PROSTTE; PS00422; HTH_HUXR_FAMILY; 1.
PROSTTE; PS00422; HTH HUXR_FAMILY; 1.
PROST
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28-FEB-2003 (Rel. 41, Last amotation update)
Transcriptional regulatory protein uhpA.
UppA OR SYM3790.
Salmonella typhimurium.
Bacteria, Proteobacteria, Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
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Island M.D., Wei B.-Y., Kadner R.J.;
Structure and function of the uhp genes
"ransport system in Bscherichia coli and
J. Bacteriol, 174:2754-2762(1992).
                                                                                                                                             EMBL; M17102; AAA24720.1; -...
EMBL; M84479; AAA24724.1; -...
EMBL; L10328; AAA24722.1; -...
EMBL; AZ000444; AAC76692.1; -...
EMBL; AZ010449; AAA3027.1; -...
EMBL; AZ016569; AAA3027.1; -...
EMBL; AZ016569; AAA38029.1; -...
EMBL; AZ015869; AAA5232.1; -...
EMBL; AZ01586; AAN45232.1; -...
EMBL; AZ01599; AAP18964.1; -...
PIR; A2622; BVECAU.
PIR; H86050; H86050.
HSSP; P10957; IRNL.
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PA_SALTY STANDARD; PR
USP 57.199 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last seque)
28-FEB-2003 (Rel. 41, Last annot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ECO2DBASE; G020.9; 6TH EDITION
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Matches
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Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Milvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.; "Complete genome sequence of Salmonella enterica sercvar Typhimurium LT2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                            -!- FUNCTION: APPEARS TO BE THE POSITIVE ACTIVATOR OF UHPT TRANSCRIPTION.
-!- SUBCELLULAR LOCATION: CYtoplasmic (Probable).
-!- PTM: PHOSPHORYLATED BY UHPB (PROBABLE).
-!- SIMILARITY: COLTAINS 1 response requiatory domain.
-!- SIMILARITY: BELONGS TO THE LUXR/UHPA FAMILY OF TRANSCRIPTIONAL REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=99303612; PubMed=10373455;
Muramatsu M., Sankaranand V.S., Anant S., Sugai M., Kinoshita K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PSG622; HTH_LUXR_FAMILY; 1.
PROSITE; PSG0110; RESPONSE_REGULATORY; 1.
PROSITE; PSG0110; RESPONSE_REGULATORY; 1.
DNA-binding; Activator; Sugar transport; Complete proteome.
DOMAIN
116; RESPONSE_REGULATORY.
MOD_RES
54 54 PHOSPHORYLATION (BY SIMILARITY).
DNA_BIND 155 1174. MOTIF (BY SIMILARITY).
SEQUENCE 196 AA; 20790 MW; 4C80FF931C69078F CRC64;
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28-FEB-2003 (Rel. 41, Last sequence update)
Activation-induced cytidine deaminase (EC 3.5.4.5) (Cytidine aminohydrolase).
ACCDA OR AID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95.0%; Score 19; DB 1; Length 196; 100.0%; Pred. No. 3.4e+02; ive 0; Mismatches 0; Indels
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Local Similarity 100.
Hes 4; Conservative
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178
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ACT_SITE 76
ACT_SITE 178
ACT_SITE 180
SEQUENCE 199 AA;
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RETE HORSE
ID RETE HORSE
AC Q28369;
DT 28-FEB-2003 (
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Best Local &
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                                                                 cells.";
J. Biol. Chem. 274:18470-18476(1999).
-!- FUNCTION: RNA-editing deaminase involved in somatic hypermutation, gene conversion, and class-switch recombination. Required for several crucial steps of B-cell terminal differentiation necessary for efficient antibody responses.
-!- CATALYTIC ACTIVITY: Cytidine + H(2)0 = uridine + NH(3).
-!- COFACTOR: Zinc (By similarity).
-!- COFACTOR: Zinc (By similarity).
                  "Specific expression of activation-induced cytidine deaminase (AID), a novel member of the RNA-editing deaminase family in germinal center B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=ATCC 35092 / DSM 1617 / P2;
MEDLINE=20165948; PubMed=10701121;
MEDLINE=20165948; PubMed=1.0701121;
Charlebois R.L., Singh R.K., Chan-Weiher C.C.-Y., Allard G., Chow C., Confalonieri F., Curtis B., Duguet M., Erauso G., Faguy D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-DEC-1998 (Rel: 37, Created)
15-DEC-1998 (Rel: 37, Last sequence update)
15-DEC-1998 (Rel: 37, Last sequence update)
16-DEC-1998 (Rel: 41, Last annocation update)
17-DEC-1998 (Rel: 41, Last annocation update)
18-DEC-1998 (Rel: 41, Last annocation upd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sulfolobus solfataricus.
Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
Sulfolobus.
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SEQUENCE FROM N.A.
STRAIN=ARCC 35092 / DSM 1617 / P2;
MEDLINE=97352706; PubWed=9209067;
Charlebois R.L., Sensen C.W., Doolittle W.F., Brown J.R.;
"Evolutionary analysis of the hisCGABdFDEHI gene cluster from the archaeon Sulfolobus solfataricus P2.";
J. Bacteriol. 179:4429-4432(1997).
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Pred. No. 3.5e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002125, C. 1.
Prosite; P805240; APOBEC_C; I.
PROSITE; P800903; CYT_DCMP_DEAMINASES; I.
MRNA processing; Hydrolase; Zinc. (BY SIMILARITY).
METAL 87 87 ZINC (BY SIMILARITY).
METAL 90 90 ZINC (BY SIMILARITY).
METAL 97 90 ZINC (BY SIMILARITY).
CROUGENCE 198 A4; Z4030 MW; 18A3BAlOCA54BEBZ CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AR132979; AAD41793.1; -. MGD; MGI:1342279; Aicda. GO; GO:0004126; F:cytidine deaminase activity; IDA. InterPro; IPR007994; APOBEC C. InterPro; IPR02125; dCMP/cyt_deam.
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100.0%; Pred. No. 3.5e+
.... 0; Mismatches
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Best Local Similarity 100.
Matches 4; Conservative
Davidson N.O., Honjo T.,
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IISS SULSO
D HISS SUL
C 033777;
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SEQUENCE FROM N.A.

STATNIS-ATCC 35092 / DSM 1617 / P2;

STATNIS-ATCC 35092 / DSM 1617 / P2;

MEDLINE-21332296; PubMed=11427726;

MAGYEZ M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,

A Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,

De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,

Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,

Charlebois R.L., Doolittle W.F., Duguet M., Gassterland T.,

Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;

The complete genome of the crenarchaeon Sulfolobus solfstaricus P2.";

The complete genome of the crenarchaeon Sulfolobus solfstaricus P2.";

Trocomplete genome of the crenarchaeon Sulfolobus solfstaricus P2.";

Trocomplete genome of the crenarchaeon Sulfolobus solfstaricus P2.";

Trocomplete genome of the presentation of PRFAR and glutamine to IGP, AICAR and glutamate. The hisH subunit provides the glutamine amidetransferase activity that produces the ammonia necessary to hisF for the synthesis of IGP and AICAR (By similarity).

This CATALYITY: A CITYTY: - I (5-phospho-1-deoxyribulos-1-deoxyribulos-1-deoxyribulos-1-deoxyribulos-1-deoxyribulos-1-deoxyribulos-1-deoxyribulos-1-deoxyribulos-1-deoxyribulos-1-deoxyribulos-1-deoxyribulos-1-deoxyribulos-1-deoxyribulos-1-deoxyribulos-1-deoxyribulos-1-deoxyribulos-1-deoxyribulos-1-deoxyribulos-1-deoxyribulos-1-deoxyribulos-1-deoxyribulos-1-deoxyribulos-1-deoxyribulos-1-deoxyribulos-1-deoxyribulos-1-deoxyribulos-1-deoxyribulos-1-deoxyribulos-1-deoxyribulos-1-deoxyribulos-1-deoxyribulos-1-deoxyribulos-1-deoxyribulos-1-deoxyribulos-1-deoxyribulos-1-deoxyribulos-1-deoxyribulos-1-deoxyribulos-1-deoxyribulos-1-deoxyribulos-1-deoxyribulos-1-deoxyribulos-1-deoxyribulos-1-deoxyribulos-1-deoxyribulos-1-deoxyribulos-1-deoxyribulos-1-deoxyribulos-1-deoxyribulos-1-deoxyribulos-1-deoxyribulos-1-deoxyribulos-1-deoxyribulos-1-deoxyribulos-1-deoxyribulos-1-deoxyribulos-1-deoxyribulos-1-deoxyribulos-1-deoxyribulos-1-deoxyribulos-1-deox
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Gaasterland T., Garrett R.A., Gordon P., Jeffries A.C., Kozera C., Kushwaha N., Lafleur B., Medina N., Peng X., Penny S.L., She Q., St Jean A., van der Oost J., Young F., Zivanovic Y., Doolittle W.F., Ragan M.A., Sensen C.W.
                                                                                                                                                                                             "Gene content and organization of a 281-kbp contig from the genome the extremely thermophilic archaeon, Sulfolobus solfataricus P2."; Genome 43:116-136 (2000).
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PIR; H90206; H90206.
HAMAP: MF 00218; -; I.
InterPro; IPR000991; GATase-1.
Pfam; PF00117; GATase; I.PE0117; GATASE TYPE I; PALSE NEG.
Histidine biosynthesis; Transferase; Glutamine amidotransferase;
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Lettinol-binding protein precursor (PRBP) (RBP).
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; 17DB1A86724CE095 CRC64;
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100.0%; Pred. No. 3.5e+02;
ive 0; Mismatches 0;
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MEDLINE=22388257; PubMed=12477932;
A Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
A strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
A straush R.D., Collins B., Wagner L., Schemen C.M., Schuler G.D.,
A lischul S.F., Zeeberg B., Buttow K.H., Schemen C.M., Bath N.K.,
A plachul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A blachenko L., Marushia R., Farmer A.A., Rubin G.M., Hong L.,
A stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Ginbarance P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Muzny D.M., Sodergen E.J., Lu X., Gibbs R.A.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Chener A., Schmutz J., Myarza R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Chener A., Schmutz J., Myarza M.A.,
Chener C.D., Schmutz J., Myarza M.A.,
Chener C.D., Schmutz J., Myarza M.A.,
Chener D.M., Marza M.A.,
Chener D.M., Marza M.A.,
Chener D.M., Schmutz J., Myarza M.A.,
Chener D.M., Schmutz J., Myarza M.A.,
Chener D.M., Schmutz J., Myarza M.A.,
Chener D.M., Schmutz J., Wyarza M.A.,
Chener D.M., Schmutz J., Schmutz 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 18-201 FROM N.A.
TISSUE=Fetal liver;
Zhang C., Yu Y., Zhang S., Wei H., Zhang Y., Zhou G., Bi J., Liu M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Structural and functional studies of vitamin A-binding proteins."; Ann. N.Y. Acad. Sci. 359:79-90(1981).
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SEQUENCE OF 1-189 FROM N.A.

D'Onofine 66055755; PubMed=2988779;
D'Onofine C., Colantuoni V., Cortese R.;
"Structure and cell-specific expression of a cloned human retinol structure and cell-specific expression of a cloned human retinol structure and cell-specific expression of a cloned human retinol specific transcriptional signals.";

EMBO J. 4:1981-1989 (1985).
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MEDILINE-88019004; PubMed-24440, Peterson P.A.;

Rask L., Anundi H., Follman J., Peterson P.A.;

"The complete amino acid sequence of human serum retinol-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 19-183.
MEDLINE=80004132; PubMed=573217;
Rask L., Anundi H., Peterson P.A.;
"The primary structure of the human retinol-binding protein.";
FEBS Lett. 104:55-58(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 19-201.
MEDLINE-81254137; PubMed=6942701;
Rask L., Anundi H., Boehme J., Eriksson U., Ronne H., Sege K.,
Peterson P.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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MEDLINE=91017498; PubMed=2217163;
retinol-binding protein.";
Nucleic Acids Res. 11:7769-7776(1983)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ups. J. Med. Sci. 92:115-146(1987).
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MEDLINE=95395382; PubMed=7666002;
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                                                                             SEQUENCE FROM N.A.
        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                            Gaps
                           Eguus caballus (Horse).
Eukaryota, Metazoa; Chordata; Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Eguus.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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MEDLINE-84069802; PubMed=6316270;
Colambuoni V., Romano V., Bensi G., Santoro C., Costanzo F.,
Raugei G., Cortese R.;
"Cloning and sequencing of a full length cDNA coding for human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00179; LIPOCALIN.
PROSITE; PS00213; LIPOCALIN; 1.
Plaema; Vitamin A; Retinol-binding; Transport; Liver; Signal;
Lipocalin. 1 POTENTIAL.
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PLASMA RETINOL-BINDING PROTEIN.
BY SIMILARITY.
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BY SIMILARITY.
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100.0%; Pred. No. 3.5e+02;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro, IPR002345; Lipocalin.
InterPro, IPR00566; Lipocln_cytFABP.
Pfam; PF00061; lipocalin, 1.
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201
178 BY
192 BY
147 BY
23022 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        201 AA;
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Best Local Similarity
                                                                                                                                     [1]
SEQUENCE FROM N.A.
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                                                                                                         NCBI_TaxID=9796;
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DISULFID

SEQUENCE

Matches

Pfam, PR00061, lipocalin, 1.
PRINTS; PR00179; LIPOCALIN.
PROSITE; PS00213; LIPOCALIN.
PLSCAMA; Vitamin A; Retinol-binding; Transport; Liver; Signal; Lipocalin; Disease mutation; Vision; 3D-structure.
SIGNAL

Min, Co. 000561s, C:extracellular space, T GO, GO:0005501; F:retinoid binding; TAS. InterPro; IPR002345; Lipocalin. InterPro; IPR00566; Lipocalin\_cytFABP.

MIM; 180250; -.

PDB; 1BRP; 31-JAN-94. PDB; 1BRQ; 31-JAN-94. PDB; 1QAB; 09-APR-99. SWISS-2DPAGE; P02753; HUMAN. Siena-2DPPAGE; P02753; -. Genew; HGNC:9922; RBP4.

PLASMA RETINOL-BINDING PROTEIN,

/FTId=VAR\_009276. G -> D (in RBP deficiency). /FTId=VAR\_009277. F -> L (IN REF. 1 AND 3). LGSGR -> WAA (IN REF. 1 AND 3).

CONFLICT CONFLICT STRAND HELIX

STRAND

TURN

STRAND

TURN

-> N (in RBP deficiency)

201 178 192 147 59

138 138 59

DISULFID DISULFID DISULFID

CHAIN

VARIANT /ARIANT

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DISEASE: Defects in RBP4 are a cause of retinol-binding protein deficiency [MIM:180250]. This condition causes night vision problems. It produces a typical "fundus xerophthalmicus," featuring a progressed atrophy of the retinal pigment epithelium. DISEASE: A deficiency of vitamin A blocks secretion of the binding supply of vitamin to the epidermal cells in defective delivery and supply of vitamin to the epidermal cells (a condition associated with a dermatosis).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHARACTERIZATION OF VARIANTS ASN-59 AND ASP-93.

MEDLINE=99247593; PubMed=10232633;
Blessladki H.K., Frank J., Beck S.C., Heinrich F., Illek B., Reifen R.,
Gollnick H., Seeliger M.W., Wisshager B., Zrenner E.,
"Blochemical but not clinical vitamin A deficiency results from
mutations in the gene for retinol binding protein.";
Am. J. Clin. Nutr. 69:931-936(1999).
-!- FUNCTION: Delivers retinol from the liver stores to the peripheral
tissues. In plasma, the RBP-retinol complex interacts with
transthyretin, this prevents its loss by filtration through the
kidney glomeruli.
-!- SUBCELLULAR LOCATION: Secreted.
-!- MASS SPECTROMETRY: MW=21063.46; MW_ERR=1.88; METHOD=Electrospray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [12]
VARIANTS RBP DEFICIENCY ASN-59 AND ASP-93.
WARDLINE=99103495; PubMed=988420;
Seeliger M.W. Biesalski H.K., Wissinger B., Gollnick H., Gielen S., Frank J., Beck S., Zrenner E.;
Phenotype in retinol deficiency due to a hereditary defect in retinol binding protein synthesis.";
Invest. Ophthalmol. Vis. Sci. 40:3-11(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS) OF COMPLEX WITH TTR. MEDLINE=99162254; PubMed=10052934; Naylor H.M., Newcomer M.B.; "The structure of human retinol-binding protein (RBP) with its carrier protein transthyretin reveals an interaction with the carboxy terminus of RBP.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: Belongs to the lipocalin family.
DATABARS: NAME=Matations of the RBP4 gene;
NOTE=Retina International's Scientific Newsletter;
WWW="http://www.retina-international.com/sci-news/rlbp4mut.htm".
Jowan S.W., Newcomer M.E., Jones T.A.;
"Crystallographic refinement of human serum retinol binding protein
                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY.
MEDLINE=92322903; PubMed=1623143;
Monaco H.L., Zanotti G.;
"Three-dimensional structure and active site of three hydrophobic molecule-binding proteins with significant amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochemistry 38:2647-2653(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lopolymers 32:457-465(1992).
                                                                                                                              Proteins 8:44-61(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           similarity.";
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Trout W.B., MoDonnall J.J., Kramer K.K., Baumbach G.A., Roberts R.M.;
"The retinol-binding protein of the expanding pig blastocyst:
molecular cloning and expression in trophectoderm and embryonic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (1.65 ANGSTROMS), AND REVISIONS TO 134 AND 185.
MEDLINE-98437649; PubMed-9757135;
Zanotti G., Panzalorto M., Marcato A., Malpeli G., Folli C., Berni R. "Structure of pig plasma retinol-binding protein at 1.65-A
                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Merazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                              Length 201;
                                                                                                                                                                                                                                                                                                                                              95.0%; Score 19; DB 1; Length 201
100.0%; Pred. No. 3.5e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1992 (Rel. 23, Created)
15-UUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Plasma retinol-binding protein precursor (PRBP) (RBP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   201 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disc.";
Mol. Endocrinol. 5:1533-1540(1991);
                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                      60 VAEF 63
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223
231
24
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ID RETB_PIG
AC P27485;
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PSECURATE OF 19-201.

NEDLINE-85207643; PubMed=1838985;
NEDLINE-85207643; PubMed=1838985;
NEDLINE-85207643; PubMed=1838985;
NEDLINE-85207643; PubMed=1838985;
NEDLINE-85207643; PubMed=1838985;
NEDLINE-85207643; PubMed=1838985;
Nederok L., Eriksson U., Aakerstroem B., Jones A., Newcomer M., As Peterson P.A., Rask L.; Rask L.; As Peterson P.A., Rask L.; As Peterson P.A., Rask L.; Takinologies between rabbit, rat, and human serum RT retinol-binding proteins: ", and retinologies between rabbit, rat, and human serum retinol-binding proteins: ", and retinologies between rabbit, rat, and human serum RT retinol-binding proteins: ", and retinologies between rabbit, rat, and human serum retinologies bring to retinol from the peripheral CC -: FUNCTION: Delivers retinol from the liver stores to the peripheral transfer in plasma, the RBP-retinol complex interacts with the kidney glomeruli.

CC -: SUBCELULAR LOCATION: Secreted.

CC -: SUBCELULAR FIFTY: Belong to the lipocalin family.
                                                                                                                  Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteléostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                              MEDLINE=93011736; PubMed=1339354;
Lee S.Y., Ubels J.L., Soprano D.R.;
"The lacrimal gland synthesizes retinol-binding protein.";
Exp. Eye Res. 55:163-171(1992).
      01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Plasma retinol-binding protein precursor (PRBP) (RBP).
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                         NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 VAEF 5
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SEQUENCE
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resolution.";
Acta Crystallogr. D 54:1049-1052(1998).
-!- FUNCTION: Delivers retinol from the liver stores to the peripheral tissues. In plasma, the RBP-retinol complex interacts with transthyretin, this prevents its loss by filtration through the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, M68860, AAA31113.1; -
PIR, A39466, A39466.

PDB; 1AQB; 28-JAN-98

InterPro; IPR003566; Lipocalin.
InterPro; IPR003656; Lipocalin.
PRO061; Lipocalin; 1.
PRO061; Lipocalin;
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100.0%; Pred. No. 3.5e+02;
iive 0; Mismatches 0;
                                                                                                                                 kidney glomeruli.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the lipocalin family.
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                 EMBL; 845958; AAB22582.1; -.
PIR; A49178; VARB.
HSSP; P18902; PFEN.
InterPro; IPR002345; Lipocalin.
InterPro; IPR000566; Lipocalin.
Pfam; PF00061; Lipocalin; 1.
PRINTS; PR00179; LIPOCALIN; 1.
PROSTIE; P800213; LIPOCALIN; 1.
PROSTIE; P800213; LIPOCALIN; 1.
Plasma; Vitamin A; Retinol-binding; Transport; Liver; Lipocalin;
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0
                                                                                                                                                                                                                                                                                                                                                                                                     PLASMA RETINOL-BINDING PROTEIN.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
4153FCF050184136 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Length 201;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1992 (Rel. 23, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein yigZ.
YIGZ OR B3848.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.0%; Score 19; DB 100.0%; Pred. No. 3.5 tive 0; Mismatches
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19 201 PLL
22 178 BY
88 192 BY
138 147 BY
201 AA; 23102 MW;
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YIGZ_ECOLI
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201 AA.

SULT 58
THE RABIT STANDARD;
PO6512;
PO6512;
01-JAN-1988 (Rel. 06, Created)

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                                                                                                                                                                                                                                                                               MEDLINE=94147996; PubMed=8313894; Koomin B.V., Bork P., Sander C.; "Yeast chromosome III: new gene functions."; EMBO J. 13:493-503(1994).
                                              Gaps
                                                                                                                                                                                                      Nakahigashi K., Inokuchi H.; "Nucleotide sequence between the fadB gene and the rrnA operon from Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI TaxID=9606;
          Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein; Complete proteome.
CONFLICT 125 125 L -> V (IN REF. 2).
SEQUENCE 204 AA; 21757 MW; 97E48163FE899DBE CRC64;
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100.0%; Pred. No. 3.6e+02;
iive 0; Mismatches 0;
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16-0CT-2001 (Rel. 40, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 205 AA.
                                                                                                                                                                                                                                            Nucleic Acids Res. 18:6439-6439(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, M87049, AAA67645.1, ALT INIT.
EMBL, AE000460, AAC76851.1, ALT INIT.
EMBL, X54687, CAA38501.1, ALT INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EcoGene, EG11484, yigZ.
InterPro, IPR019022, EFG III.V.
InterPro, IPR01498, UPF0029.
IEM, PF01205, UPF0029; 1.
TIGRPAMS, TIGR00257, TIGR00257; 1.
PROSITE; PS00910, UPF0029; 1.
                                                                                                                                                                                         MEDLINE=91057145; PubMed=2243799;
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Best Local Similarity luv...
4; Conservative
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Escherichia coli.
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                                      NCBI_TaxID=562;
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ID21_HUMAN
D_MD21_HUMAN
.C_Q13257;
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TISSUE=Bone marrow, and Muscle;

WEDLINE=22388557; Pubmed=12477932;

REDLINE=22388557; Pubmed=12477932;

Strausberg R.L., Teingold E.A., Grouse L.H., Derge J.G.,

Riausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

A lischul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahr N.K.,

A lischul S.F., Jordan H., Moore T., Max S.I., Mang J., Hsich F.,

Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

A stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Morley K.C., Hale S., Garrina R.D., Mullahy S.J.,

Raha S.S., Morley K.C., Hale S., Garria A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glbbs R.A.,

Rahay J., Helton E., Ketteman M., Madan A., Rodiffaus G.G.,

Nhiting M., Madan A., Young A.C., Shevohenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.L., Skalska U., Smallus D.E.,

"Generation and initial analysis of more than 15,000 full-length

Thuman and mouse cDNA sequences",

"Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Structure of the Mad2 spindle assembly checkpoint protein and its interaction with Cdc20.";
Nat. Struct. Balol. 7:224-229(2000).

-I. FUNCTION: REQUIRED FOR THE EXECUTION OF THE MITOTIC CHECKPOINT WHICH MONITORS THE PROCESS OF KINETOCHORE-SPINDLE ATTACHMENT AND DELAYS THE ONSET OF ANAPHASE WHEN THIS PROCESS IS NOT COMPLETE. IT INHIBITS THE ACTIVITY OF THE ANAPHASE PROMOTING COMPLETE. IT SEQUESTERING CDC20 UNTIL ALL CHROMOSOMES ARE ALIGNED AT THE METAPHASE PLATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-9945864; PubMed-10527948;
Nelson K.K., Schlondorff J., Blobel C.P.;
Nelson K.K., Schlondorff J., Blobel C.P.;
"Evidence for an interaction of the metalloprotease-disintegrin tumour necrosis factor alpha convertase (TACE) with mitotic arrest deficient 2 (MAD2), and of the metalloprotease-disintegrin MDC9 with a novel MAD2-related protein, MAD2-beta.";
Biochem. J. 343:673-680(1999).
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MEDLINE=98301442; PubMed=9637688;
Fang G., Yu H., Kirschner M.W.;
"The checkpoint protein MAD2 and the mitotic regulator CDC20 for ternary complex with the anaphase-promoting complex to control anaphase initiation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Klebert S., Barnikol-Watanabe S., Kratzin H.D., Hilschmann N., Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                Li Y., Benezra R.; "Identification of a human mitotic checkpoint gene: hsMAD2."; Science 274:246-248(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRUCTURE BY NAW OF 11-195.
MEDLINE-20165182; PubMed=10700282;
Luo X., Fang G., Coldiron M., Lin Y., Yu H., Kirschner M.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NODOR1 T.; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                  Jin D.-Y., Jeang K.-T.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases
[1]
SEQUENCE FROM N.A.
MEDLINE=96421709; PubMed=8824189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genes Dev. 12:1871-1883(1998).
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Wagner G.,
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SEQUENCE FROM N.A.

STRAIN=129;
MEDILINE=20348739; PubMed=10892650;
Dobles M., Liberal V., Scott M.L., Benezra R., Sorger P.K.;
Chromosome missegregation and apoptosis in mice lacking the mitotic checkpoint protein Mad2.";
Cell 101:635-642000).
-!- FUNCTION: REQUIRED FOR THE EXECUTION OF THE MITOTIC CHECKPOINT CELL 101:635-642000.
-!- FUNCTION: REQUIRED FOR THE EXECUTION OF THE MITOTIC CHECKPOINT CELL INTERIOR THE PROCESS OF KINETOCHORE-SPINDLE BY SEQUESTERING CDC20 UNTIL ALL CHROMOSOMES ARE ALIGNED AT THE METAPRASE PLATE (BY SIMILARITY).
-!- SUBDMIT: INTERACTS WITH CDC20.
-!- SUBDMIT: INTERACTS TO THE MAD2 PAMILY.
-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
-!- SIMILARITY: Contains I HORMA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EVBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
 MAD2LI OR MAD2A.
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutebria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
                                                                                           [1] ____SEQUENCE FROM N.A.
STEATH=CS7EL/6J; TISSUE=Embryo;
STEATH=CS7EL/6J; TISSUE=Embryo;
Jin D.-Y. Jeang K.-T.;
"Identification of a novel component of the spindle assembly checkpoint in mammalian cells.";
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R MBEL; AFZ61319; AAF69525.1; -.
R HSSP; Q123.7; LDUJ.
R RGD; MG11860374; Mad211.
R GO; GO:0000776; C:kinetochore; IDA.
R GO; GO:0000776; C:kinetochore; IDA.
R GO; GO:0000709; P:mitotic chromosome segregation; R GO; GO:0007094; P:mitotic chromosome segregation; R GO; GO:0007094; P:mitotic chromosome segregation; R GO; GO:0007094; P:mitotic chromosome segregation; IMP.
R GO; GO:007094; P:mitotic chromosome segregation; IMP.
R Ffam; PF02301; HORMA; 1.
R PROSITE; PS50815; HORMA; 1.
Cell cycle; Altosie; HORMA; 1.
DOMAIN.
14 197 HORMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95.0%; Score 19; DB 1; Length 205; 100.0%; Pred. No. 3.6e+02; ive 0; Mismatches 0; Indels
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178 C -> S (IN REF. 1).
201 T -> I (IN REF. 1).
23598 MW, A9F3F28BC4C9738E CRC64;
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(Rel. 29, Last sequence update)
(Rel. 40, Last annotation update)
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205 AA;
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Best Local Similarity
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01-JUN-1994
16-OCT-2001
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ID YACI LEG
AC P37033;
DT 01-JUN-:
DT 01-JUN-:
DT 16-OCT-:
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-i- SUBUNIT: INIBACAL.
-i- SUBCELLULAR LOCATION: Nuclear.
-i- SUMILARITY: BELONGS TO THE MAD2 FAMILY.
-i- SIMILARITY: Contains 1 HORVA domain.
-i- DATABASE: NAME-Atlas Genet. Cytogenet. Oncol. Haematol.;
WWW="http://www.infobiogen.fr/services/chromcancer/Genes/WAD2L1ID304.html".
                                                                                                 WWW="http://www.infobiogen.fr/services/chromcancer/Genes/MAD2LIID304.ht
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or send an email to license@isb-sib.ch).
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21 MOUSE
MD21_MOUSE
STANDARD; PRT; 205 AA.

Q921B5; Q9J153;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2003 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Mitotic spindle assembly checkpoint protein MAD2-like 1).
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205 AA;
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Best Local Similarity
Matches 4; Conserv
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                                                                                                    STRAIN=Philadelphia 1;
MEDLINE=93374864; PubMed=8366052;
MEDGAUG J.M., Horwitz M.A.;
Mengaud J.M., Horwitz M.A.;
"The major iron-containing protein of Legionella pneumophila is an aconitase homologous with the human iron-responsive element-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=Biotype gravis / NCTC 13129;
MIEDLINE=2296543; PubMed=14602910;
Cardeno-Tarraga A.M., Efstration A., Dover L.G., Holden M.T.G.,
Pallen M., Bentley S.D., Besra G.S., Churcher C., James K.D.,
De Zoysa A., Chillingworth T., Cronin A., Dowd L., Feltwell T.,
Hamlin N., Holroyd S., Agels K., Moule S., Quail M.A.,
Rabbinowitsch E., Rutherford K.M., Thomson N.R., Unwin L.,
Whitchead S., Barrell B.G., Parkhill J.;
"The complete genome sequence and analysis of Corynebacterium
diphtheriae NCTC13129.";
Nucleic Acids Res. 31:6516-6523(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
              Legionella pneumophila.
Bacteria, Proteobacteria, Gammaproteobacteria, Legionellales,
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Corynebacterineae, Corynebacteriaceae, Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                           95.0%; Score 19; DB 1; Length 208; 100.0%; Pred. No. 3.6e+02; ive 0; Mismatches 0; Indels
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Hypothetical protein.
SEQUENCE 208 AA; 23714 MW; IESC75E63A20C800 CRC64;
Hypothetical 23.7 kDa protein in acn 5'region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-DEC-1998 (Rel. 37, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
HAWO OR DIP1669.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  215 AA
                                                                                                                                                                                 protein.";
J. Bacteriol. 175:5666-5676(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97158681; PubMed=9006041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hemoglobin.";
J. Bacteriol. 179:838-845(1997),
                                                                                                                                                                                                                                                                                                                                                   EMBL; L22081; AAA25294.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Corynebacterium diphtheriae.
                                     Legionellaceae; Legionella.
NCBI_TaxID=446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Conservative
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P71119;
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                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its mes by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINES 96050477 FubMed=7561763;

MEDLINES 96050477 FubMed=7561763;

MCGATVEY P.B., Tousignant M., Geletka L., Cellini F., Kaper J.M.;

MCGATVEY P.B., Tousignant M., Geletka L., Cellini F., Kaper J.M.;

"The complete sequence of a cucumber mosaic virus from Ixora that is deficient in the replication of satellite RNAs.";

Gen. Virol. 76:2257-2270 (1995).

-i. SIMILARITY: Belongs to the cucumoviruses/bromoviruses coat protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IRON (HEME AXIAL LIGAND) (BY SIMILARITY).

E -> K (IN REF. 1).

A -> V (IN REF. 1).

A -> V (IN REF. 1).

N -> H (IN REF. 1).
-!- FUNCTION: Allows the bacteria to use the host heme as an iron source. Involved in the oxidation of heme and subsequent release of iron from the heme moiety.
-!- CATALYTIC ACTIVITY: Heme + 3 AH(2) + 0(2) = biliverdin + Fe(2+) + CO + 3 A + 3 H(2)0.
-!- SIMILARITY: Belongs to the heme oxygenase family.
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Cucumber mosaic virus (strain Ixora) (CMV).
Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
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PIR, D71392; D71392; D71392.
InterPro; IRR002347; Cucumovirus coat.
InterPro; IPR008975; Viral_cap_coat.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam, PF01126, Heme oxygenase; 1. PRINYS, PRODO88, HAEMOXYGNASE. PROSITE, PS00593; HEME_OXYGENASE; 1. Heme; Oxidoreductase.
                                                                                                                                                                                                                                                                                                                                                      EMBL; U73860; AAC4432.1; -.
EMBL; BXX48358; CAES0198.1; -.
HASP; P09601; 1008.
InterPro; IPR002051; Heme_oxygenase.
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34 B
60 A
93 DG
192 N
24116 MW;
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ID COAT CMVIX
AC Q66120;
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CONFLICT
CONFLICT
SEQUENCE
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SULT 65

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MEDLINE-98049343; PubMed=9389475;
MEDLINE-98049343; PubMed=9389475;
MEDLINE-98049343; PubMed=9389475;
MEDLINE-98049343; PubMed=9389475;
METCHUM K.A., Dodayton R.A., Tomb J.-F., White O., Nelson K.E.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
Peterson S., Reich C.I., Wandell L.K., Badger J.H., Glodek A., Zhou L.,
Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
Badow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
-!- FUNCTION: Probably involved in degradation of a variety of RNA species; could act a RNA-binding component of the exosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- SUBUNIT: Component of the archaeal exosome multienzyme ribonuclease complex (Potential).
-i- SUBCELLULAR LOCATION: (Stoplasmic (Potential).
-i- SIMILARITY: Contains 1 KH domain.
-i- SIMILARITY: Contains 1 S1 motif domain.
                                                                                                      Archaea; Buryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
    10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Probable exosome complex RNA-binding protein 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE001070; AAB90745.1; -. PIR; D69311; D69311.
                                                                                      Archaeoglobus fulgidus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     209 VAEF 212
                                                                                                                                                  NCBI_TaxID=2234;
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RAN_TETPY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polyhedrosis virus genome.", Virology 229:381-399(1997).
-!- FUNCTION: COULD BE INACTIVE AS THE ACTIVE SITE CYSTEINE IS MODIFIED TO TRYPTOPHAN.
-!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein tyrosine + phosphate.
-!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-TYROSINE PHOSPHATASE FAMILY: CDC14 SUBFAMILY.
                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE=9126251; MEDLINE=97271300; PubMed=9126251; Ahrens C.H., Russell R.R., Funk C.J., Evans J., Harwood S., Rohrmann G.F., "The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Orgyia pseudotsugata multicapsid polyhedrosis virus (OpMNPV).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.
NCBI_TaxID=164623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SITE 162 162 EQUIVALENT OF ACTIVE SITE CYS. SEQUENCE 220 AA; 25234 MW; D3FC093F1953D425 CRC64;
                                                                                                                          95.0%; Score 19; DB 1; Length 218; 100.0%; Pred. No. 3.8e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95.0%; Score 19; DB 1; Length 220; 100.0%; Pred. No. 3.9e+02; tive 0; Mismatches 0; Indels
                                                                                  218 AA; 24185 MW; 130E82D17BD75224 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Putative protein-tyrosine phosphatase 1 (EC 3.1.3.48).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000387; TYR phosphatase.
PROSITE; PS00383; TYR PHOSPHATASE 1; FALSE_NEG.
PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                            220 AA.
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Pfam; PF00760; Cucumo coat; 1.
PRINTS; PR00222; CUCUMOCOAT.
ProDom; PD001284; Cucumovirus_coat; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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R1 ARCFU
CSCR1 ARCFU STANDARD;
10-OCT-2003 (Rel. 42, Created)
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Best Local Similarity 100...
4; Conservative
                                                                                                                     Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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                                                              Coat protein
SEQUENCE 2:
                                                                                                                                                                                                                                                                                                                                   P1_NPVOP
PTP1_NPVOP
O10274;
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SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE 223 AA; 24725 MW; A11B7F1A26972833 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50126; XH TYPE 1; 1.
PROSITE; PS50126; S1; 1.
Exosome; RNA-binding; Complete proteome.
DOMAIN 135 127 KH.
                                                                                                                                                                                                                                                                                                                                  TIGR; AF0492; -.

HAWAR, MF 00623; -; 1.

INTERFO, IPR004087; KH dom.

INTERFO; IPR004088; KH type 1.

INTERFO; IPR008994; NuCleic_acid_OB.

INTERFO; IPR003029; S1.

Pfam; PF00513; KH; 1.

SWART; SM00322; KH; 1.

SWART; SM00316; S1; 1.
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Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
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InterPro; IPR002699; ATPSYNt_Dsub.
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nes 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=5911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 VAEF 5
                                    NCBI_TaxID=274;
                                                                                                                                                                                                                                                                                        (+) (Out)
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Matches
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RAN_TETTH
δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                               Gene 144:123-125(1994).
-!- FUNCTION: GTP-binding protein involved in nucleocytoplasmic transport. Required for the import of protein into the nucleus and also for RNA export. Involved in chromatin condensation and control of cell cycle (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
V-type ATP synthase subunit D (EC 3.6.3.14) (V-type ATPase subunit D).
Thermus thermophilus.
                                                                                       GTP-binding nuclear protein RAN/TC4.
Tetrahymena pyriformis.
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
Tetrahymenina; Tetrahymena.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLUIAR LOCATION: Nuclear (By similarity),
SIMILARITY: Belongs to the small GTPase superfamily. Ran family.
                                                                                                                                                                                                                             STRAIN=W, MEDILIBE-94299154; PubMed-8026746; MEDILIBE-94299154; PubMed-8026746; Medita K.-I., Takemasa T., Alam S., Hattori T., Watanabe Y., Nozawa Y.; Takemasa T., Alam S., Hattori T., Watanabe Y., "Cloning of cDNAs encoding a cell-cycle-regulatory GTP-binding low-M(r) (GBLM) protein, Ran/TC4, from micronucleated Tetrahymena thermophila and amicronucleated Tetrahymena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          r protein, Protein transport.
25
GTP (BY SIMILARITY).
70
GTP (BY SIMILARITY).
126
GTP (BY SIMILARITY).
143
18B (BY SIMILARITY).
25422 MW, 5474DADB5ABF0977 CRC64;
                                    (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 41, Last annotation update)
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  223 AA.
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InterPro; IPR002041; RAN.
InterPro; IPR001806; Rag trinsfrung.
InterPro; IPR001806; Rag trinsfrung.
InterPro; IPR005225; Small_GTP.
Pf.M. PR0057; Tash, GTPRANTC4.
PR.NTS; PR00642; GTPRANTC4.
PR.NTS; PR00449; RASTRNSFRWNG.
SWART; SW00176; RAN, 1.
ITGRFAMS; TIGROCA31; small_GTP; 1.
PROSITE; PS01115; RAN, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; D21825; BAA04849.1; -. HSSP; P17080; 1A2K.
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  STANDARD;
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223 AA;
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Best Local Similarity
                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                P41<u>9</u>14;
01-NOV-1995
                                                                           28-FEB-2003
                                                        01-NOV-1995
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  TETPY
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D_VATD_THE
C_0878\( \text{80} \);
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Nozawa Y.;
"Cloning of cDNAs encoding a cell-cycle-regulatory GTP-binding
"Cloning of cDNAs encoding a cell-cycle-regulatory GTP-binding
low-M(r) (GBLM) protein, Ran/TC4, from micronucleated Tetrahymena
thermophila and amicronucleated Tetrahymena pyriformis.";
Gene 144:123-125(1994).
-!- FUNCTION: GTP-binding protein involved in nucleocytoplasmic
transport. Required for the import of protein into the nucleus and
also for RNA export. Involved in chromatin condensation and
control of cell cycle (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FSB-2003 (Rel. 41, Last annotation update)
GTP-binding nuclear protein RAN/TC4.
Tetrahymena thermophila.
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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-!- SUBCELLULAR LOCATION: Nuclear (By similarity)
-!- SIMILARITY: Belongs to the small GTPase superfamily. Ran family.
                                                                                                                  Yokoyama K., Ohkuma S., Taguchi H., Yasunaga T., Wakabayashi T., Yoshida M.;
Yoshida M.;
Yoshida M.;
Yoryoe H.-ATPBase/synthase from a thermophilic eubacterium, Thermus thermophilus. Subunit Erructure and operon.";
J. Biol. Chem. 275:13955-13961(2000).
-!-FUNCTION: Prociduces ATP from ADP in the presence of a proton
                                                                                                                                                                                                                                                                                                                                                                                   gradient across the membrane. 
 -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.0%; Score 19; DB 1; Length 223; 100.0%; Pred. No. 3.9e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: Belongs to the V-ATPase D subunit family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF01813; ATP-synt_D; 1.
Prodom; PD004122; ATPsynt Dsub; 1.
TIGREAMS; TIGR00309; V, ATPase subD; 1.
Hydrolase; ATP synthesis; Hydrogen ion transport.
SEQUENCE: 223 AA; 24677 WW; B666AE00DFE0B08B CRC64;
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SEQUENCE FROM N.A.
STRAIN=HB8 / ATCC 27634;
MEDLINE=20250964; PubMed=10788522;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
01-MOV-1997 (Rel. 35, Last annocation update)
11-MOV-1997 (Rel. 35, Last annocation update)
01-MOV-1997 (Rel. 36, Wha procesin in PP34-EXO intergenic region (ORF 4).
01cgyia pseudotsugata multicapsid polyhedrosis virus (OpMNPV).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis virus genome."; Virology 229:381-399 (1997).
-!- SIMILARITY: TO CORRESPONDING ORF IN ACMMPV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=97271300; PubMed=9126251;
Ahrens C.H., Russell R.R., Funk C.J., Evans J., Harwood S.,
Rohrmann G.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            225 AA; 25649 MW; 69F8B8409AF703F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95.0%; Score 19; DB 1; Lr
100.0%; Pred. No. 3.9e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00176; RAN; I.
TIGREAMS; TIGR00231; small_GTP; I.
PROSITE; PS01115; RAN; I.
GTP-binding; Nuclear protein; Protein transport.
NP_BIND

18
25
GTP (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       228 AA
                                                                                                                                                                                                                                                                                                        INCEMPIC; IPRO02041; RAN.
INTERPIC; IPR001806; Ras trnsfrmug.
INCEMPIC; IPR005225; Small_GTP.
PELM; PF00071; ras; 1.
PRINTS; PR00627; GTPRANTC4.
PRINTS; PR00449; RASTRNSFRMIG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IBB
                                                                                                                                                                                                                                             EMBL; D17748; BAA04600.1; -. HSSP; P17080; 1A2K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 100.
les 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleopolyhedrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=164623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=89294089.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VAEF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VAEF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32 NPVOP
7132 NPVOP
P24080;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ~
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NP BIND
NP BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HAMAP; WF_00244; -; 1.
InterPro; IPR04880; Cytidylyltransf.
Pfam; PF01467; CTP transf_2; 1.
Pyridine nucleotide blosynthesis; Transferase; Nucleotidyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Holmes M.,
                                                                                                                                                                                                                                                                                                                                10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Probable nicotinate-nucleotide adenylyltransferase (EC 2.7.7.18)
(Deamido-NAD(+) pyrophosphorylase) (Deamido-NAD(+) diphosphorylase)
(Nicotinate mononucleotide adenylyltransferase) (NaMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H., Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J., Chris Lee P., Nelson W., White O., Peterson J., Khouri H., Hance I., Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzez A., Utterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H., Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S., Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Frotecbacteria; Gammaprotecbacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                          ö
                                                                                                            DB 1; Leus.
o. 4e+02;
0; Indels
                                                                                                                        Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete genome sequence and comparative analysis of the
                                                                            l protein, Late protein.
228 AA; 25962 MW; F0766AD21F60039D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          230 AA; 25291 MW; 4CF04E8F70E48941 CRC64;
                                                                                                                                                                                                                                                                                                     230 AA.
                                                                                                                      95.0%; Score 19; DB 100.0%; Pred. No. 4e+tive 0; Mismatches
                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=22423060; PubMed=12534463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas putida (strain KT2440)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE016792; AAN70379.1; -.
               D13796; BAA02952.1; -. D13929; BAA03030.1; -. U75930; AAC59129.1; -.
                                                                                                                                                          4; Conservative
                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAD; Complete proteome.
SEQUENCE 230 AA; 252
                                                                                                                                                                                                                                                                                                                                                                                                                                 adenylyltransferase).
NADD OR PP4810.
                                                         PIR; D30857; D30857
Hypothetical protein
SEQUENCE 228 AA;
                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=160488;
                                                                                                                                                                                                                         84 VAEF 87
                                                                                                                                                                                        2 VAEF 5
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                                                                                                                           Query Match
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               EMBL;
                              EMBL:
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230 AA

PRT;

44

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STANDARD;
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QBNT39;
 UBIE_COREF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 74
UBIE CORGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                           01-007-1996 (Rel. 34, Created)
01-007-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Chloroplast 30S ribosomal protein 53.
RPS3.
Porphyra purpurea.
Chloroplast.
Chloroplast.
Eukaryota, Rhodophyta, Bangiophyceae, Bangiales, Bangiaceae, Porphyra.
NCBI_TAXID=2787;
                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                       STRAIN=Avonport;
Reith M.E., Munholland J.;
"Complete nucleotide sequence of the Porphyra purpurea chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                  genome.";
Plant Mol. Biol. Rep. 13:333-335 (1995).
-!- SUBUNT: Part of the 30S ribosomal subunit.
-!- SUBCELLULAR LOCATION: Chloroplast.
-!- SUBCELLULAR belongs to the S3P family of ribosomal proteins.
-!- SIMILARITY: Contains 1 KH type-2 domain.
                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
Query Match 95.0%; Score 19; DB 1; Length 230; Best Local Similarity 100.0%; Pred. No. 4e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95.0%; Score 19; DB 1; Length 230; 100.0%; Pred. No. 4e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (S)
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR, $73229; $73229.

HAMAP; MF 01309; -; 1.

InterPro; IPR000408; KH dom.

InterPro; IPR004049; KH TYPE 2.

InterPro; IPR004044; KH TYPE 2.

InterPro; IPR004045; Ribosomal 83 C.

InterPro; IPR005704; Sact.

Pfam; PF00013; KH; 1.

Pfam; PF00013; KH; 1.

Pfam; PF00013; KH; 1.

Pfam; PF00013; KH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U38804; AAC08194.1; -. PIR; S73229; S73229.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100..
                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 VAEF 121
                                                                                     42 VAEF 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 VAEF 5
                                                           2 VAEF 5
                                                                                                                                                           RR3 PORPU
P51308;
                                                                                                                              ESULT 72
R3_PORPU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- FUNCTION: Methyltransferase required for the conversion of dimethylmenaquinone (DMKH2) to menaquinone (MKH2) (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Comparative complete genome sequence analysis of the amino acid replacements responsible for the thermostability of Corynebacterium efficiens"; Genome Res. 13:1572-1579(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
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10-0cT-2003 (Rel. 42, Last sequence update)
10-0cT-2003 (Rel. 42, Last annotation update)
Menaquinone biosynthesis methyltransferase ubiz (EC 2.1.1.-).
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
MEDLINE=22723752; Pubmed=12840036;
Nishio Y., Nakamura Y., Kawarabayasi Y., Usuda Y., Kimura E.,
Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,
Gojobori T.;
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Menaquinone biosynthesis methyltransferase ubis (BC 2.1.1:-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Corynabacterium glutamicum (Brevibacterium flavum).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynabacterineae; Corynabacteriaceae; Corynabacterium.
                                                                                                                                                                                  Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95.0%; Score 19; DB 1; Length 230; 100.0%; Pred. No. 4e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAMAP; WF _01813; _; 1.
InterPro; IPR001601; Methyltranef.
InterPro; IPR0000501; SAM bind:
InterPro; IPR0004033; UDiE/COG5 Metrf.
Pfam; PF01209; Ubie_methyltran; 1.
PR0SITE; PS01183; UBIE_1; PALSE_NBG.
PROSITE; PS01184; UBIE_2; PALSE_NBG.
Menaquinone biosynthesis; Transferase; Methyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          230 AA; 25366 MW; E10DCB602A1CD886 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   s-adenosyl-L-homocysteine + menaquinol.
-!- PATHWAY: Menaquinone biosynthesis; last step.
-!- SIMILARITY: Belongs to the ubiE family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AP005215; BAC17291.1; ALT_INIT.
                                                                                                                            UBIE OR CE0481. Corynebacterium efficiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 100.
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                                                                                                                                                                                                                                        NCBI_TaxID=152794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete proteome
SEQUENCE 230 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 VARF 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                               "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
-!-FUNCTION: Methyltransferase required for the conversion of
dimethylmenaquinone (DMKH2) to menaquinone (MKH2) (By similarity).
-!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + demethylmenaquinol = s-adenosyl-L-homocysteine + menaquinol.
-!- PATHWAY: Menaquinone blosynthesis; last step.
-!- SIMILARITY: Belongs to the ubiE family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES=E.col1;
MEDLINE=92223101; PubMed=1314093;
Yang T.-P., Depew R.E.;
"Nucleotide sequence of a region duplicated in Escherichia coli toc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN=KI2 / MG1655;
SEDCIRES=8.coli; STRAIN=KI2 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Flunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shigella flexneri.
Bacteria; proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI TaxID=562, 217992, 623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.0%; Score 19; DB 1; Length 230; ilarity 100.0%; Pred. No. 4e+02; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS01183; UBIE 1; FALSE NEG.
PROSITE; PS01184; UBIE 2; FALSE NEG.
Menaquinone biosynthesis; Transferase; Methyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            230 AA; 25244 MW; A8548173B7901400 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein ygiB.
YGIB OR B3037 OR C3783 OR SF3077 OR S3282.
Escherichia coli,
Escherichia coli O6, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mutants.";
Biochim. Biophys. Acta 1130:227-228(1992)
                                                                                                                                                                                                                                                                                                                                                                                             HAMAP; MF_01813; -; 1.
InterPro; IPR001601; SAM bind.
InterPro; IPR004033; UbiE/CQG_Metrf.
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SEQUENCE FROM N.A.
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SEQUENCE S. COll; STRAIN=06:HI / CFT073 / ATCC 700928;
MEDLINE=22388234; PubMed=12471157;
Welch R.A., Burcles B.L., Liou S.-R., Boutin A., Hackett J., Stroud D., Mayhew G.F., Rose D.J., Zhou S.-R., Boutin A., Hackett J., Stroud D., Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mesaic structure revealed by the complete genome sequence of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
MEDLINE=22272406; PubMed=12384590;
Jin Q., Yann Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Jin Q., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Zhao Z., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
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Eccdene; EG11164; yqiB.

Hypothetical protein; Complete proteome.

SEQUENCE 234 AA; 24868 MW; 08D5DE931072C966 CRC64;
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01-CCT-2001 (TrEMBLrel. 18, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin regulatory light chain 2 (MLC-2) (Fragment)
Bombyx mor! (Silk moth).
Bombyx mor! (Silk moth).
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
Bombycidae; Bombyx.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=93224468; PubMed=8385668; MEDLINE=93224468; PubMed=8385668; MCTavish H., LaQuier F., Arciero D., Logan M., Mundfrom G., McTavish H., LaQuier F., Arciero D., Logan M., Mundfrom G., Fuchs J.A., Hooper A.B.; Fuchs J.A., Hooper A.B.; Fuchs J. Logan Society of genes coding for electron transport proteins in the bacterium Nitrosomonas europaea."; J. Bacterium Nitrosomonas europaea."; J. Bacteriul. 175:2445-2447(1993).
SEQUENCE 22 AA; 2549 MW; C22664F5EBICE75F CRC64;
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MEDIANE=21177481; PubMed=11280994;
Zhong B.X.;
"Protein database for several tissues derived from five instar of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cytochrome P-460 (Fragment).
Nitrosomonas europaea.
Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
Nitrosomonadaceae; Nitrosomonas.
NCBI TaXID=915;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95.0%; Score 19; DB 2; Length 22; 100.0%; Pred. No. 3.4e+02; tive 0; Mismatches 0; Indels
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Pred. No. 4.7e+02;
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Last annotation update)
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100.0%;
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01-MAY-2000 (TrENBLrel. 13, C
01-MAY-2000 (TrENBLrel. 13, L
01-UNA-2000 (TrENBLrel. 14, L
Cytochrome P-460 (Fragment).
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    2 VAEF 5
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SEQUENCE
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197827 rattus norv

197222 cricetulus
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28n6a0 homo sapien
27wx56 alcaligenes
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 25, Last annotation update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Cytotoxin-binding protein (Fragment).
Cytotoxin-binding protein (Fragment).
Braryota; Merazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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MEDLINE=94039134; PubMed=7693466;
Lutz F., Mohr M., Grimmig M., Leidolf R., Linder D.;
Lutz F., Mohr M., Grimmig M., Leidolf R., Linder D.;
"Pseudomonas aeruginosa cytotoxin-binding protein in rabbit
erythrocyte membranes. An oligomer of 28 kDa with similarity to
transmembrane channel proteins.";
Eur. J. Biochem. 217:1123-1128 (1993).
PIR; $39049; $39049.
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95.0%; Score 19; DB 6; Length 20;

Best Local Similarity 100.0%; Pred. No. 3.18+02;

Matches 4; Conservative 0; Mismatches 0; Indels
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0005215; F:transporter activity; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR000425; MIP.
Pfam; PF00230; MIP; 1.
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O30168
Q9XSF7
Q83UD0
Q7WZ93
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Q8ECB9
Q8ECB9
Q8FEC9
Q87771
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Q95779
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Q9CAH5
Q854X2
Q8LAG7
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Q9TQR7;
Q1-MAY-2000 (TEMBLrel.
01-MAY-2000 (TEMBLrel.
01-CTT-2003 (TEMBLrel.
Transferrin (Fragment).
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Best Local Similarity
Matches 4; Conserv
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                          18 VAEF
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Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G., Fleischmann R.D., Ketchum K.A., Klenk H.-F., Gill S., Dougherty B.A., Nelson K., Quackenbush J., Zhou L., Kirkness B.F., Peterson S., Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A., McKenney K., Flizderald L.M., Lee N., Adams M.D., Hickey B.K., Cergon D.E., Goczyne J.D., Utterback T.R., Peterson J.D., Kelley J.M., Cotton M.D., Waldman J.M., Fujii C., Bowman C., Matthey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
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Gaps
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Bacteria, Proteobacteria, Epsilonproteobacteria, Campylobacterales,
Helicobacteraceae, Helicobacter.
MCBI_TaxID=210;
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Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The complete genome sequence of the gastric pathogen Helicobacter
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STRAIN=IN2 / ATCC 51768 / DSW 7523;
MEDLINE21664397; PubMed=11792869;
Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
Miller J.H.;
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    Indels
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Archaea; Crenarchaeota; Thermoprotei; Thermoproteacea;
Thermoproteaceae; Pyrobaculum.
NCBI_TaxID=13773;
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Nature 388:539-547(1997).
BERL: AD007950.1; --
PIR; G64625; G64625.
TIGR: HP0847: pretein; Complete proteome.
SEQUENCE 33 AA; 3704 MW; FA3F52631C0DB943 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                          025518;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein HP0847.
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(TrEMBLrel. 20, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
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Mismatches
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4; Conservative
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Best Local Similarity
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                                                                                                                                                13 VAEF 16
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                                                                        2 VAEF 5
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01-JUN-2003 (
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01-NOV-1996 (TERMELRE). 01, Created)
01-NOV-1996 (TERMELRE). 01, Last sequence update)
01-NOV-1996 (TERMELRE). 25, Last annotation update)
Hypothetical protein (Fragment).
Hybothetical protein (Fragment).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Klebsiella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Perissodactyla, Equidae, Equus.
NCBI_TaxID=9796;
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5.4e+02;
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EMBL; AE009770; AAL62822.1; -.. Hypothetical protein; Complete proteome. SEQUENCE 35 AA; 3934 MW; A324B4F94F6A14BB CRC64;
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(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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Pred. No. 5.6e+02;
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GO; GO:0006879; F:ferric iron bindestasis; IEA.
GO; GO:0006826; F:fron ion transport; IEA.
Pfen:Pro; IPR001156; Transferrin.
Pfam; PF00405; transferrin; 1.
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                                                                                                    05.0%; Score 19; DB Similarity 100.0%; Pred. No. 5.4 4; Conservative 0; Mismatches
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100.0%; Pred
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SEQUENCE FROM N.A.
STRAIN=26657 / AICC 700392;
STRAIN=26657 / AICC 700392;
TOMD J.-F.; White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Tomb J.-F.; White O., Kerlavage A.R., Klenk H.-P., Gill S., Dougherty B.A.,
Releachmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
Nelson K., Quackenbush J., Zhou L., Klikness E.F., Peterson S.,
Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey B.K.,
Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
Cotton M.D., Weldman J.M., Fujil C., Bowman C., Watthey L., Wallin E.,
Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                            Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
NCBI_TaxID=210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22735913; PubMed=12835416; Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T., Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T., Schlesner F., Beck A., Borzym K., Heitmann K., Rabus R., Schlesner H., Amann R., Reinhardt R., "Complete genome sequence of the marine planctomycete Pirellula strain 1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria, Planctomycetes, Planctomycetacia, Planctomycetales,
Planctomycetaceae, Pirellula.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95.0%; Score 19; DB 16; Length 48; 100.0%; Pred. No. 7.38+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein; Complete protecme.
SEQUENCE 48 AA; 5492 MW; ED5911D96F57BFEB CRC64;
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60F62389C0FDA6A7 CRC64;
                                                  01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein HP0789.
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Last annotation update)
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EMBL; BX294135; CAD71991.1; -.
Hypotherical process. Compiler proteome.
SEQUENCE S1 AA; 5951 MW; 60F62389C0FDA6A7 CRC6
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(TrEMBLrel. 25, Last seq.
(TrEMBLrel. 25, Last anno
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EMBL, AAE000591, AAD07847.1; -.
PIR, EG4618, E64618.
TIGR, HP0789; -
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nes 4; Conservative
                                    PRELIMINARY;
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01-OCT-2003 (TrEMBLre
Hypothetical protein.
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                                  025478
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Q7UXLS;
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RESULT 9
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SETAILWEYSB3, ATCC 700802;
MEDLINE=2250857; PubMed=12663927;
Paulsen I.T., Banerjei L., Myers G.S.A., Nelson K.E., Seshadri R.,
Paulsen I.T., Fourts D.E., Eisen J.A., Gilli S.R., Heidelberg J.F.,
Tettelin H., Dodson R.J., Umayam L., Brinkac L., Beanan M.,
Daugherty S., DeBoy R.T., Durkin S., Kolonay J., Madupu R., Nelson W.,
Vamathevan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H.,
Utterback T., Radune D., Kectoum K.A., Dougherty B.A., Fraser C.M.;
"Role of mobile DNA in the evolution of vancomycin-resistant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q830H9;
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein.
ER2805.
Enterococcus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
NCBI_TAXID=1351;
              "Investigation of the Klebsiella pneumoniae 1,3-propanediol pathway: Characterization and expression of glycerol dehydratase and 1,3-propanediol oxidoreductase.";
propanediol oxidoreductase.";
Thesis (1994), Chemical Engineering, University of Wisconsin-Madison.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      44 AA; 4537 MW; 39851658FF88E734 CRC64;
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SEQUENCE 45 AA; 5278 MW; 89CB55F5CB4C014A CRC64;
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100.0%; Pred. No. co.
... 0; Mismatches
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ses 4; Conserv
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Best Local Similarity
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DB 16; Length 51;

Score 19;

95.08;

Query Match

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Hypothetical protein.
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Plasmid pCP301.
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MEDLINE=2107:H7 / EDD933 / ATCC 700927;
MEDLINE=2107:H35; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Grocheck E.J., Davins N.W., Lim A., Dimalanta B.T., Potanousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blatner F.R.,
"Genome sequence of enterohaemorrhagic Bscherichia coli 0157:H7.";
Nature 409:529-531 (2001).
RMB1; AE005369; AAG56425.1; -.
PIR; E85745; E85745.
Hypothetical protein; Complete proteome.
SEQUENCE 54 AA, 6507 MW, BBEFACD6BE6140CE CRC64;
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"Cloning, characterization, and inactivation of the Bacillus brevis
"Cloning, characterization, and inactivation of the Bacillus brevis
J. Bacteriol. 174:2281-2287 (1982).
J. Bacteriol. 174:2281-2287 (1982).
PIRI, A42375; A42375, PIRI, A42375; A42375; A5558 MW; 5D689099F84F9AAF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus brevis (Brevibacillus brevis).
Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Brevibacillus.
NCBI_TaxID=1393;
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Becherichia coli 0157:H7.
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
NCBI_TaxID=83334;
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                                                     Indels
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                       Pred. No. 7.8e+02;
Mismatches 0;
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100.08;
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Q44941;
01-NOV-1996 (TrEMBLrel. 01, C.
01-NOV-1996 (TrEMBLrel. 01, L.
01-JUN-2003 (TrEMBLrel. 24, L.
Short ORP.
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                    Best Local Similarity 100.
Matches 4; Conservative
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                                                                                                                                                             31 VAEF 34
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X3Y8
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Gaps
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STRAIN=301,
Jin O., Zhang J.Y., Liu H., Yang J., Yang F., Zhang X.B., Wang J.H.,
Jin O., Zhang J.Y., Liu H., Young J., Yang F., Zhao A.L., Gao Y.S.,
Yang G.W., Wu H.T., Dong J., Sun L.L., Xue Y., Zhao A.L., Gao Y.S.,
Yang G.W., Wan B., Chen S.X., Yao Z.J., He B.K., Chen R.S., Ma D.L.,
Yuan Z.H., Xu J.G., Wang Y., Shen Y., Lu W.C., Qiang B.Q., Wen Y.M.,
Hou Y.D.;
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                                                                                                                                                                                                                Escherichia coli 06.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=217992;
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Enterobacteriaceae; Shigella.
NCBI_TaxID=42897;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein, Complete proteome.
SEQUENCE 54 AA; 5322 MW; 6B3C3D0F21ED4376 CRC64;
                                                            01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hyporhetical protein.
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002);
EMBL; AE016759; AAN79938.1; -.
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   54 AA
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PRT;
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PRELIMINARY;
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SEQUENCE FROM N.A.
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Matches
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                                      Gaps
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IISSUE=Liver;
Zhang C., Yu Y., Zhang S., Wei H., Zhang Y., Zhou G., Bi J., Liu M.,
                                                                                                                                                                               Q9P166 PRELIMINARY, PRT; 61 AA.
Q9P166;
Q1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
PRO2435.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES-Heliocoverpa armigera nucleopolyhedrovirus G4;
Deng F., Chen X., Vlak J.M., Arif B.M., Hu Z.;
"Sequence analysis of the gp3? gene of Heliothis armigera single-
nucleocapsid nucleoplyhedrovirus.";
Zhongguo Bingduxue 15:35-42(2000).
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01-JUN-2001 (TrEMBLrel: 17, Created)
01-JUN-2001 (TrEMBLrel: 17, Last sequence update)
01-JUN-2003 (TrEMBLrel: 25, Last annotation update)
01-OCT-2003 (TrEMBLrel: 25, Last annotation update)
0R-90 (Hypochetical protein) (Unkown).
Helicoverpa area single nucleocapsid nucleopolyhedrovirus,
Helicoverpa armigera nucleocopylyhedrovirus 64, and
Helicoverpa armigera nuclear polyhedrovirus 64, and
Helicoverpa armigera nuclear polyhedrosis virus.
Viruses; dabNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.
Nucleopolyhedrovirus.
Nucleopolyhedrovirus.
 95.0%; Score 19; DB 2; Length 61; 100.0%; Pred. No. 9.3e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95.0%; Score 19; DB 4; Length 61; 100.0%; Pred. No. 9.3e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      by analysis of cDNA clones from human fetal liver."; submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF119881; AAF69635.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleopolyhedrovirus.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
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SPECIES-Heliocoverpa armigera nucleopolyhedrovirus G4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 AA; 7467 MW; 6433950D4657C1D4 CRC64;
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Query Match
Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity 100.
Matches 4; Conservative
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Fang M., Hu Z., Chen X., Vlak J.M.;
"Genetic organization of the HindIII-L region of Helicoverpa armigera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Wang H., Hu Z., Sun X., Vlak J.M., Chen X.;
"Sequence analysis of the lap3 gene of Heliothis armigera single-
nucleocapsid nucleopolyhedrovirus.";
Zhongguo Bingduxue 15:43-49(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPECIES=Heliocoverpa armigera nucleopolyhedrovirus G4;
MEDLINE=21064569; PubMed=1122177;
Chen X., IJKel W.F., Tarchini R., Sandbrink H., Wang H.,
Peters S., Zuidema D., Lankhorst R.K., Vlak J.M., Hu Z.;
"The sequence of the Helicoverpa armigera single-nucleocapsid
nucleopolyhedrovirus genome.";
J. Gen. Virol. 82:241-257(2001).
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Sheng Wu Hua Heueh Yu Sheng Wu Li Hsueh Pao 33:179-184(2001)
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                                                                                                                                                                                                          SPECIES=Heliocoverpa armigera nucleopolyhedrovirus G4, MEDLINE=21078302; PubMed=11210934; Mang H., Chen X., Wang H., Arif B.M., Vlak J.M., Hu Z.; "Nucleotide sequence and transcriptional analysis of a putati: DNA-binding protein of Helicoverpa armigera polyhedrovirus."; Virus Genes 22:113-120(2001).
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Chen X., IJKel W.F., Tarchini R., Sun X., Sandbrink H., Wang '
Peters S., Zuidema D., Lankhorst R. K., Vlak J. M., Hu Z.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
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Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF334030; AALS6194.1; -.
EMBL; AF271059; AAGS3791.1; -.
EMBL; AF303045; AAKG6298.1; -.
EMBL; AF303045; AAKG4316.1; -.
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Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases
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68 AA; 7962 MW; 61B7718BFBB195FF CRC64;
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01-UIN-2003 (TrEMELrel. 24, Created)
01-UIN-2003 (TrEMELrel. 24, Last sequence update)
01-UIN-2003 (TrEMELrel. 24, Last annotation update)
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Helix-turn-helix protein, CopG family
NE0289.
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ATTAINESTEROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SET STRAINESTEL1, Str-2, Str-3, Str-4, Str-9, Str-10, and Str-11;

MEDLINE=21359292; PubMed=12140239;
Antumes A., Templeton A.R., Guyomard R., Alexandrino P.;

Antumes A., Templeton A.R., Guyomard R., Alexandrino P.;

Antumes A., Templeton A.R., Guyomard R., Alexandrino P.;

The role of nuclear genes in intraspecific evolutionary inference:

STR STREAM 
                                                                                                                                                                                                                                                                                                       "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032."; Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases. BMBL; AP005280; paBB9300.1; -- BMBL; PR005280 bass 2000.1; -- BYDCthetical protein; Complete proteome. SEQUENCE 69 AA; 7815 WW; COEZA072C2295DD2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OTT-2003 (TrEMBLrel. 25, Last annotation update)
Transferrin (Fragment).
Salmo trutta (Brown trout).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                             Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95.0%; Score 19; DB 13; Length 71; 100.0%; Pred. No. 1.1e+03; Live 0; Mismatches 0; Indels
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Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
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                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
Nakagawa S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 AA
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PRINTS; PR00422; TRANSFERRIN.
NON TER 1 71 71
SEQUENCE 71 AA; 7546 MW; 8
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Best Local Similarity 100.00
Best Local 4; Conservative
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QBAUQ2;
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Q8AUQ2
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Liu Y.L., Mu J., Yu Z., Chen L., Fan D.L., Weng Q.J., Zhang L.,
Liu Y.Q., Yu S.L., Liu X.H., Lu T.T., Zhang Y.J., Lu Y.J. Li C., Li T.,
Zhang Y., Hu H., Jia P.X., Qian Y.M., Ying K., Zhou B., Chen Z.H.,
Rao P., Zhang L., Wu M., Zhang R.Q., Guan J.P., Fu G., Wang S.Y.,
Ren S.X., Lv G., Lin W., Gu W.Q., Zhu G.F., Tu Y.F., Jia J., Yin H.P.,
Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y., Shao C.Y., Sun Y.,
Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W., Sheng H.H.,
Gu J.L., Chen S.T., Ni L., Zhu F.H., Hong G.F.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AL731509; CABG5527.1;
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                                                                                                                             SECUENCE FROM N.A.

STRAINA-RACC 19718 / IFO 14228;

STRAINA-RACC 19718 | Dubbed=12700225;

Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M.,

Alauser L., Hooper A.B., Kilotz M.G., Norton J., Sayavedra-Soto L.A.,

Arciero D.M., Hommes N.G., Whitraker M.M., Arp D.J.;

"Complete genome sequence of the ammonia-oxidizing bacterium and

J. Bacteriol. 188:2752-2773 (2003).

EMBL; BX321857; CAD84200.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
05-OCT-2003 (TrEMBLrel. 25, Last annotation update)
05-JNBA0044M19.22 procein (OSJNBA0053B21.1 protein).
05-JNBA0044M19.22 OR OSJNBA0053B21.1.
05-JNBA0044M19.22 POSJNBA0053B21.1.
05-JNBA0044M19.1.
05-JNBA0044M19.1.
05-JNBA0044M
Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
Nitrosomonadaceae; Nitrosomonas.
NCBI_TaxID=915;
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1-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein Cgl1907.
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Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity 100
Matches 4; Conservative
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2 VAEF 5
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Q82MX0
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Q97JU4
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MEDLINE=97251358; PubMed=9097040;
MEDLINE=97251358; PubMed=9097040;
Kasai H., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T.,
Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y.,
Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y.,
Sivasundaram S., Tagami H., Takeda J., Takemoto K., Wada C.,
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Enterobacteriaceae; Escherichia.
NCBI_TaxID=562;
                                                                                                                                                                                                                                  01-MAR.2003 (TrEMBLrel. 23, Created)
01-MAR.2003 (TrEMBLrel. 23, Last sequence update)
01-MAR.2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Transferrin (Fragment).
Salmo salar (Atlantic salmon).
Salmo salar (Atlantic salmon).
Actinoptery Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Actinoptery Metazoa, Chordata, Teleostei, Bueleostei, Protacanthopterygii, Salmoniformes; Salmonidae; Salmo.
NCBI_TAXID=8030;
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE STAIN-Ssa-1, and Ssa-2;

A MEDINE-213592; PubMed=12140239;
Antunes A., Templeton A.R., Guyomard R., Alexandrino P.;

"The role of nuclear genes in intraspecific evolutionary infegenealogy of the transferrin gene in the brown trout.";

Mol. Biol. Evol. 19:127-1287 (2002).

R EMBL; AF48883; AAN17017.1; -.

R EMBL; AF488841; AAN17017.1; -.

R EMBL; AF488842; AAN1702.1; JOINED.

R GO; GO:0005576; C:extracellular; IEA.

GO; GO:0006879; F:ferric iron binding; IEA.

GO; GO:0006879; P:iron ion transport; IEA.

R GO; GO:0006879; P:iron ion transport; IEA.

R GO; GO:0006879; P:iron ion transport; IEA.

R DF4m; PF00405; transferrin; 1.

R PF4m; PF00405; TRANSFERRIN.

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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
Late control gene D protein (Fragment).
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Matches 4; Conservative
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SEQUENCE FROM N.A.
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STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE=21359325; PubMed=11466286;
Moelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
Tatusto N.L., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
"Genome sequence and comparative analysis of the solvent-producing
bacterium Clostridium acetobutylicum.";
J. Bacteriol. 183:4823-4838(2001).
EMBL, AB007632, AAK79151.1;
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Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
NCBI_TaxID=1488;
Yamamoto Y., Horiuchi T.;

"A 460-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 40.1-50.0 min region on the linkage map.";
DNA Res. 3:379-392 (1996).

EMBL; D90847; BAA1549.1; -.

EMBL; D90846; BAA15938.1; -.

SROŪTER 1 1 SEQUENCE 72 AA; 8099 MW; 42A63B25B00EADCB CRC64;
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Bacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
'NOB_TaxID=33903;
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STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=21477403; PubMed=11572948;
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Hypothetical protein; Complete proteome.
SEQUENCE 74 AA; 8747 MW; 633633CB0A0C293A CRC64;
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Q97JU4;
Q1-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein CAC1179.
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Last annotation update)
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01-JUN-2003 (TrEMBLrel. 24,
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Best Local Similarity 100.
Matches 4; Conservative
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Virology 263:254-262(1999)
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Best Local Similarity luv..
...a 4; Conservative
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Submitted (DEC-1995)
                       Hypothetical protein
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                                                                                                                       NCBI_TaxID=1590;
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EMBL: AB099952; BACS6442.1; --
IINTEPPO: IRPROJS11: DNAbind_HORMA.
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                                                                                                                                                                                                                                                             "Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis.";
Nat. Biotechnol. 21:826-531(2003).
EMBL; AP005027; BAC692431.1;
Hypothetical protein; Complete protecome.
SEQUENCE 74 AA; 7960 MW; DBCE71C8B08AEB01 CRC64;
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Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C., Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T., Kikuchi H., Shiba T., Sakaki Y., Hattori M.; "Genome sequence of an industrial microorganism Streptomyces avermitiils: deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                                                                                                    95.0%; Score 19; DB 16; Length 74; 100.0%; Pred. No. 1.1e+03; ative 0; Mismatches 0; Indels
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                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=NA-4680 / ATCC 31267 / NCIMB 12804 / NRL 8165;
MEDLINE=22608306; PubMed=12692562;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OTT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to MAD2 protein (Fragment)
Bos taurus (Bovine)
                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001)
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01-JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 24,
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Best Local Similarity 100.
Matches 4; Conservative
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SULT 25

Q88VS7 SULT 26 18VS7

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Kilegrebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,
Riegrebezem M., Ider R., Tarchini R., Peters S., Sandbrink H.M.,
Riapers O.P., Leer R., Tarchini R., Peters S., S., Sandbrink H.M.,
Riegres M.W.E.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,
Boffer S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing B.,
De Vos W.M., Siezen R.J.,
Bromere genome sequence of Lactobacillus plantarum WGFS1.";
Proc. Natl. Acad. SG1. U.S.A. 100:1990-1995(2003).
BMB., AL935257, CAD64344.1.;
BMB., AUGOSEST, CADGAGA44.1.;
SEQUENCE 77 AA, 8618 MM, COUEZBFFID401F2F CRG64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDINE-20478054; PubMed=11021991;
Sun L., Gurnon J.R., Adams B.J., Graves M.V., Van Etten J.L.;
"Characterization of a beta-1,3-glucanase encoded by chlorella virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NEDLINE=20013326; PubMed=10544099; Kaiser A., Vollmert M., Tholl D., Graves M.V., Gurnon J.R., Xing W., Lisec A.D., Nickerson K.W., Van Etten J.L.; "Chlorella virus PBCV-1 encodes a functional homospermidine synthase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=96400190; PubMed=8806566;
Kutish G.F., Li Y., Lu Z., Furuta M., Rock D.L., Van Etten J.L.;
Kanalysis of 76 kb of the chlorella virus PBCV-1 330-kb genome: map positions 182 to 258.",
Virology 223:303-317(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Paramecium bursaria chlorella virus 1 (PBCV-1).
Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Chlorovirus.
VCBI_TaxID=10506;
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0
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                                                        Larchoscillus plantarum.
Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
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Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
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01-FBB-1997 (TrEMBLrel. 02, Created)
01-FBB-1997 (TrEMBLrel. 02, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
A532L protein.
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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100.0%; Pred. No. 1.2e+03;
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STRAIN=NCIMB 8826 / WCFS1;
MEDLINE=22480296; PubMed=12566566;
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43 VAEF 46
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SEQUENCE FROM N.A.
Winans S.C., Zhu J., Oger P.M., Schrammeijer B., Hooykaas P.J.,
Farrand S.K.;
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Plasmid Ti.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiamacaes, Rhizobium/Agrobacterium group; Agrobacterium.
                                                                                                                                                                                                                                                                       95.0%; Score 19; DB 12; Length 79; 100.0%; Pred. No. 1.2e+03; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Octopine-type Ti plasmid sequence.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF242881; AAF77180.1; -.
GQ; GO:0046821; C:extrachromosomal DNA; IEA.
Plasmid.
SEQUENCE 80 AA; 8723 MW: 4F8470cm10077700
                                                                   SEQUENCE FROM N.A.
Graves M.V., Van Etten J.L.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                      Graves M.V., Van Etten J.L.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
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Gurnon J.R., Graves M.V., Van Etten J.L.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, 142580; AA956899.1; -.
PIR; 118034; T18034.
SEQUENCE 79 AA, 8698 MW; B191C627F5D5C5A7 CRC64;
                              Van Etten J.L.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
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01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
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Best Local Similarity
Matches 4; Conserv
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SEQUENCE FROM N.A.
                                                                                                                            SEQUENCE FROM N.A.
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Q9KI36;
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89WL6
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9KI36
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"Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).

EMBL, AP001514; BAB05901.1; -...

PIR; F83922; F83922.

PIR; F83922; F83922.

SEQUENCE 84 AA; 9669 WW; GCDE3768ED9F5D84 CRC64;
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                                                                                                                                                             MEDLINE=22484998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Matanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
Tabata S.;
                                                                                                                                                                                                                                                                                   "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";
DNA Res. 9:189-197(2002).
EMBL; APO05937; BAC45927.1; -.
Complete proteome.
SEQUENCE 81 AA; 9235 MW; D512A9FFED0DA6C7 CRC64;
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STRAIN=C-125 / JCM 9153;
MEDLINE=20512582; PubMed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamira Y., Ogasawara N., Kuhara S.,
Horikoshi K.;
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
NCBI_TaxID=375;
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=86665;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UT-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein BH2182.
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0821D2

1D 0821D2

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DE HYPOTI

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Tu G.F., Achen M.G., Aldred A.R., Southwell B.R., Schreiber G.;
"The distribution of cerebral expression of the transferrin gene is species specific.";
J. Biol. Chem. 266:6201-6208(1991).
-!- FUNCTION: TRANSFEREINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE.
                                                                                                                                Stephenson S. -A., Maclean D.J., Manners J.M.;

Stephenson S. -A., Maclean D.J., Manners J.M.;

"Disruption of a novel pathogenicity gene of Colletotrichum gloeosporioides results in a hypersensitive response in the host Stylosanthes guianensis."

Stylosanthes guianensis."

Stylosanthes guianensis."

Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.

RMBL; U94183; AB95222.1; -.

CG, GO:0003677; F:DNA binding; IEA.

RMBL; SNAGS77; F:DNA binding; IEA.

R Pfan; PF01381; HTH 3. 1.

R Pfan; PF01381; HTH 3. 1.

R Pypothetical protein.

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SEQÜENCE 85 AA; 9316 MW; BFB9A0E5F44E9CF2 CRC64;
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
             Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;
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Similarity 100.0%; Pred. No. 1.3e+03;
4; Conservative 0; Mismatches 0; Indels
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Last annotation update)
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GO; GO:0005576; C:extracellular; IEA.
GO; GO:0008199; P:ferric iron binding; IEA.
GO; GO:0006819; P:iron ion homeostasis; IEA.
GO; GO:0006826; P:iron ion transport; IEA.
InterPro; IPR001156; Transferrin.
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PROSITE; PS00205; TRANSFERIN_1; 1.
Iron transport; Metal-binding.
NON_TER 1 1 1
NON_TER 7 4 45
SEQUENCE 87 AA; 9433 MW; AA464B2A
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MEDLINE=91177867; PubMed=1848850;
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                                                  NCBI_TaxID=5457;
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Geng M.M., Schuhmacher A., Muchldorfer I., Bensch K.W., Schaefer K.P.,
Geng M.M., Schuhmacher A., Muchldorfer I., Melchers K.,
Schneider S., Pohl T., Essig A., Marre R., Melchers K.,
The genome sequence of Chlamydia pneumoniae TW183 and comparison with
other Chlamydia strains based on whole genome sequence analysis.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
BMBL, AE017159; AAP98704.1; -.
BYDOCHELICAL protein.
SEQUENCE 84 AA; 9260 MW; 7786DF8DD7B3AB8 CRC64;
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                                                                                                                                                                                                                                             "Genome sequence of Chlamydophila caviae (Chlamydia paittaci GPIC): examining the role of niche-specific genes in the evolution of the Chlamydiaceae.";
Nucleic Acids Res. 31:2134-2147(2003).
EMBL; ARO16997; AAP05749.1;
TIGR; CCA01010;
                                                                                                  STRAIN=GPIC;
MEDILINE-S2569155; PubMed=12682364;
MEDILINE-S25569155; PubMed=12682364;
Read T.D., Myers G.S.A., Brunham R.C., Nelson W.C., Paulsen I.T.,
Heidelberg J., Holtzapple E., Khouri H., Federova N.B., Carty H.A.
Umayam L.A., Haft D.H., Peterson J., Beanan M.J., White O.,
Salzberg S.L., Hsia R.-C., McClarty G., Rank R.G., Bavoil P.M.,
Fraser C.M.;
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CPBJ0775.
Chlamydia pneumoniae (Chlamydophila pneumoniae).
Racteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
NCBI_TaxID=83557;
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01-UIN-1998 (TrEMBLrel. 06, Created)
01-UIN-1998 (TrEMBLrel. 06, Last sequence update)
01-UCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment).
Colletotrichum gloeosporioides (Anthracnose fungus) (Glomerella
cingulata).
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
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Similarity 100.0%; Pred. No. 1.3e+03;
4; Conservative 0; Mismatches 0; Indels
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SEQUENCE 84 AA; 9191 MW; 7DF6009729C7093A CRC64;
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Last sequence update)
Last annotation update)
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Plasmid pMT-1.
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Q9ZGY2;
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Q9ZGY2
RESULT 37
Q41185
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                                                                                                     01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypotherical protein.
Bacteriophage PY54.
Viruses, dabba viruses, no RNA stage; Caudovirales; Siphoviridae.
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Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
Nitrosomonadaceae; Nitrosomonas.
NCBI_TaxID=915;
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                                                                                                                                                                                                                                                                                          Hertwig S.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AJS64013; CAD91786.1; --
EXXONUCLEASE; Hypothetical protein.
SEQUENCE 87 AA; 8538 MW; D17D7A7E3075459B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9S590;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UJN-2001 (TrEMBLrel. 17, Last annotation update)
Cytochrome P460 (Fragment).
                                                                                           87 AA
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Best Local Similarity 100.
Matches 4; Conservative
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                                    13 VAEF 16
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MEDLINE=91013065; PubMed=1398114;
MEDLINE=91013065; PubMed=1398114;
Shih M.C., Heinrich P., Goodman H.M.;
Shih M.C., Heinrich P., Goodman H.M.;
"Cloning and chromosomal mapping of nuclear genes encoding chloroplast and cytosolic glyceraldehyde-3-phosphate-dehydrogenase from Arabidopsis thaliana."
Gene 119:317-319 (1992).
EMBL, 845911; AAB23533.1; -.
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MEDLINE=99043988; PubMed=9826348;
Lindler L.E., Plano G.V., Burland V., Mayhew G.F., Blattner F.R.;
Lindler L.E., Plano G.V., Burland V., Mayhew G.F., Blattner F.R.;
Complete DNA sequence and detailed analysis of the Yersinia pestis
XIMS plasmid encoding murine toxin and capsular antigen.";
Infect. Immun. 66:5731-5742(1998).
BMBL, AROYAGLI, AAC82761.1; -.
PREMI, AROYAGLI, AAC82761.1; -.
PREMI, TISO18; TISO18.
GO, GO:0046821; C:extrachromosomal DNA; IEA.

InterPro; IPRO3006; IG MHC.
Hypothetical protein; Plasmid.
SEQUENCE 89 AA; 10736 MW; 72B4221126023EE4 CRC64;
                                                                                                                                                                                                                                             Chloroplast.

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Magnollophyta; eudicotyledons; core eudicots; rosids;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                             Q41185;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UDN-2003 (TrEMBLrel. 24, Last annotation update)
Glyceraldehyde-3-phosphate-dehydrogenase subunit GapB (Fragment).
GAPB.
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Enerobacteriaceae; Yersinia.
NCBI_TaxID=632;
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Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                            Arabidopsis thaliana (Mouse-ear cress)
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PRT;
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Matches 4; Conservative
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   PRELIMINARY;
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Query Match
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QBIZX3;
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Q81ZX3
ID Q81ZX:
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"The complete genome sequence of the lactic acid bacterium Lactococcus lactis sep. lactis IL1403.";
[Genome Res. 11:731-753(201).
EMBL; AE006385; AAK05648.1; -.
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Ypde OR L11550.
Lactococcus lactis (subsp. lactis) (Streptococcus lactis).

Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
NCBI_TAXID=1360;
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May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
"Complete genomic sequence of Pasteurella mulcocida Pm70.";
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
HSSP; P80378; 1AB3
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Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Pasteurella.
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GO; GO: 0005840; C: riboscome; IEA.
GO; GO: 0003735; F: structural constituent of riboscome; IEA.
GO; GO: 0006412; F: structural constituent of riboscome; IEA.
InterPro; IPR005699; Riboscomal_S15.
InterPro; IPR005290; Riboscomal_S15.
Pfan; PF00312; Riboscomal_S15; I.
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Hypothetical protein; Complete proteome.
SEQUENCE 89 AA; 10403 MW; D90DF3CF71D12D06 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89 AA; 10184 MW; F796E0AB5283ED0E CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
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Probom, PD157043; RS15 bact; 1.
TIGREAMS; TIGREAMS; TIGREAMS; TIGREAMS; 1 PS00362; RIBOSOMAL_S15; 1.
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MEDLINE=21235186; PubMed=11337471;
                                                                                                                                                                          PRT;
                                                                                                                                                                                                      Q9CNX1;
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-OCT-2003 (TREMBLREL. 25,
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3 VAEF 6
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RPS15 OR PM0301.
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Best Local
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Al-Mahrouki A.A., Irwin D.M., Youson J.H.;

Molecular cloning of preproinsulin cDNA from the rock bass.";

Molecular cloning of preproinsulin cDNA databases.

L. Submitted (OCT-1999) to the EMBL/GORBANK/DDBJ databases.

-: SINDILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.

R. MEBL, AF19584, AAX28708.1; -.

R. HSSP; PO1308; ILPH.

R. GO; GO:0005179; Fibramone activity; IEA.

R. GO; GO:0005179; Fibramone activity; IEA.

R. GO; GO:0005179; Fibramone activity; IEA.

R. MINTERPO; IPRO04825; Ins/IGF/relax.

R. PERNYS; PRO049; Insulin; 1.

R. PRINYS; PRO049; INSULINB.

R. SWART; SMO0078; ILGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
VCBI_TaxID=9606;
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   Length 89;
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Yin F., Fan D.M.;
"Identifying a new variant of MAD2L1.";
Submitted (JUN-2011) to the EMBL/GenBank/DDBJ databases.
EMBL, AF394735; AAN74648.1; -.
InterPro; IPR003511; DNAbind_HORMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF02301; HORMA; 1.
PROSITE; PS50815; HORMA; 1.
SEQUENCE 90 AA; 10335 MW; 8209F5A7A7D8D09B CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Preproinsulin (Fragment)
Ambloplites rupestris (Rock bass).
                                                                                                                                                                                                                                                                                                                                                                                                       01-WAR.2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last amnotation update)
MADD mitotic arrest deficient-like 1 variant.
95.0%; Score 19; DB 16; 100.0%; Pred. No. 1.3e+03; iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                 90 AA.
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      Query Match
Best Local Similarity 100.
Matches 4; Conservative
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Q8U8Q1;
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Q89WX7
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Cevallos M.A., Izquierdo J., Porta H., Tun C., Davila G., Brom S.;

Cevallos M.A., Izquierdo J., Porta H., Tun C., Davila G., Brom S.;

Rhizobium etli CE3 contains at least three plasmids of the RepABC family. A structural and an evolutionary analysis.";

Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AR313446; AAM88940.1; -.

EMBL; AR313446; C:extrachromosomal DNA; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-070-1998 (TrEMBLrel. 06, Created)
01-070-1998 (TrEMBLrel. 06, Last sequence update)
01-070-1998 (TrEMBLrel. 25, Last annotation update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Aquaporin 1 (Fragment).
0ryctolagus cuniculus (Rabbit).
Bukaryota, Metazoa; (Dordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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Plasmid p42b.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobium/Agrobacterium group; Rhizobium.
NCBI_TaxID=29449;
                                                 Query Match

95.0%; Score 19; DB 13; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 94;
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                      91 91
91 AA; 10100 MW; E86C8B256DC69D39 CRC64;
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94 AA; 10222 MW; CO9D6EA3DFF1E2BA CRC64;
                                                                                                                                                                                                01-0CT-2002 (TrEWBLrel. 22, Created)
01-0CT-2002 (TrEWBLrel. 22, Last sequence update)
01-0TN-2003 (TrEWBLrel. 24, Last annotation update)
Putative transcriptional regulator (Fragment).
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Local Similarity 100.0%; Pred. No. 1.4e+03;
les 4; Conservative 0; Mismatches 0;
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PROSITE; PS00262; INSULIN; 1.

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SEQUENCE
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Matches
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046425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The genome of the natural genetic engineer Agrobacterium tumefaciens {\sf C58."}_i,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Agrobacterium tumefaciens (strain C58 / ATCC 33970).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
VCBI_TaxID=176299;
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                                                                                                                                                                                                                                                                                                    Length 94;
                                                                                                                                                                                                                                                                                                    95.0%; Score 19; DB 6; Length 94; ilarity 100.0%; Pred. No. 1.4e+03; Conservative 0; Mismatches 0; Indels
EMBL, AE009334; AAL44840.1; -.
PIR; AB3053; AB3053.
PYR; AB3051 AB3053.
SEQUENCE 96 AA; 11193 MW; FBD635894B46ABAE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein Atu4039.
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Last annotation update)
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Best Local Similarity
Matches 4; Conserval
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Matches 4; Conserv
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Hepatitis A virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
Hepatovirus.
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STRAIN=EGD-e / Serovar 1/2a;
MEDLINE=21537279; PubMed=11679669;
                                                                                                                                                                      J. Hepatol. 13:8146-5151(1991).
EMBL; S44109; AAB22740.2; -.
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InterPro, IPR007138; ABM.
Pfam, PF03992; ABM; 1.
Hypothetical protein; Compl.
SEQUENCE 97 AA; 10979 MM
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                                            NCBI_TaxID=12092;
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Matches
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                                                                                                                MEDLINE-22484999; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
                                                                                                                                                                                         "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";

Bradyrhizobium japonicum USDA110.";

BMD., 8-9:189-197(2002).

EMBL, AP005936; BAC4516.1;

GO, GO:0016020; C:membrane; IEA.

InterPro; IPR003425; Unk_YGGT.

Complete proteome.

SEQUENCE 96 AA; 10976 WW; A9E11F9AA4BC7734 CRC64;
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STRAIN=VC1 / DSM 3638 / ATCC 43587 / JCM 8422;
Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
Wiss Complete sequence of the Pyrococcus furiosus genome.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
BMBL, ABOI0262; AAL81744.1;
Hypothetical protecin; Complete protecome.
SEQUENCE 96 AA; 10804 MW; D6DAE09D096D577A CRC64;
         Bradyrhizobium japonicum.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
VOLE_TaxID=375;
                                                                                                                                                                                                                                                                                                                                               95.0%; Score 19; DB 16; Length 96; 100.0%; Pred. No. 1.46+03; ative 0; Mismatches 0; Indels
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01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein FF1620.
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Last sequence update)
Last annotation update)
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Best Local Similarity 100.000
1 4; Conservative
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Best Local Similarity 100.
Matches 4; Conservative
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                                                                           [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pyrococcus.
NCBI_TaxID=2261;
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SULT 48 6535

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Glaser P., Eargeul L., Buchieser E., de Darwar A., Dehoux P.,
Charbit A., Cherouani F., Couve E., de Darwar A., Dehoux P.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget C.,
Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
Adutier L., Geobel W., Ganez-Lopez N., Hauf T., Hauf D., Jückson D.,
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
Nordeisek G., Novella S., de Pablos B., Perez-Dlaz J.-C., Purcell R.,
Remmel B., Rose M., Schlueter T., Simces N., Tierrez A.,
Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.,
Comparative genomics of Listeria species.",
ESTEL, AL591983; CADO657.1, -.
SEQUENCE FROM N.A.
STRAIN=L6H/S;
MEDLINE=203488833; PubMed=1668326;
Fineschi N., Cavalieri F., Garelick H., Prugnola A., Pellegrini V.,
Zuckerman A.J.;
"Characterization of a hepatitis A virus strain suitable for vaccine
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Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                               Length 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Listeria monocytogenes.
Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
NCBI_TaxID=1639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                   al protein, Complete proteome.
97 AA; 10979 MW; 9E758586E94218E0 CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein lmo2579.
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Local Similarity 100.0%; Pred. No. 1.5e+03;
les 4; Conservative 0; Mismatches 0;
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Q9HZ38

ESULT 50 9HZ38

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Gaps

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Indels

ESULT 51

Matches

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SEQUENCE FROM N.A.
STRAIN=ATCC 55739;
Nam S.J., Kim J.H.;
Nam S.J., Kim J.K.;
Park J.Y., Ha Y.L., Kim J.H.;
Nam S.J., Kina J.K.;
Park J.Y., Ha Y.L., Kim J.H.;
Nam J.H.;
Submitted (JUL-2011) to the EMBL/GenBank/DDBJ databases.
EMBL, AF401482; AAA60142.1;
EMBL, AF401482; AAA60142.1;
EMBL, AF401481; P:translation elongation factor activity; IEA.
GO; GO:0006414; P:translational elongation; IEA.
InterPro; IPR01816; EF TS.
Pfam, PF00889; EF TS; 1.
SEQUENCE 101 AA; 11650 MW, BBCF30D941DB2B9B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M., Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A., Arciero D.M., Hommes N.G., Whittaker M.M., Arp D.J.; Complete genome sequence of the ammonia-oxidizing bacterium and obligate chemolithoautorroph Nitrosomonas europaea."; J. Bacteriol. 185:2759-2773 (2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales; Nitrosomonadaceae; Nitrosomonas. NCBI_TaxID=915;
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Lactobacillus.
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100 AA; 10836 MW; 82DC1153BABFAE27 CRC64;
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Last annotation update)
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Last annotation update)
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100.0%; Pred. No. 1.5e+03;
ive 0; Mismatches 0;
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         Pred. No. 1.5e+03;
                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=ATCC 19718 / IFO 14298;
MEDLINE=22586410; PubMed=12700255;
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100.0%;
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Q8VS54;
Q1-MAR-2002 (TEMBLEEL: 20,
Q1-MAR-2002 (TEMBLEEL: 20,
Q1-JUN-2003 (TEMBLEEL: 24,
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24,
25,
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Pfam; PF03795; YCII; 1.
Hypothetical protein; Compl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 4; Conservative
                                    4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nitrosomonas europaea.
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   Best Local Similarity Matches 4; Conserv.
                                                                                                                                                       62 VABF 65
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Q82UR2;
01-JUN-2003 (
01-JUN-2003 (
01-OCT-2003 (
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                                                                                                                                                                                                                                                       RESULT 52
Q82UR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 53
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                                                                                                                                                       셤
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SITRAIN=DC3000;
Buell R., Joardar V., Khouri H., Fedorova N., Tran B., Russell D.,
Buell R., Joardar V., Van Aken S., Feldblyum T., Gwinn M.,
Dodson R., DeBoy R., Durkin A., Kolonay J., Madupu R., Daugherty S.,
Brinhac L., Beanan M., Haft D., Selengut J., Nelson W., Davidsen T.,
White O., Fraser C., Collmer A.;
"Complete sequence of Pseudomonas syringae.";
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, ARO18862; ARO55228.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-ATC 15692 / PA01;
STRAIN-ATC 15692 / PA01;
Strover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowallik D.J., Lagrou M.,
Bickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowallik D.J., Lagrou M.,
Brody L.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
Brody L.L., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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01-0TN-2003 (TrEMBLrel. 24, Last sequence update)
01-0TN-2003 (TrEMBLrel. 25, Last annotation update)
01-0TS-2003 (TrEMBLrel. 25, Last annotation update)
PSPT01808
PSPT01808
PSEUdomonas syringae (pv. tomato).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                     Pseudomonas aeruginosa.
Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales,
Pseudomonnadaceae, Pseudomonas.
NCBI_TaxID=287,
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                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UNV-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein PA3202.
                                                                        99 AA
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Indels

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SEQUENCE FROM N.A.
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NON_TER
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Q722N2;
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Q9F368;
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209736
AC 09736
AC 09736
DT 01-MAD DT 01-MAD DT 01-MAD DT 01-MAD DE NYPOUL BY ON SCOOL SECTE ON STRAILS RA BEDLII RA
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MEDLINE-21332959; PubMed=11427726;
MEDLINE-21332959; PubMed=11427726;
MEDLINE-21332959; PubMed=11427726;
Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,
Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
Charlebois R.L., Doolittle W.F., Duguet M., Gasterland T.,
Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
"The complete genome of the crenarchaeon Sulfolobus solfataricus P2.",
                                                                              Gaps
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MEDLINE-22608414 PubMed=12721629;

Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T.,

Nelson K.B., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,

Holtzapple E.K., Okstad O.A., Helgason E., Rilstone J., Wu M.,

Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.,

DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,

Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
Sulfolobus.
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95.0%; Score 19; DB 17; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels
                     Length 101;
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=198094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003799; DUF196.
Pfam; PF02647; DUF196; 1.
TICRFAMS; TIGR01573; cas2; 1.
Wypotherical protein; Complete proteome.
SEQUENCE 101 AA; 11936 MW; A7C338AD76202E17 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein SSO1404.
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01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein.
                  Score 19; DB 2; L/
Pred. No. 1.5e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001)
EMBL; AE006755; AAK41639.1; -.
PIR; H90297; H90297.
95.0%; Scc...
100.0%; Pred. No. 1....
'... 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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            Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                               62 VAEF 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=2287;
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7YC2
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1R27
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Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
Berry K.J., Plaut R.D., Wolf A., Watkins K.L., Nierman W.C.,
Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S.L.,
Thomason B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,
Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2003 (TrEMBirel. 25, Created)
01-OCT-2003 (TrEMBirel. 25, Last sequence update)
01-OCT-2003 (TrEMBirel. 25, Last annotation update)
EXISOC2.6 (Putative novel protein similar to APOBECI (Apolipoprotein mRNA editing protein) and Phorbolin) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gabs
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                                                                                                                                                   "The genome sequence of Bacillus anthracis Ames and comparison to closely related bacteria.";
Nature 423.81-86(2003)
BMBL; AE017031; AAP26109.1; -.
TIGR; BA2232; --
Hypothetical protein; Complete proteome.
SEQUENCE 102 AA; 11925 MW; 13B8E296C8A341B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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SEQUENCE FROM N.A.
STRAINN=21996410; PubMed=12000953;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 13, Last annotation update)
Hypothetical protein SCO4420.
SCO4420 OR SC6F11.18
Streptomyces coelicolor.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
                                                                                                                                                                                                                                                                                                                                                                                       Length 102;
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Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases
EMBL; AL022318; CAB45276.1; -.
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Pred. No. 1.5e+03;
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Les 4; Conservative
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01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24,
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Matches 4; Conservative
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Matches 4; Conservative
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       SEQUENCE FROM N.A.
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Q8SVK0;
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Q8SVK0
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1D 0856T
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Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Farser A., Goble A., Hidalgo J., Horneby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22484998, PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashina K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
Tabata S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete genomic sequence of nitrogen-fixing symbiotic bacterium bradyrhicobium japonicum USDA110.";
DNA Res. 9:189-197(2020).
EMBL; AP005950; BAC49378.1; -.
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Wicobacteriophage Barnyard.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
[1]
                                                                                                                                                                                                            "Complete genome sequence of the model actinomycete Streptomyces
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
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                                                                                                                                                                                                                            coelicolor 33.2).";
Nature 41:141-147(2002).
BMB:, AL939120; CAC08429.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 103 Aa; 11387 MW; 55C2B80589EB75B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome.
SEQUENCE 103 AA; 11104 MW; BF27CB9F90FBB723 CRC64;
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Last annotation update)
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100.0%; Pred. No. 1.5e+03;
ative 0; Mismatches 0;
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01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last seqn
01-JUN-2003 (TrEMBLrel. 24, Last ann
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Best Local Similarity 100.
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Best Local Similarity 100.
Matches 4; Conservative
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Mycobacteriophage Corndog.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
NCBI_TaxID=205875;
MEDLINE=222660; PubMed=12705866; MEDLINE=222660; PubMed=12705866; MEDLINE=222660; PubMed=12705866; MEDLINE=222660; PubMed=12705866; MEDLINE=222660; MEDLINE=222660; MEDLINE; M
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NCBI_TaxID=6035;
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100.0%; Pred. No. 1.6e+03;
iive 0; Mismatches 0; Indels
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
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EMBL, ALS90445; CAD26596.1; -.
Hypothetical protein.
SEQUENCE 105 AA; 11897 MW; 08059108C05D3BB9 CRC64;
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01-UNY-2002 (TrEMBLrel. 21, Last sequence update)
01-UNY-2002 (TrEMBLrel. 21, Last annotation update)
Hypotherical protein ECU05_0770.
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Last sequence update)
Last annotation update)
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100.0%; Pred. No. 1.6e+03;
iive 0; Mismatches 0;
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Kessler P.S., McLarnan J., Leigh J.A.;
"Nitrogenase phylogeny and the molybdenum dependence of nitrogen fixation in Methanococcus marripaludis.";
J. Bacteriol. 179:541-543 (1997).
EMBL; U75887; AAC45519.1;
PIR; T10097; T10097.
InterPro. IPR00971 DUPIS3.
Pfam; PF02579; Nitro FeMo-Co; 1.
SEQUENCE 106 AA; I1862 MW; 4734D89CFED33F3B CRC64;
                                                                                                                                                                                                                                                                                                                                               Blank C.E., Kessler P.S., Leigh J.A., Genetics in methanogens: transposon insertion mutagenesis Methanococcus maripaludis niff gene.", Bacteriol. 177:5773-5777 (1995).
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               Archaea; Euryarchaeota; Methanococci; Methanococcales;
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MEDLINE=97144542; PubMed=8990309;
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                                                             Methanococcaceae, Methanococcus, NCBI_TaxID=39152;
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                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN=LL;
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Matches
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRANB-2CM 10545 / 7;
MEDLINE-21456156; PubMed=11572479;
MEDLINE-21456156; PubMed=11572479;
MEDLINE-21456156; PubMed=11572479;
MEDLINE-21456156; PubMed=11572479;
MEDLINE-21465156; PubMed=11572479;
Medline N., Baba S.-I., Ankai A., Fukui S.,
Nagai Y., Nishijima K., Otsuka H., Hosoyama A., Fukui S.,
Nagai Y., Nishijima K., Otsuka H., Makazawa H., Takamaya M., Kato Y.,
Noshizawa T., Kauchi H.;
Noshizawa T., Kakuchi H.;
Complete genome sequence of an aerobic thermoacidophilic
Crenarchaeon, Sulfolobus tokodaii strain?.";
Complete genome sequence of an aerobic thermoacidophilic
Crenarchaeon, Sulfolobus tokodaii strain?.";
DNA Res. 8:123-146(2001).
EMBL; AP000988; BAB67095.1; -
InterPro; IPR006743; Transposase 29.
Fram; PP04693; Transposase 29.
Fram; PP046993; Transposase 29.
Fram; PP04693; Transposase 29.
Fram; PP046993; Transposase 29.
Fram; PP04699; Transposase 29.
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ENDURINCE FROM N.A.

MEDLINE=225966, PubMed=12705866,
Pedulla M.L., Ford M.E., Houtz J.M., Karthikeyan T., Wadeworth C.,
Pedulla M.L., Ford M.E., Houtz J.M., Karthikeyan T., Wadeworth C.,
Lewis J.A., Jacobs-Sera D., Falbo J., Gross J., Pannunzio N.R.,
Brucker W., Kumar V., Kandaeamy J., Keenan L., Bardarov S.,
Kriakov J., Lawrence J.G., Jacobs W.R. Jr., Hendrix R.W.,
Hatfull G.F.,
Hatfull G.F.,
Crigins of highly mosaic mycobacteriophage genomes.",
Cell 113:171-182(2003).
EMBL; AX129335; AAN01935.1, -.
SEQUENCE 105 AA; 11955 MW; 7DDEC09F5F2AF2DD CRC64;
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096231;
01-DEC-2001 (TEMBLrel. 19, Created)
01-DEC-2001 (TEMBLrel. 19, Last sequence update)
01-UJW-2003 (TEMBLrel. 24, Last annotation update)
Hypothetical protein ST2000.
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Last sequence update)
Last annotation update)
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100.0%; Pred. No. 1.6e+03;
tive 0; Mismatches 0;
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Methanococcus maripaludis.
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Sest Local Similarity 100.
Matches 4; Conservative
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01-JUN'2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Matrilysin (Fragment).

Ovis aries (Sheep).

Ovis aries (Sheep).

Mammalla, Butheria, Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
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SEQUENCE FROM N.A.

TISSUB-Endometrium;
Submitted (MAY.2000) to the EMBL/GenBank/DDBJ databases.
Submitted (MAY.2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF267158; AAG59846.1; -.
RESP: POS237; 1MMQ.
MEROPS; MIO.0085.-.
GO; GO:0004222; F:metallomopeptidase activity; IEA.
GO; GO:0004222; F:metallomopeptidase activity; IEA.
GO; GO:0004222; F:metallomopeptidase activity; IEA.
GO; GO:0006508; -: P:metallomopeptidase activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR006026; Peptidase M.
InterPro; IPR00138; Pepti MIOA MI2B.
REAM; PR00138; MATRIXIN.
SMART; SM00235; ZnMc; 1.
NON TER 106 106
SEQÜENCE 106 AA; 11578 MW; EBDB271054928018 CRC64;
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Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels
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P71530 SULT 63 1530

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"Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AP062776; BAB98308.1; -.
InterPro; IPROJ138; ABM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gardier M.J., Hall M., Fung E., White O., Berriman M., Hyman R.W., Garlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K., Elsen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S., Chan M.-S., Nene V., Shallom S.L., Suh B., Peterson J., Angiuoli S., Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B., Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A., McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C., Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W., Praser C.M., Barrell B.;
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmodium falciparum (isolate 3D7).
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=36329;
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95.0%; Score 19; DB 3; Length 107;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMEL; AE014842; AAN36006.1; -.
Hypothetical protein.
SEQUENCE 107 AA; 12714 MW; CA351258FCF46EF5 CRC64;
                                                                                                                                                                                                                                                                                                                                                   Q81HV3 PRELIMINARY; PRT; 107 AA.
Q81HV3;
Q1-MAR-2003 (TFEMBLrel. 23, Last sequence update)
01-MAR-2003 (TFEMBLrel. 23, Last sequence update)
01-MAR-2003 (TFEMBLrel. 23, Last annotation update)
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                               .6e+03;
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STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
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                               100.0%; Pred. No. 1.6 ive 0; Mismatches
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MEDLINE=22255705; PubMed=12368864;
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Query Match
Best Local Similarity 100.0°
Bernag 4; Conservative
                                                               4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 419:498-511(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
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                               Best Local Similarity
Matches 4; Conserv
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                                                                                                                                 2 VAEF 5
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Query Match
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QBNRX6
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MEDLINE=21135672; PubMed=11238395;

Bean L.E., Dvorachek W.H. Jr., Braun E.L., Errett A., Saenz G.S.,

Giles M.D., Werner-Rashburne M., Nelson M.A., Natvig D.O.;

"Analysis of the pdx-1 (snz-1/sno-1) region of the Neurospora crassa
"Analysis of the pdx-1 (snz-1/sno-1) region of the Neurospora crassa
genome. Correlation of pyridoxine-requiring phenotypes with mutations
in two structural genes.";
Genetics 157:1067-1075(2001).

EMBL; AF319689; ARXO7845.1; -.

HSSP; P80028; 1TOF.
                                                                                                                                                                                                                         01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JAN-1998 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Cathepsin B-like cysteine proteinase (Fragment).
T7123.13.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TAXID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
STRAIN=cv. Columbia;
Federspiel N.A., Conway A.E., Conway A.R., Davis K., Brendel V.,
Palm C.J., Au M., Araujo R., Chung E., Kurtz D.B., Bushler E.,
Dewar K., Feng J., Kim C., Li Y., Shinn P., Sun H., Oji O.,
Osborne B., Shen Y.K., Toriumi M., Vyotskaia V., Yu G., Theologis
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h Similarity 100.0%; Score 19; DB 10; Length 106; Similarity 100.0%; Pred. No. 1.6e+03; 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ECKET J., Davis R.W.;
"Genomic sequence of Arabidopsis BAC T7123.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL: 199595; AAC24377.1; -
NON_TER 106 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Putative thioredoxin G6G8.7.
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107 AA; 11676 MW;
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                                                                                                                                                                 PRELIMINARY;
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Best Local Similarity
Matches 4; Conserv
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SEQUENCE 10
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01-JUN-2001
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ESULT 66

Gaps ö us-09-594-978a-3.rspt

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Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.
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Matches 4; Conservative
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Best Local Similarity
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SEQUENCE 109 AA;
                                                                                                                SEQUENCE FROM N.A
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Q7TX28;
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Q7TX28
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STRAIN=H37Rv;
MEDLINE=9829597; PubMed=9634230;
MEDLINE=9829597; PubMed=9634230;
Gole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
Gordon S.V., Biglmeler K., Gas S., Barry C.B. III, Tekaia F.,
Badcock K., Basham D., Chillingworth T., Connor R.,
Badcock K., Basham D., Strown D., Chillingworth T., Connor R.,
Bavies R., Devlin K., Peltwell T., Gentles S., Hamlin N., Holroyd S.,
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
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                                                                  Gaps
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2003 (TrEMBLrel. 24, Last annotation update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Retinol binding protein (Fragment).
Crocodylus miloticus (Nile crocodile) (African crocodile).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Crocodylidae; Crocodylinae; Crocodylius.
                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20022983; PubMed=10555283;
Hughes S., Zelus D., Mouchiroud D.;
"Warm-blooded isochore structure in nile crocodile and turtle.";
"Mol. Biol. Evol. 16:1521-1527(1999).
EMBL; AJ011392; CAB56418.1; -.
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Corymebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
                               Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 95.0%; Score 19; DB 13; Length 109; Best Local Similarity 100.0%; Pred. No. 1.6e+03; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                 0; Indels
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12373 MW; B5ACF23621078018 CRC64;
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-1998 (TrEMBLrel. 05, Last annotation update)
Hypothetical protein Rv3183.
Rv3183 OR MTV014.27 OR MT3275.
Mycobacterium tuberculosis.
                             95.0%; Score 19; DB 16; Lilarity 100.0%; Pred. No. 1.6e+03; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0005515; F:transporter activity; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR002345; Lipocalin.
InterPro; IPR00566; Lipocalin.
Pfam; PF00061; Lipocalin; 1.
PRINTS; PR00179; LIPOCALIN.
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 107 AA;
                               Query Match
Best Local Similarity
Matches 4; Conserv
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                                                                                                                                22 VAEF 25
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STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback F., Weidman J., Khouri H., Gill J., Mikula A.,
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STRAIN=AFRIZZ/97;
STRAIN=AFRIZZ/97;
PATAINE=22709107; PubMed=12788972;
Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
Payor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,
Payor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,
Parkil B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
"The complete genome sequence of Mycobacterium bovis.";
Parkl. Acad. Sci. U.S.A. 100:7877-7882(2003).
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                                                                                                                                                                                                                                                                                                                                                                                                                                       "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains.";
Submitted (APR.2001) to the EMBL/GenBank/DDBJ databases.
BMBL, AL021646; CAA16648.1; -.
BMBL, RE00140; AAK47615.1; -.
PIR; E70942; E70949.
Ruter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1765;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGR; MT3275; -.
Tubercullst; Rv3183; -.
GO, GO, 200577; F:DNA binding; IEA.
GO, GO, 200577; F:DNA binding; IEA.
FEM: PF01381; HTH 3; 1.
SMART; SM0530; HTH 3; 1.
SMART; SM0530; HTH 3x 1.
SMART; SM0530; HTH 3x 1.
SEQUENCE 109 AP; 11802 MW; A66DBE160D79613A CRC64;
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Possible transcriptional regulatory protein.
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100.0%; Pred. No. 1.6e+03;
ative 0; Mismatches 0;
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100.0%; Pred. No. 1.6e+03;
tive 0; Mismatches 0;
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Pyrococcus furiosus.
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                                                          73 VAEF 76
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2 VAEF 5
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Q8U296;
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Q8U296
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Lopez-Estebaranz J.L., Esteban M., Martin-Gallardo A.;
Lopez-Estebaranz J.L., Esteban M., Martin-Gallardo A.;
Lopez-Estebaranz J.L., Esteban M., Martin-Gallardo A.;
of a Random DNA Sequencing, Computer-Based Approach for the Generation
of a Gene Map of Mollusum Contagiosum Virus.";
Virus Genes 0:0-0(1997).
EMBL; U86919; AABS7977.1; -.
NON_TER 110 110
NON_TER 110 110
SEQÜENCE 110 AA; 11856 MW; 6AE9CE25FC3DB780 CRC64;
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MEDLINE=22423060; PubMed=12534463;
Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
Nartins Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,
Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,
Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzez A.,
Utterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H.,
Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
Kiewitz C., Eisen J., Timmis K.N., Duesterhoeft A., Tuemmler B.,
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                                                                                  011343;
01-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUL-1997 (TrEMBLrel. 19, Last sequence update)
X1-5 protein (Fragment).
X1-5 protein (Fragment).
X1-5 protein (Fragment).
Molluscum contagiosum virus subtype 1 (MCVI).
Northese; dspNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
Molluscipoxvirus.
NCBL TaxID=10280;
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Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=160488;
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95.0%; Score 19; DB 16; Length 110;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels
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Q88EG3;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
YCII-related domain protein.
                                                                    110 AA
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                                                                    PRT;
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Pfam; PF03795; YCII; 1.
Complete proteome.
SEQUENCE 110 AA; 11775 M
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                                                                    PRELIMINARY;
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NCBL_TAXID=2261;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sluder A.; "Explosive lineage-specific expansion of the orphan nuclear receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa, Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                     Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
Whist complete sequence of the Pyrococcus furiosus genome.";
Submitted (FEB-202) to the EMBL/GenBank/DDBJ databases.
EMBL, AR010208; AAL61067.1;
InterPro; IPR007842; HEPN.
Pfam; PF05168; DUF712; 1.
PROSITE; PS50910; HEPN.
Hypothetical protein; Complete proteome.
SEQUENCE 111 AA; 13379 MW; CGA005A6B2B6CA4E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95.0%; Score 19; DB 17; Length 111; 100.0%; Pred. No. 1.7e+03; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HNP4 in nematodee.";
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, #2204162; #2030166.1;
GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR008946; Str_ncl_receptor.
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SEQUENCE 112 AA; 12826 MW; 44FC60A4E3744791 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Nuclear receptor NHR-1 (Fragment).
Caenorhabditis elegans.
                                          01-JUN-2002 (TIEMBLrel. 21, Created)
01-JUN-2002 (TIEMBLrel. 21, Last sequence update)
01-OCT-2003 (TIEMBLrel. 25, Last annotation update)
Hypothetical protein PF0943.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
PRELIMINARY;
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